Phenotypes for novel functional traits of dairy cattle¹

J.B. Cole

Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD, USA, 20705-2350

Abstract

Modern dairying uses sophisticated data collection systems to maximize farm profitability. This includes information on cows and their environments. As on-farm automation increases many more phenotypes can be collected. There are two principal sources of data: farms and laboratories. On-farm data typically are recorded by farmers, but it is now common for information to be collected by other experts. For example, claw health data often are recorded by hoof trimmers. Automated milking systems provide detailed information about individual milkings, including time and conductivity for mastitis detection, and tools exist to assay progesterone in real-time. However, those systems often integrate poorly with the software used to interface with milk recording programs. Some farms have automated stations to record climate data, but much environmental information is not captured in on-farm systems, e.g., housing and flooring types and ration composition. Many phenotypes are based on the laboratory analysis of milk samples, and spectroscopic analysis is used to determine milk and fat concentrations in milk. Recent research suggests that many other phenotypes can be collected from those data, including milk fatty acid composition and methane production. The latter trait may provide a more economical measure of feed efficiency than individual intakes. There are also milk ELISAbased tests for diseases such as paratuberculosis and leucosis to provide early identification of carriers. Many young animals are genotyped, but only summary data are stored on the farm. Some phenotypes, most notably haplotypes associated with reduced fertility and increased perinatal mortality, can be generated directly from data collected in national databases. There are now more than a dozen of these recessives tracked in the US and other countries. The most substantial challenge faced by many dairy managers will be the effective use of the many new phenotypes that now are available.

Keywords: novel phenotypes, dairy cattle, health and fitness traits

Introduction

¹ Mention of trade names or commercial products in this article is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the US Department of Agriculture. The USDA is an equal opportunity provider and employer.

Modern genetic selection programs in dairy cattle are based on objectives that incorporate many economically important traits into a single value used to rank and select animals (Philipsson et al., 1994). Total merit indices used in the Nordic countries were the first to include fertility and health traits (Philipsson and Lindhé, 2003), and were important in demonstrating the value of selection objectives including lowly heritable traits. Selection objectives for genetic improvement programs in dairy cattle typically have focused on production traits (VanRaden, 2004), but over the last 20 years increasing emphasis has been placed on health and fitness traits in many different countries (Miglior et al., 2005). However, additional phenotypes are needed to describe the performance, health, and fitness of the modern high-performing dairy cow.

New sources of on-farm data

Data have typically been recorded by farmers, but it is now common for information to be collected by other experts, too. For example, claw health data often are recorded by hoof trimmers, and those data are being used to select for improved claw health (van der Linde et al., 2010; Chapinal et al., 2013). Automated milking systems time (e.g., Berger and Hovav, 2013) provide detailed information about individual milkings, and tools exist to measure progesterone in real-time. Those systems also can record cow body weights, which are associated with changes in health status and feed efficiency (Veerkamp, 1998). Automated systems are appealing because they help control labor costs, which are growing quickly in most countries. However, those systems often integrate poorly with the software used to interface with milk recording programs. Some farms have automated stations to record climate data, but much environmental information is not captured in on-farm systems, such as housing and flooring types. Calus et al. (2005) demonstrated that those data can be used to construct predictive models of cow performance.

New sources of laboratory data

Many new phenotypes are based on the laboratory analysis of milk samples, including spectroscopic. Many phenotypes can be collected from those data, including milk fatty acid composition (Soyeurt et al., 2011) and methane production (Dehareng et al., 2012). The latter trait may be a more economical measure of feed efficiency than individual intakes (Hegarty et al., 2007). There are also milk ELISA-based tests for the detection of diseases such as paratuberculosis and leukosis, and those data can be used in selection programs to improve disease resistance (Attalla et al., 2010). Some US laboratories are partnered with milk recording organizations so that test results can use the same data flow as more traditional data.

Novel traits and genomics

Many young animals are now genotyped, and low-density genomic tests on cows can be used to increase the economic value of calves produced (De Vries et al., 2011), particularly if used in genomic mating programs (Sun et al., 2013). Those genotyped cows will be needed to achieve reliabilities suitable for selection of novel functional traits (Buch et al., 2012), and data are already available in the US to select for improved health using producer-recorded data (Parker Gaddis et al., 2014). Haplotypes associated with reduced fertility and increased stillbirth (VanRaden et al., 2011) can be generated directly from data in national databases, and there are now 19 such recessives tracked in the US and other countries (Cole et al., 2013).

Non-farm uses of functional data

Consumers are willing to pay higher prices for products that they perceive to be healthier or associated with improved animal welfare (e.g., organic milk, cage-free eggs), and it is possible that health and fitness data could be incorporated into welfare certification programs, which that would require the consent of the farmers who provide the data. Milk fatty acid and protein composition can be changed by genetic selection (Bovenhuis et al., 2013), and milk processors may be willing to pay incentives for milk with desirable effects on human health.

Conclusions

Modern dairying is an increasingly complex and technological enterprise. In order to achieve both farm-level goals such as profitability, and societal goals such as environmental sustainability, additional measurements describing cattle performance are needed. Effective selection for novel functional traits is possible using traditional genetic evaluation methods, but is greatly enhanced by the use of genomic tools.

List of references

- Attalla, S.A., A.J. Seykora, J.B. Cole, and B.J. Heins. 2010. Genetic parameters of milk ELISA scores for Johne's disease. J. Dairy Sci. 93:1729–1735.
- Berger, R., and A. Hovav. 2013. Using a dairy management information system to facilitate precision agriculture: The case of the AfiMilk® system. Info. Sys. Mgmt. 30:21–34.
- Bovenhuis, H., M.H.P.W. Viskera, and A. Lundén. 2013. Selection for milk fat and milk protein composition. Adv. Anim. Biosci. 4: 612–617.
- Buch, L.H., M. Kargo, P. Berg, J. Lassen, and A. C. Sørensen. 2012. The value of cows in reference populations for genomic selection of new functional traits. Animal 6:880–886.
- Calus, M.P.L., J.J. Windig, and R.F. Veerkamp. 2005. Associations among descriptors of herd management and phenotypic and genetic levels of health and fertility. J. Dairy Sci. 88:2178– 2189.

- Chapinal, N., A. Koeck, A. Sewalem, D.F. Kelton, S. Mason, G. Cramer, and F. Miglior. 2013. Genetic parameters for hoof lesions and their relationship with feet and leg traits in Canadian Holstein cows. J. Dairy Sci. 96:2596–2604.
- Cole, J.B., P.M. VanRaden, D.J. Null, J.L. Hutchison, and T.A. Cooper. 2013. AIPL Research Report GENOMIC3: Haplotype tests for recessive disorders that affect fertility and other traits. Available: http://aipl.arsusda.gov/reference/recessive_haplotypes_ARR-G3.html. Accessed April 2, 2014.
- De Vries, A., J.B. Cole, and D.T. Galligan. 2011. Economics of reproduction and genetics: the quality of the pregnancy. Southeast Dairy Herd Management Conference. Nov. 2, 2011, Macon, GA. pp. 45-56.
- Dehareng, F., C. Delfosse, E. Froidmont, H. Soyeurt, C. Martin, N. Gengler, A. Vanlierde, and P. Dardenne. 2012. Potential use of milk mid-infrared spectra to predict individual methane emission of dairy cows. Animal 6:1694–1701.
- Hegarty, R.S., J.P. Goopy, R.M. Herd, and B. McCorkell. 2007. Cattle selected for lower residual feed intake have reduced daily methane production. J. Anim. Sci. 85:1479–1486.
- Miglior, F., B.L. Muir, and B.J. Van Doormaal. 2005. Selection indices in Holstein cattle of various countries. J. Dairy Sci. 88:1255–1263.
- Parker Gaddis, K.L., J.B. Cole, J.S. Clay, and C. Maltecca. 2014. Genomic selection for producer-recorded health event data in U.S. dairy cattle. J. Dairy Sci. Published online before print March 7, 2014. doi:10.3168/jds.2013–7543.
- Philipsson, J., G. Banos, and T. Arnason. 1994. Present and future uses of selection index methodology in dairy cattle. J. Dairy Sci. 77:3252-3261.
- Philipsson, J., and B. Lindhé. 2003. Experiences of including reproduction and health traits in Scandinavian dairy cattle breeding programmes. Livest. Prod. Sci. 83:99–112.
- Soyeurt, H., F. Dehareng, N. Gengler, S. McParland, E. Wall, D.P. Berry, M. Coffey, P. Dardenne. 2011. Mid-infrared prediction of bovine milk fatty acids across multiple breeds, production systems, and countries. J. Dairy Sci. 94:1657–1667.
- Sun, C., P.M. VanRaden, J.R. O'Connell, K.A. Weigel, and D. Gianola. 2013. Mating programs including genomic relationships and dominance effects. J. Dairy Sci. 96(12):8014–8023.
- van der Linde, C., G. de Jong, E.P.C. Koenen, and H. Eding. 2010. Claw health index for Dutch dairy cattle based on claw trimming and conformation data. J. Dairy Sci., 93:4883–4891.
- VanRaden, P.M. 2004. Invited review: Selection on net merit to improve lifetime profit. J. Dairy Sci. 87:3125–3131.
- VanRaden, P.M., K.M. Olson, D.J. Null, and J.L. Hutchison. 2011. Harmful recessive effects on fertility detected by absence of homozygous haplotypes. J. Dairy Sci. 94:6153–6161.
- Veerkamp, R.F. 1998. Selection for economic efficiency of dairy cattle using information on live weight and feed intake: a review. J. Dairy Sci. 81:1109–1119.