Can Genomics Be Used To Improve Feed Efficiency?

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Take Home Messages

- Feed efficiency is a trait that will benefit from genomic selection.
- Efforts are underway to assemble large datasets necessary for utilizing genomics to predict genetic merit for feed efficiency.
- Care must be taken to optimally apply selection for improved feed efficiency.

Introduction

Feed efficiency is a trait that has received much attention recently because of its importance to the economic success and environmental stewardship of the dairy industry. However, very little selection pressure for improved feed efficiency is practiced worldwide. The primary reason for this is a lack of systematic data collection for feed intake traits. Traditionally, the estimation of genetic merit for use in genetic improvement programs has relied on the availability of phenotypic records from the animals being evaluated or their relatives (progeny). Because of the time and labor required to acquire feed intake data, genetic evaluation for feed efficiency has not been possible. However, genomics offer the opportunity to predict the genetic merit of animals based on their DNA sequence, often in the absence of phenotypic data on the animal and its close relatives. In this way, genomics data can facilitate the inclusion of feed efficiency in genetic evaluation programs and selection indexes. Current data indicate that genetic variation for feed efficiency exists among dairy cows, and that this variation is regulated in part by genetics. Therefore, selection for improved feed efficiency should be successful at increasing the quantity of milk (or milk solids) per feed consumed. However, large data sets of genotypic and phenotypic data are needed to initially establish the relationships between genotypes and genetic merit, and careful consideration must be given to determining the most appropriate strategies for improving feed efficiency.

▪ How Is Genomic Information Used?

Genomic data are used for two primary purposes: to understand the genetic architecture and physiological processes that influence traits of interest, and to predict the genetic value, often presented as predicted transmitting ability (PTA), of animals for traits of interest. This paper will focus on the latter application.

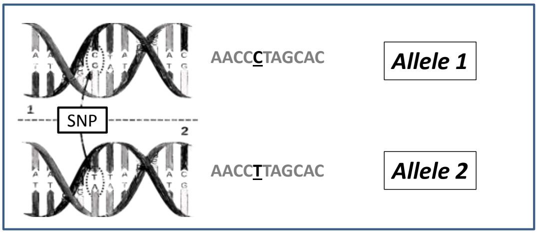

Figure 1: DNA sequences representing the same region of the genome are shown for 2 individuals. The difference in DNA sequence represents a single nucleotide polymorphism (SNP). Alternate sequences for the same region of DNA are known as alleles. http://en.wikipedia.org/wiki/Single-nucleotide_polymorphism

Genomic data include the genotypes of animals at thousands of single nucleotide polymorphisms (SNP) distributed throughout the DNA of each individual. These SNP represent locations in the genome where animals differ in their DNA sequence by a single nucleotide (Figure 1). Differences in the DNA sequence are referred to as polymorphisms, and alternate sequences for a given region of DNA are known as alleles. The genomes of all mammals have two copies of each DNA region (except for DNA of the Y chromosome). Individuals are considered homozygous if they have two copies of the same allele, or heterozygous if they have one copy of each of two alleles. When working with SNP, genotypes are often coded as 0, 1 or 2 where the genotype represents the number of copies of a specific allele.

Several approaches exist for using SNP genotypes to predict the genetic value of dairy cattle. One approach is based on the premise that each allele of each SNP contributes a certain value to the overall PTA. Once the value of each allele is determined, the PTA of additional animals can be determined by summing the value of each of their alleles, which are known from SNP genotypes. When using this approach, the most important and challenging step is determining the value of each SNP allele. This is accomplished using a Training Data Set that includes both genotypes and phenotypes for the trait of interest (Figure 2).

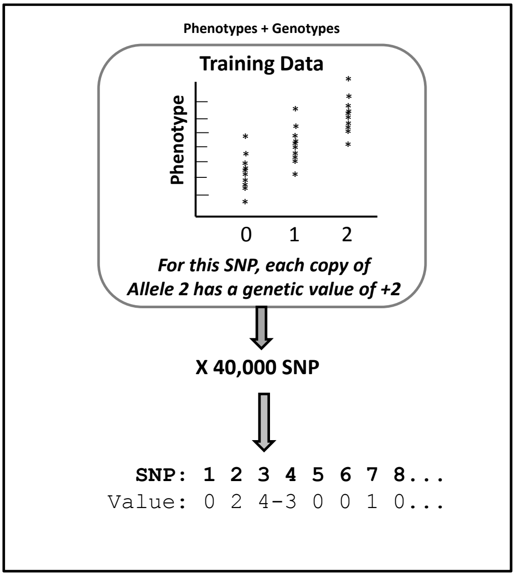

Figure 2: A Training Data Set is used to estimate the value of each allele of each SNP.

For each SNP, animals with different genotypes are compared to determine if differences in phenotype are associated with genotype for that particular SNP. The value of the SNP may be calculated as the difference in phenotype that is observed when one allele is replaced by another. This analysis is then repeated for each SNP that has been genotyped, often approximately 40,000 SNP. As a result of this analysis of the Training Data, a SNP ‘key’ is produced. This key shows the genetic value of one allele for every SNP genotyped, and can be used to predict genetic value of any genotyped animal. One of the most critical aspects for genomic prediction is having enough animals of the appropriate genetic background in the Training Data Set so that accurate estimates of SNP effects can be calculated.

Once the SNP Key is calculated, it is used to predict the PTA for any genotyped animal (Figure 3). This is done by multiplying the value of one allele at a SNP by the number of copies of that allele found in an animal, and then summing the values over all SNP to generate a genomic PTA (gPTA). Typically, the accuracy of the SNP Key is estimated using a subset of data from animals that have both phenotype and genotype data available. The accuracy of the SNP Key is determined from the relationship between the predicted gPTA and the observed phenotype. This validation process is often used to optimize methods used to generate the SNP Key, and contribute to calculation of reliability values for gPTA. Ultimately, the goal of genomic prediction is to predict gPTA for animals with no phenotypic data available, such as young bulls or heifers.

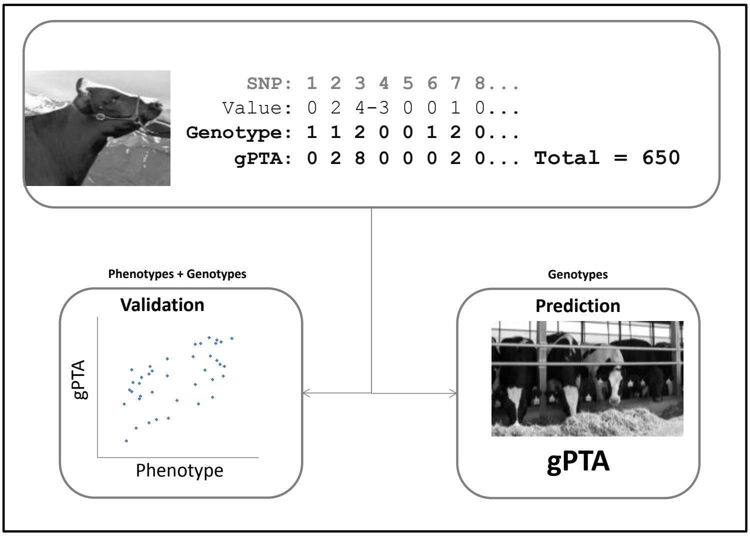

Figure 3: The SNP Key may be used to evaluate the accuracy of predictions, and to estimate genomic PTA.

Genomic prediction is well suited to the dairy industry in part because the dairy industry has mechanisms in place to capture large amounts of phenotypic data from lactating cows. These data are used to estimate the genetic value of sires using traditional genetic evaluation methods, and a SNP Key for prediction of PTA of young animals. As of November 2013, the USA national database included genotypes from over 109,000 bulls and 345,000 females (USDA-AIPL). All animals with a traditional genetic evaluation are included in the Training Data Set. Based on current estimates, the accuracy of gPTA for young sires with no daughter records is approximately equivalent to traditional PTA calculated from 30 to 40 daughters for most traits. Estimated genetic values are in turn used in the Training Data Set to generate a SNP Key with improved accuracy

■ Are the Necessary Data Available For Feed Efficiency?

The greatest challenge to implementing genomic prediction for novel traits such as feed efficiency is the collection of data for a suitable Training Data Set. Because measurement of individual daily feed intake requires substantial investment in facilities and labor, it is not likely to be measured on a routine basis in the field. Therefore, data for a Training Data Set must be collected from research herds. Several projects throughout the world are currently in progress and share the overall goal of being able to select dairy cattle for improved feed efficiency using genomic prediction.

In the USA, the National Program for Improvement of Feed Efficiency in Dairy Cattle represents an international consortium that is collecting data for feed intake, production traits, body weight and body condition score from US and international collaborators. The goal of this project is to assemble a Training Data Set including approximately 8,000 animals so that gPTA for feed efficiency can be predicted in the USA. In particular, this project is exploring the use of residual feed intake (RFI), or the difference between an animals observed feed intake and that predicted based on her production and maintenance requirements, as a measure of feed efficiency. This project is led by Dr. Mike VandeHaar, Michigan State University and is described in more detail in his paper in these proceedings.

An international consortium, Global DMI, led by Dr. Roel Veerkamp, Wageningen University, Netherlands, is collecting feed intake data. This project includes data from approximately 10,000 heifers and cows from around the world, and is focusing on the prediction of gPTA for dry matter intake. To date, this project has dealt with many challenges associated with combining data from varied sources and has begun to explore the impact of genetic differences among dairy cattle from different regions of the world (deHaas et al., 2012).

Researchers in Australia and New Zealand have been collaborating for many years on a project to study RFI. For this research, feed efficiency was measured as RFI in growing heifers and used to predict efficient versus inefficient animals. These heifers were followed into lactation where it was found that they differed in RFI as lactating cows, but the difference was much less than that observed earlier in the animals’ lives. The RFI data from growing heifers are also being used for prediction of gPTA for RFI (Pryce et al., 2012). Finally, a Scandinavian consortium is also working to collect feed intake with a goal of selecting for improved feed efficiency.

Perhaps the most important feature of these projects is that many participants and much of the data are shared across projects. Although each project has the goal of improving feed efficiency, each is approaching this goal in a slightly different manner. Communication among the projects has been effective for sharing early findings and results from each approach. The fact that some data are shared among projects also helps to interpret results coming from each study, as there are direct genetic ties among the different data sets. Ultimately, each of these projects will likely generate gPTA and supporting SNP Keys for their traits of interest. The next, and perhaps more important step, will be determining how to incorporate those gPTA into an overall selection program.

■ Can We Expect To Make Genetic Progress For Improved Feed Efficiency?

What Are Selection Criteria For Improving Feed Efficiency?

On the surface, feed efficiency seems to be a relatively simple concept – cows that produce more milk from less feed are efficient. However, feed efficiency is a trait for which selection is quite complex. The most intuitive definition of feed efficiency is the ratio of milk production (accounting for components) over dry matter intake. This ratio is useful for monitoring changes in herds over time, and for making comparisons across herds. However, ratios are often undesirable traits for selection due to certain statistical properties. In the case of feed efficiency, selection for efficiency defined as the ratio of milk production over intake is largely driven by selection for milk production. This relationship is the reason the dairy industry has made tremendous improvements in efficiency without selecting directly for the trait. However, it is believed that additional improvement in efficiency can be achieved by including more sophisticated definitions of feed efficiency in breeding goals.

One approach is to select for reduced dry matter intake, while maintaining selection pressure for production traits. If done appropriately, this strategy should result in the selection of cows that maintain desirable levels of production but consume less feed throughout lactation. One of the challenges for this strategy is that milk production and feed intake are highly correlated. It is not yet clear how successful selection will be at breaking apart this correlation and simultaneously improving milk production while decreasing intake.

An alternative strategy is to define feed efficiency such that it is independent of milk production. This is one feature of RFI, which represents the difference between observed feed intake and that predicted based on the cow's production and maintenance requirements. In this way, selection for reduced RFI favors cows that consume less feed to produce a similar quantity of milk, after accounting for differences in maintenance requirements. Although selection for RFI has the advantage of being independent of milk production, it also has limitations for inclusion in a selection index. Residual feed intake is itself an index, and it may be more appropriate to account for the component traits of RFI (milk production, DMI, and body size) individually in a selection index, rather than including an index within an index. Additionally, RFI accounts for differences in maintenance requirements thereby 'forgiving' larger cows the additional feed they consume to support their larger size. Although this may not be appropriate, it can also be argued that selection for smaller body size could be included as an additional term in a selection index.

Finally, it must be recognized that improved RFI is associated with cows that eat less than expected, and will therefore have negative RFI values.

Ultimately these different strategies, if appropriately implemented, will likely yield similar results. However, PTA for ‘feed efficiency’ may be presented quite differently depending on the way feed efficiency is defined. Currently, selection for improved feed efficiency is moving forward in many countries, although different approaches are being taken to accomplish this goal (Berry and Crowley, 2013; Pryce et al., 2013).

Genetic Progress – The Key Equation

The rate of genetic improvement per year depends upon four key factors: the accuracy of selection, the intensity of selection, the genetic standard deviation for a trait, and the generation interval.

$$\text{Genetic Change per Year} = \frac{\text{Accuracy x Intensity x Genetic Standard Deviation}}{\text{Generation Interval}}$$

Accuracy of selection depends on how accurately the selection criteria (PTA, phenotype, etc.) rank animals according to their genetic merit for a trait, while the intensity of selection describes how ‘choosy’ one is when bringing new animals into the population. The genetic standard deviation is a function of the genetics of the population, and describes how much variation exists among animals. Finally, the generation interval defines how long it takes to replace one generation with the next. Typically, genomic information contributes to increased genetic change by improving the accuracy of selection and decreasing the generation interval. Genomics may also increase the intensity of selection by providing information on additional animals, thereby creating a larger population from which to select. Genomic information will contribute to improved feed efficiency via each of these mechanisms.

The greatest contribution of genomic data will be in facilitating the estimation of gPTA for feed efficiency that would otherwise be unattainable. Although considerable effort is being put forth to collect feed intake data in research herds throughout the world, these efforts are insufficient for a national evaluation of feed efficiency in the absence of genomic data. By using genomics to establish a SNP Key and predict genetic merit, the value of the research data is extended throughout dairy cattle populations. Ultimately, genomics will enable PTA to be predicted with reasonable accuracy for all animals with genomic data. In the absence of genomic data, these PTA would not be estimable.

Despite the promise of genomics to deliver PTA for feed efficiency, one challenge will be maintaining the accuracy of the SNP Key generated from the

Training Data Set. This occurs for most traits as additional data become available on lactating cows and the Training Data Set is continuously updated with new information. However, new feed intake data may not be available to continuously flow into the system and keep estimates of the SNP Key current for feed efficiency traits. The research projects currently underway are primarily funded to generate the initial Training Data Set and SNP Key. The dairy industry will likely need to determine the value of updating the SNP Key, and a mechanism to fund the ongoing collection of feed intake data in order to maintain the accuracy of gPTA for feed efficiency long term.

A final consideration is that the genetic improvement of feed efficiency will be defined by the nature of the genes regulating the trait. Genetic improvement for any trait is defined in part by the amount of genetic variation, or the genetic standard deviation, for the trait. It has been suggested that the genetic variation for feed efficiency defined as RFI is very low in dairy cattle (Kennedy et al., 1993). However, that conclusion was based on a limited amount of data that may have been affected by phenotypic correlations among traits (Veerkamp et al., 1995). Current data indicate that a meaningful amount of variation in RFI exists, and that RFI is a trait that should respond to selection (Tempelman et al., 2013). Additionally, selection for altered RFI has been successful in beef cattle, pigs, laying hens, and mice, further supporting RFI as a viable selection criteria for improving feed efficiency in dairy cattle (Spurlock and VandeHaar, 2014).

■ Summary and Conclusions

Feed efficiency is a trait that is time consuming and costly to evaluate on an individual animal basis. For this reason, genetic evaluation programs for improved feed efficiency will in large part depend on genomic evaluations. Currently, a limitation to conducting genetic evaluations for feed efficiency is a lack of data that are needed to estimate effects of alternate SNP alleles. Several projects are underway to address this need, and overlap among these projects demonstrates the collaborative efforts of scientists working in this area. Finally, careful consideration must be given to determining how to best implement selection for improved feed efficiency. Strategies that select for reduced feed intake or improved RFI are both likely to be successful, but present their own unique challenges. In summary, genetic improvement of feed efficiency is feasible with the aid of genomics. Selection for improved feed efficiency should be achievable, but care must be taken to appropriately incorporate this selection into existing breeding goals.

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