Feature Article

The future of phenomics in dairy cattle breeding

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Implications

- Increasingly complex dairy cattle production systems require that all aspects of animal performance are measured across individuals' lifetimes.
- Selection emphasis is shifting away from traits related to animal productivity toward those related to efficient resource utilization and improved health and welfare/resilience.
- The goal of phenomics is to provide information for making decisions related to on-farm management, as well as genetic improvement.

Key words: analytics, big data, dairy cattle, machine learning, phenomics, sensors

Introduction

Genetic selection has been a very successful tool for the long-term improvement of livestock populations, and the rapid adoption of genomic selection over the last decade has doubled the rate at which some dairy cattle populations are improving (García-Ruiz et al., 2016). While details differ somewhat between livestock species, the general objective of breeding programs is the same: the identification of genetically superior males and females that are used as the parents of the next generation. However, the expression of genetic potential also requires that animals are placed in environments that support such performance. For example, Figure 1 shows the increase since 1970 in milk protein yield in U.S. Holstein cattle, partitioned into gains due to increased genetic potential and those associated with improved environment (housing, feeding, etc.). Improved animal efficiency has also resulted in reduced environmental impacts throughout the production chain, which is of importance to consumers around the world (Capper and Cady, 2019).

Improved animal efficiency may be in conflict with improved health and resilience of animals because of trade-offs (Poppe et al., 2020). Resilience is the capacity of animals to be minimally affected by environmental perturbations, such as diseases or heat waves, or to rapidly return back to the state it had before the perturbation (Berghof et al., 2019). One example is to have cattle that can adapt to climate change, for example, cows that are heat tolerant (Pryce at al., 2018). Big data offer opportunities to better breed dairy cattle with a balanced emphasis on efficiency and resilience. This work will review the current literature related to deep phenotyping of dairy cattle, identify opportunities and challenges associated with new technology for measuring animal performance, and discuss how promising tools may be applied in practice.

The Importance of Measurement

The phenotype, a measurement of some property or feature of an individual, is the basis of all genetic improvement programs, although its meaning is often assumed and definitions are sometimes rare (e.g., Lush, 1994). While livestock breeders have long used complex selection indices that combine many traits into a single measurement of performance (Cole and VanRaden, 2017), there is a renewed interest in the collection of high-dimensional data on individual animals driven by various genome-mapping initiatives (Houle et al., 2010), environmental challenges (Grossi et al., 2019), and promising new technologies for low-cost phenotyping (e.g., Halachmi et al., 2019). A recent white paper focused on high-throughput

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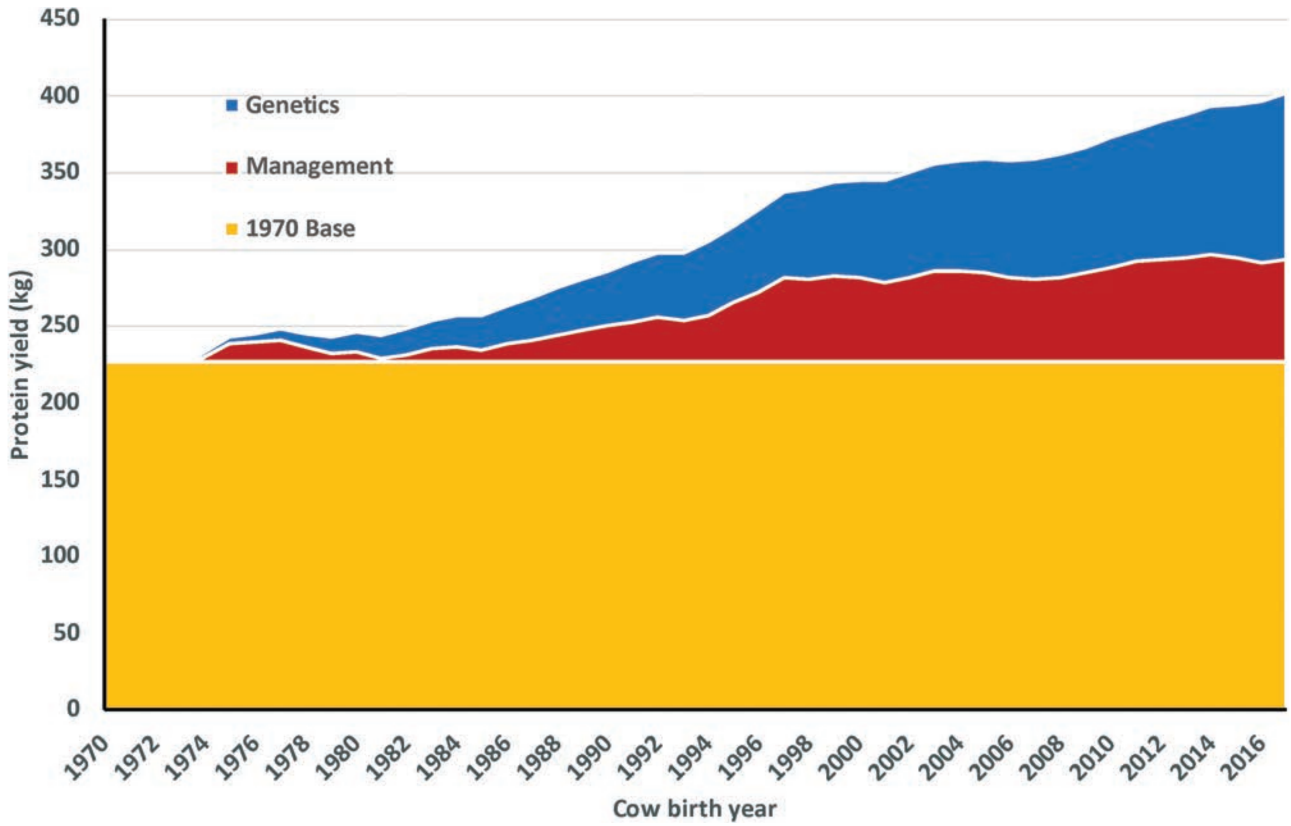

Figure 1. Improvements in genetic potential and cow management have contributed to a sustained increase in productivity per animal, such as for protein yield of U.S. Holstein cows (Source: Council on Dairy Cattle Breeding).

phenotyping in livestock species (Koltes et al., 2019), and the U.S. Department of Agriculture's latest 10-yr blueprint for animal genomics research emphasizes the importance of closing the genome-to-phenome gap (Rexroad et al., 2019). The ultimate goal of these efforts is to understand in detail how information encoded in the genome is translated into a phenotype to support the production of nutritious food from healthy animals.

It is important to recognize that the dairy industry has many constituents (dairy producers, dairy processors, breeding companies, etc.), each of which has a different interest in measures of animal performance than do scientists. In the United States, 42 traits of economic importance (5 yield traits; 8 measures of health, fertility, and longevity; 6 direct measures of health; 5 calving traits; and 18 conformation traits) are currently evaluated in the Holstein breed. Each of these traits is directly related to cow profitability, and selection indices are commonly used to combine information from many traits into a single quantity that can be used for animal ranking and selection (Figure 2).

Among researchers, there is interest in many other phenotypes, notably those related to milk composition and manufacturing properties, but there is currently little interest from dairy producers because there is no way for them to be paid directly for those traits. An exception is breeding for A2 beta casein, which is gaining popularity and premium supermarket shelf-space in some countries. When the phenotypic recording of these measures does not directly lead to greater farm income, it is a challenge to incentive dairy producers to contribute data, although they are willing to look to the future (e.g., breeding for kappa casein). In addition, dairy processors feel that technological innovations are a more cost-effective solution than genetic improvement for manufacturing properties. This disconnect can give the impression that dairy producers are not willing to change the direction of their selection programs, but actually reflects a lack of market signals.

It is tempting to assume that genomic selection provides an answer to all of the problems of the past. However, while genomics helps improve the rate of genetic gain (García-Ruiz et al., 2016), the emphasis on genotypes has often detracted from the importance of phenotypes. Genomic selection can improve only what is measured. Figure 3 shows the often-discussed example of decreased cow fertility associated with selection for increased milk production in U.S. Holsteins. When fertility was not included in the breeding goal, days open increased by approximately 1 d/yr and has only recently begun to show a favorable genetic trend.

Opportunities Associated With New Phenotyping Technologies

One of the key drivers of recent interest in animal phenotypes is the development of a new generation of electronic sensors that can be used to collect detailed, high-frequency measurements about animal performance and their environments in

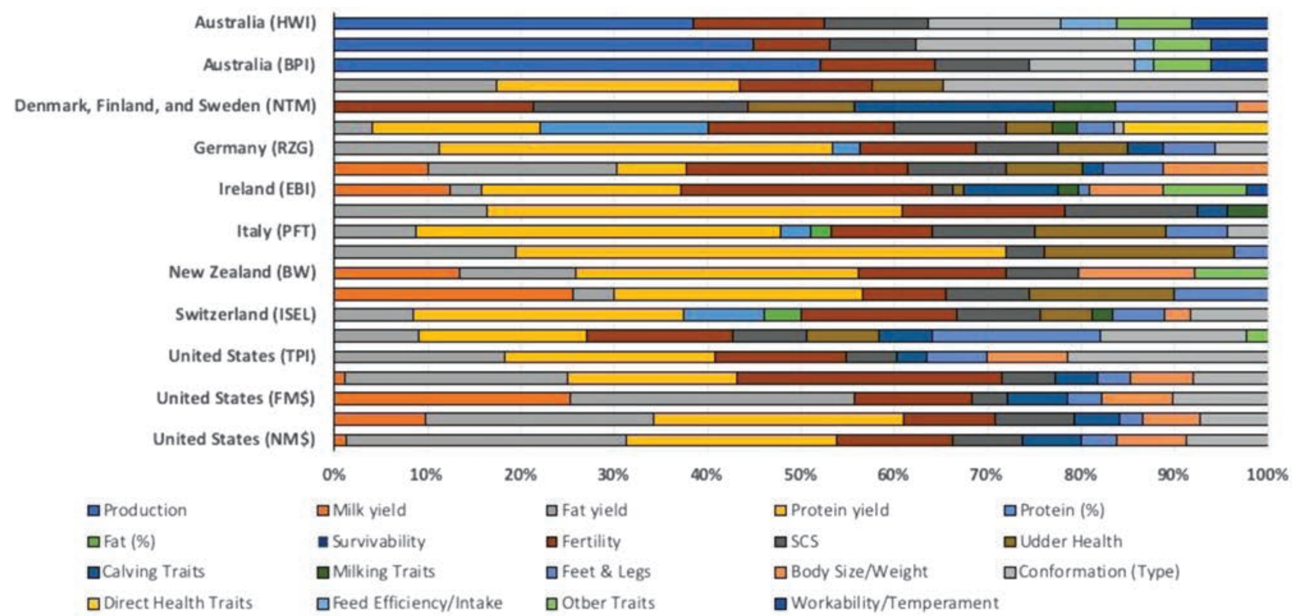

Figure 2. Phenotypes included in 21 total merit indices used to rank dairy cattle for profitability of the United States and 16 other countries. Data were collected from genetic evaluation centers and purebred cattle associations for Australia (ADHIS, 2014); Canada (CDN, 2017); Denmark, Finland and Sweden (NAV, 2017); France (Genes Diffusion, 2014); Germany (VIT, 2017); Great Britain (AHDB Dairy, 2017); Ireland (ICBF, 2017); Israel (SION, 2015); Italy (ANAFI, 2016); Japan (Holstein Cattle Association of Japan, 2010); New Zealand (DairyNZ, 2017); Spain (CONAFE, 2019); Switzerland (Holstein Association of Switzerland, 2013); The Netherlands (CRV, 2017); and the United States (Holstein Association USA Inc., 2017; VanRaden, 2017). Index abbreviations are HWI = health-weighted index; TWI = type-weighted index; BPI = balanced performance index; LPI = lifetime profit index; NTM = Nordic total merit; GDM = genes diffusion merit; RZG = Relativ Zuchtwert Gesamt (total merit index); £PLI = profitable lifetime index; EBI = economic breeding index; PD11 = Israeli 2011 breeding index; PFT = production, functionality and type index; NTP = Nippon total profit; BW = breeding worth; ICO = Índice de Mérito Genético Total (total genetic merit index); ISEL = Index de Sélection Totale (total selection index); NVI = Netherlands cattle improvement index; TPI = total performance index; GM$ = grazing merit; FM$ = fluid merit; CM$ = cheese merit; NM$ = net merit. (Source: after Figure 4 in Cole and VanRaden, 2017).

real time or near real time (e.g., Halachmi et al., 2019). Figure 4 provides a summary of data that can be collected using some of these systems.

The goal of these efforts should not necessarily be to replace existing phenotypes with new ones but to identify new sources of correlated information that can be collected on a large scale. For example, it would not be desirable to stop collecting somatic cell count (SCC) records that are correlated with udder health just because a new mastitis phenotype becomes available (Martin et al., 2018). There are several national databases that contain millions of observations for SCC that are used to compute high-reliability breeding values. New phenotypes, even those based on low-cost, easily collected observations, will require many years for sufficient data to accumulate to match the reliability that current evaluations based on SCC, longevity, and fertility data already have. There is likely more value in using new technologies to supplement data for existing phenotypes that are difficult or expensive to measure, such as computer vision-based measures of feed intake in place of weight-based intakes (Halachmi et al., 2019; Li et al., 2020).

On-Farm Analytics

Precision management is needed in order to provide the optimal environment for high-performing dairy cows, as well as to make timely management decisions (e.g., Kaniyamattam and De Vries, 2014). This includes a more frequent sampling of milk components (fat, protein, lactose, milk urea nitrogen, and somatic cell counts) and activity monitoring to identify changes in cow behavior associated with the onset of estrus, lameness, or disease and integration of real-time farm-level information (e.g., feed composition and weather). Alternative information about health comes from data recorded by automatic milking systems and electronic milking systems, such as milk yield per milking (Poppe et al., 2020), udder and teat characteristics (Poppe et al., 2019), or other electronic devices, such as sensors or cameras (Song et al., 2019). A recent, multi-institutional effort to develop a "Virtual Dairy Farm Brain" has been organized by Liang et al. (2018) in order to combine expertise from scientists, dairy producers, and industry professionals for the purpose of improving whole-farm decision-making.

The prediction of phenotypic performance using new data has not been studied in as much depth in the animal sciences as in the plant sciences (Mir et al., 2019), perhaps, because it is easier to run a seedling through an instrument for deep phenotyping than it is a calf. However, there is growing interest in this topic and the literature is growing (e.g., Goddard et al., 2016; Ho et al., 2019). The most important question overall might be, "How do we provide real-time feedback to dairy producers so that they can take advantage

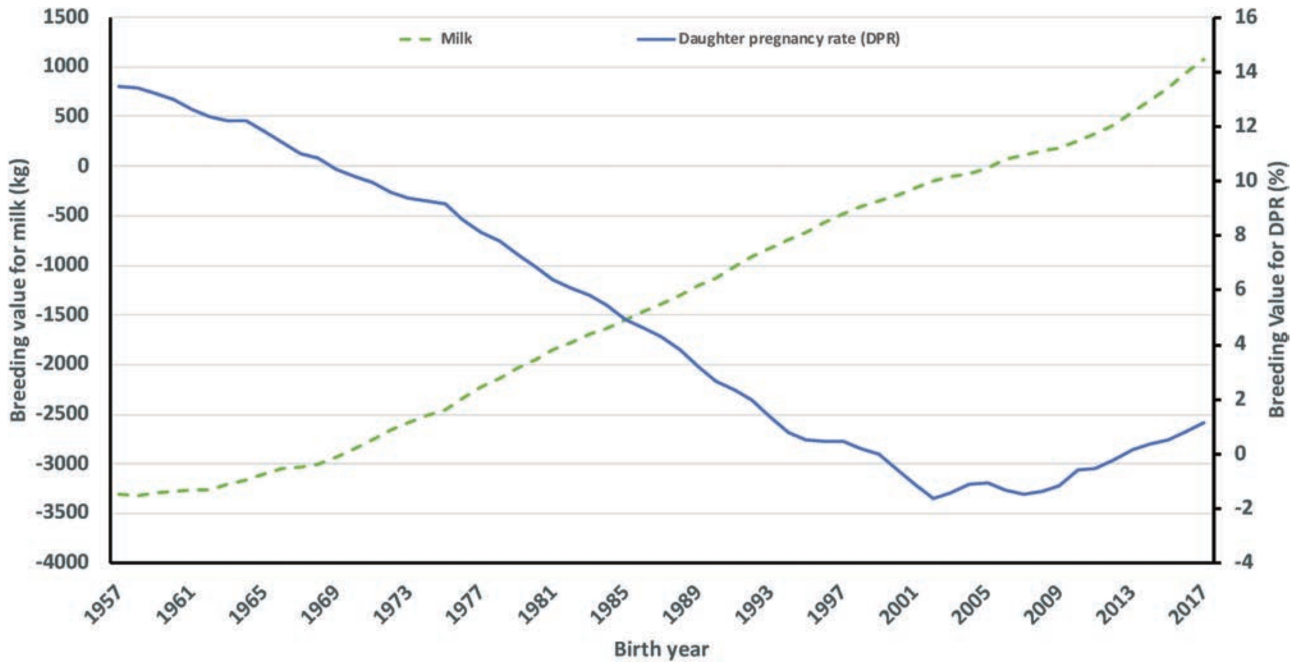

Figure 3. Changes in genetic merit of Holstein bulls for the production (milk yield, broken green line) and fertility (daughter pregnancy rate, solid blue line) of their daughters from 1957 to 2017 (Source: Council on Dairy Cattle Breeding).

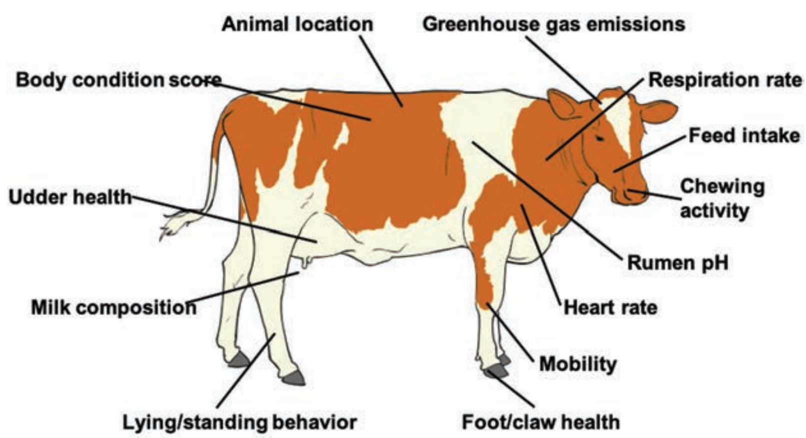

Figure 4. Phenotypes that can be collected at the cow level using sensor-based recording devices (Source: after Figure 5 of Halachmi et al., 2019).

of opportunities and avoid problems before they become acute?" This is driven in part by the biological variability among animals, exacerbated by genotype-by-environmental effects, and the high value of an individual animal. A key opportunity will be to use data and new analytics to rigorously evaluate current management practices to identify assumptions that either no longer hold or, perhaps, never held at all. That is, when presented in a timely and comprehensible manner, data can supplement intuition and guide herd managers to better decisions.

It is also critical that the dairy sector does not ignore growing demands from consumers for greater transparency about their food and how it is produced. For example, real-time monitoring of animal health and welfare may have great value as a marketing tool as is the ability to trace food to farms of origin (this is already possible in some markets, e.g., the Red Tractor logo on UK products is designed to give consumers confidence in quality and traceability of products; https://www.redtractor.org.uk/). Advanced analytics may also be necessary if consumers, and the milk processors that are the intermediate between dairy producers and consumers, demand that reproductive hormones are no longer used for routine management. Negative consumer perceptions of recombinant bovine somatotropin (growth hormone) led milk processors in the United States to ban its use, emphasizing that scientific and technical arguments about the value of a particular technology may be ineffective in the face of public resistance. It is better to be proactive on this front than reactive.

The Potential of the Milk Sample

Whole-animal measurements of performance are important because they provide detailed information about the physiological state of the animal but have the disadvantage that many different types of data must be integrated into decision support systems. Fine measurements considered to be precise measurements of individual physiological indicators (e.g., β-hydroxybutyrate) also provide valuable information but require individual collection and processing of samples. Unfortunately, labor, equipment, and laboratory expenses often prevent wide-spread collection of data from national herds regardless of the exact technology or assay used. Ideally, new phenotyping technologies would build on existing systems for nationwide collection and analysis of phenotypes for millions of cows without substantial additional expenses for dairy producers.

Alternatively, there is great potential for the use of test-day milk samples as the source of correlated phenotypes for many traits related to milk composition and the cow's physiological status. An absorbance spectrum can be generated by beaming infrared light through a milk sample (Figure 5), and the resulting points may be used to develop predictors of many different phenotypes (e.g., De Marchi et al., 2014; Gengler et al., 2016). While there are differences between the instruments sold by the three major vendors of milk-testing equipment, such as Bentley Instruments, Inc., FOSS, and Perten Instruments (formerly Delta Instruments), the same general approach may be used to develop equations for predicting, for example, lactoferrin, fatty acids, and coagulation properties from spectral data. In principle, it is similar to genomic prediction: phenotypes collected in a reference population are regressed on the wavelengths from the spectrum and the resulting weights used to estimate values in the larger population. This supports wide-scale, low-cost phenotyping because individual mid-infrared spectroscopy (MIR) samples can be collected at normal processing speed in milk-testing laboratories without the need for manipulation of the sample. The appeal with MIR is that it could become a cheap way of getting individual cow records for expensive and hard-to-measure phenotypes, such as methane production and metabolic profiles. For example, in a study that included data from five countries, calibration and cross-validation coefficients of determination of MIR predictions of >0.65 and 0.57 were obtained for prediction of methane emissions (Vanlierde et al., 2018).

Challenges Associated With New Phenotypes

While there is great potential associated with these new data, there also are many challenges that must be addressed by the scientific and farming communities. Many of the new technologies being offered to dairy producers are proprietary, and their methods may lack independent validation. This is a difficult challenge to overcome because of structural changes in agricultural experiment stations at land-grant universities that have limited the availability of both people and facilities needed to carry out validation studies, either in collaboration with industry or independently. Methods used for calculations are often incompletely documented or not documented at all because they are considered trade secrets. It is also common for data to be siloed or locked-away in proprietary software. Some vendors provide interfaces so that data can move into on-farm software systems, such as DairyComp 305 (VAS, Tulare, CA), others charge dairy producers for access to their data, and some provide no options for data mobility. Terms of access to data often are buried in software license agreements that do not clearly and explicitly disclose who owns data and how the data may be used. Finally, there is a serious lack of transparency in the dairy industry. Consolidation or vertical integration in which companies are acquired and small entities become a part of larger firms is becoming more common. For example, Company A may own Company B, with the license for Company A's equipment requiring that data be deposited in Company B's database. Company B then sells the data to third parties, and this relationship is not disclosed to the dairy producers purchasing Company A's equipment.

The role of new data in animal recording and genetic improvement programs also is unclear. Bodies such as the International Committee for Data Recording (Rome, Italy), as well as national milk-recording programs, provide detailed guidelines for the collection of data that are used in animal improvement programs. This includes standardized definitions of phenotypes to ensure like-with-like comparisons of data.

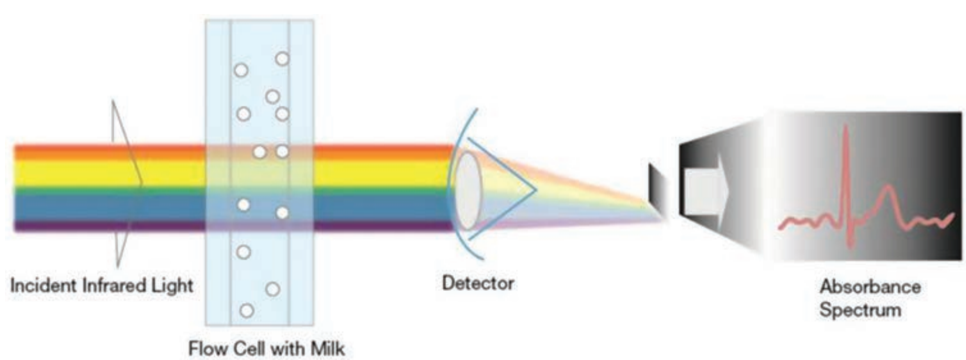

Figure 5. Creation of a mid-infrared spectral phenotype from a milk sample (Source: "MIR for Profit"; https://datagene.com.au/ct-menu-item-7/projects-industry-initiatives/mir-for-profit).

Laboratories must undergo inspection and certification, and data collection and transmission systems also must meet standards, such as those related to animal identification. Data ownership remains unresolved, as discussed above, which raises issues when data undergo quality control. For example, the Council on Dairy Cattle Breeding (Bowie, MD) requires that changes to data—such as correction of a pedigree based on genotypes—be approved by an authorized party. If it is not clear who owns the data, or who has authority to make decisions regarding those data, they cannot be easily integrated into genetic improvement or milk-recording programs.

However, the largest challenge of all remains that of how the dairy producer is to recover the costs of their investments in these new technologies. It is something of a chicken-and-egg problem: until data are available to drive new payment schemes, such as payment for higher casein or whey content in milk, there is no way for dairy producers to get paid to collect those data. The lack of access to rural broadband internet is also a growing problem because of the need to transfer data to and from farms. There are related problems on the farm, too, because the free-stall barns commonly used in the United States are constructed with steel beams and other materials that can interfere with wireless data connections, requiring the use of WiFi repeaters and other infrastructure. This imposes additional costs on top of the cost of robots, cameras, and other systems. If more technology is going to be installed on farms to meet the expectations of consumers and processors, there must also be a way for dairy producers to recover the cost of those new technologies. Even if affordable, the new technology implemented on farm must be practical and, most importantly, make work easier. The amount of data that is yielded by sensors and other on-farm precision management tools can be overwhelming and may require more labor from farm staff instead of less. This makes the integration of such technology unattractive and burdensome.

Lastly, while it is a challenge to incentivize dairy producers to collect new phenotypes, it is an equally large challenge to maintain the collection of traditional phenotypes through milk-recording programs. The number of cows enrolled in the National Dairy Herd Information Association's (Verona, WI) milk-recording programs has been declining (https://queries.uscdcb.com/publish/dhi/part.html), which is concerning. New thinking on how milk recording is perceived and used could potentially alter its uptake. For example, if MIR predictions of reproductive performance or early lactation disease risk are accurate enough, then farmers may think about milk recording in a completely different way. Procedures for the inclusion of data from automated systems in genetic improvement programs also are needed to support unbiased evaluations. It is critical that the dairy producer realizes that genetic progress is dependent on the recording of both traditional and new phenotypes. This is difficult when those who do not contribute data benefit along with those who do support the system, but no good solution to this problem has been devised. In the United States, genotyping is cheaper for participants in milk-recording programs, so there is a benefit for those who do provide data. What is not measured cannot be changed. In turn, it is similarly important that milk-recording organizations continue to provide added value to their services when there is apparent, or actual, competition between milk-recording programs and organizations that sell genomic evaluation services.

"So I Tied an Onion to My Belt, Which Was the Style at the Time."

Substantial attention has been paid recently to the growing volumes of data available in virtually all areas and the need to turn those data into actionable information with limited direct human interaction. "Big data", "machine learning", and "artificial intelligence" are all promised by their advocates to be the solution to these challenges (e.g., Cole et al., 2012; Koltes et al., 2019; Lokhorst et al., 2019). This is appealing given the rising tide of information to be interpreted, the high demand for scientists with analytics skills, and the demand from dairy producers for better tools to manage their businesses. However, these new approaches have their own challenges, ranging from bias (Castelvecchi, 2016) to interpretability (Gilpin et al., 2018), and there is a temptation to oversell outcomes. Such unrealistic expectations do not help dairy producers, consumers, or allied industry. We, as a community, need to remain focused on producing healthful food as efficiently as possible for a growing population. New analytics technologies will support that goal, but they are not infallible, and their recommendations should be tested in real-world situations.

Summary

In order to meet the growing worldwide demand for animal-sourced protein, it is essential that the dairy industry make the most efficient use possible of the cow's ability to upcycle inedible plant matter (Mottet et al., 2017; Figure 6). This will require the efficient use of all inputs needed on the farm,

Figure 6. Holstein and Jersey crossbreeds graze on American Farm Land Trust's Cove Mountain Farm in south-central Pennsylvania (Source: ARS Image Gallery, image #K8587-14; photo by Bob Nichols).

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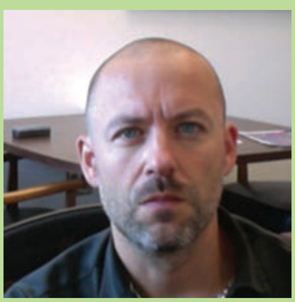

Christian Maltecca is Professor of quantitative genetics and breeding in the Department of Animal Science at North Carolina State University. His research is focused on the genomic improvement of economically relevant traits in livestock. His main interests are in the area of genomic prediction and genome-wide association for functional traits. Additional research in his group is focused on the impact of genomic selection on long-term variation and fitness.

Han Mulder is Associate Professor of animal breeding and genomics at Wageningen University and Research Animal Breeding and Genomics, The Netherlands. He is an expert in quantitative genetics, livestock breeding program design, animal resilience, genotype-by-environment interaction, and genomic selection. His current research focuses on developing resilience indicators based on big data in dairy cattle, laying hens, pigs, and tilapia, the role of GxE in designing genomic breeding programs, and investigating the role of mutation variance for long-term genomic selection.

Jennie Pryce is Principal Research Scientist of Agriculture Victoria and Professor of La Trobe University, where she leads research driving genetic gain and herd improvement in the Australian dairy industry. Her main areas of interest are genetic improvement of functional traits in dairy cattle, optimizing breeding scheme design under genomic selection, and development of dairy selection indices. She is also Lead Scientist of DataGene, participates in several groups that shape the future of dairy research in Australia, and is a member of the International Committee for Animal Recording's Working Group on Functional Traits.

reduction of undesirable outputs from animal agriculture, high-quality management of cows and their environment, and assurances to consumers that dairy animals are healthy and well cared for. Innovative technologies based on low-cost sensors and cutting-edge data analysis tools will be necessary to meet those objectives. Close collaboration between dairy producers, scientists, and allied industry will be essential to convert these technologies into practical solutions.

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Literature Cited

AHDB Dairy. 2017. £PLI—Profitable lifetime index. [accessed February 11, 2020] https://dairy.ahdb.org.uk/technical-information/breeding-genetics/%C2%A3pli/.

ANAFI (Associazione Nazionale Allevatori Frisona Italiana). 2020. Schede Calcolo Indici Aggiornato ad Aprile 2019. [accessed February 11, 2020] http://www.anafi.it/it/indici-genetici/schede-di-calcolo-indici.

ADHIS (Australian Dairy Herd Improvement Scheme). 2014. National Breeding Objective—Final report [accessed February 11, 2020] https://www.adhis.com.au/v2/downv2.nsf/(ContentByKey)/d356f55a05cac8f0ca257c78000a2677/$file/nbo%20final%20short%20report.pdf?open.

Berghof, T.V.L., M. Poppe, and H.A. Mulder. 2019. Opportunities to improve resilience in animal breeding programs. Front. Genet. 9:692. doi:10.3389/fgene.2018.00692.

Capper, J.L., and R.A. Cady. 2019. The effects of improved performance in the U.S. dairy cattle industry on environmental impacts between 2007 and 2017. J. Animal Sci. 98:1–14. doi:10.1093/jas/skz291.

Castelvecchi, D. 2016. Can we open the black box of AI? Nature 538:20–23. doi:10.1038/538020a.

CDN (Canadian Dairy Network). 2017. Lifetime performance index (LPI) formula. [accessed February 10, 2020] https://www.cdn.ca/document.php?id=443.

Cole, J.B., S. Newman, F. Foertter, I. Aguilar, and M. Coffey. 2012. Really big data: processing and analysis of large datasets. J. Animal Sci. 90:723–733. doi:10.2527/jas.2011-4584.

Cole, J.B., and P.M. VanRaden. 2017. Possibilities in an age of genomics: the future of selection indices. J. Dairy Sci. 101:3686–3701. doi:https://doi.org/10.3168/jds.2017-13335.

CONAFE (Confederación de Asociaciones de Frisona Española). 2019. Genomic evaluation of the Holstein breed in Spain. [accessed February 11, 2020] http://213.0.29.171/IndicesGen/Docs/evaluaciones_Metodologia_Genomica_EN.pdf.

CRV. 2017. About Dutch proofs. [accessed February 11, 2020] https://www.crv4all-international.com/about-crv/about-dutch-proofs/.

DairyNZ. 2017. Economic values. [accessed February 11, 2020] https://www.dairynz.co.nz/animal/animal-evaluation/interpreting-the-info/economic-values/.

De Marchi, M., V. Toffanin, M. Cassandro, and M. Penasa. 2014. Invited review: mid-infrared spectroscopy as phenotyping tool for milk traits. J. Dairy Sci. 97:1171–1186. doi:10.3168/jds.2013-6799.

Egger-Danner, C., J.B. Cole, J.E. Pryce, N. Gengler, B. Heringstad, A. Bradley, and K.F. Stock. 2015. Invited review: overview of new traits and phenotyping strategies in dairy cattle with a focus on functional traits. Animal 9:191–207. doi:10.1017/S1751731114002614.

García-Ruiz, A., J.B. Cole, P.M. VanRaden, G.R. Wiggans, F.J. Ruiz-López, and C.P. Van Tassell. 2016. Changes in genetic selection differentials and generation intervals in US Holstein dairy cattle as a result of genomic selection. Proc. Natl. Acad. Sci. USA 113:E3995–E4004. doi:10.1073/pnas.1519061113.

Genes Diffusion. 2014. GD Merit: A forward-looking synthesis. [accessed February 10, 2020] http://www.gemix.fr/bovin/GD-MERIT.aspx.

Gengler, N., H. Soyeurt, F. Dehareng, C. Bastin, F. Colinet, H. Hammami, M.L. Vanrobays, A. Lainé, S. Vanderick, C. Grelet, et al. 2016. Capitalizing on fine milk composition for breeding and management of dairy cows. J. Dairy Sci. 99:4071–4079. doi:10.3168/jds.2015-10140.

Gilpin, L.H., D. Bau, B.Z. Yuan, A. Bajwa, M. Specter, and L. Kagal. 2018. Explaining explanations: an overview of interpretability of machine learning. In: Bilof, R., editor. Proceedings of the 5th IEEE International Conference on Data Science and Advanced Analytics; October 1 to 3, 2018; Piscataway (NJ): The Institute of Electrical and Electronics Engineers, Inc.; p. 80–89.

Goddard, M.E., K.E. Kemper, I.M. MacLeod, A.J. Chamberlain, and B.J. Hayes. 2016. Genetics of complex traits: prediction of phenotype, identification of causal polymorphisms and genetic architecture. Proc. Biol. Sci. 283:20160569. doi:10.1098/rspb.2016.0569.

Gonzalez-Recio, O., M.P. Coffey, and J.E. Pryce. 2014. On the value of the phenotypes in the genomic era. J. Dairy Sci. 97:7905–7915. doi:10.3168/jds.2014-8125.

Grossi, G., P. Goglio, A. Vitali, and A.G. Williams. 2019. Livestock and climate change: impact of livestock on climate and mitigation strategies. Anim. Front. 9:69–76. doi:10.1093/af/vfy034.

Halachmi, I., M. Guarino, J. Bewley, and M. Pastell. 2019. Smart animal agriculture: application of real-time sensors to improve animal well-being and production. Annu. Rev. Anim. Biosci. 7:403–425. doi:10.1146/annurev-animal-020518-114851.

Ho, P.N., V. Bonfatti, T.D.W. Luke, and J.E. Pryce. 2019. Classifying the fertility of dairy cows using milk mid-infrared spectroscopy. J. Dairy Sci. 102:10460–10470. doi:10.3168/jds.2019-16412.

Holstein Association of Switzerland. 2013. Rapport de Gestion 2013. Posieux (Switzerland): Holstein Association of Switzerland.

Holstein Association USA Inc. 2017. TPI formula—August 2017 [accessed February 17, 2020]. http://www.holsteinusa.com/genetic_evaluations/ss_tpi_formula.html.

Holstein Cattle Association of Japan. 2010. Change to NTP formula [accessed February 11, 2020]. http://www.holstein.or.jp/english/ntp2010/ntp2010.html.

Houle, D., D.R. Govindaraju, and S. Omholt. 2010. Phenomics: the next challenge. Nat. Rev. Genet. 11:855–866. doi:10.1038/nrg2897.

ICBF (Irish Cattle Breeding Federation). 2017. What is EBI? [accessed February 11, 2020]. https://www.icbf.com/wp/?p=5772.

Kaniyamattam, K., and A. De Vries. 2014. Agreement between milk fat, protein, and lactose observations collected from the Dairy Herd Improvement Association (DHIA) and a real-time milk analyzer. J. Dairy Sci. 97:2896–2908. doi:10.3168/jds.2013-7690.

Koltes, J.E., J.B. Cole, R. Clemmens, R.N. Dilger, L.M. Kramer, J.K. Lunney, M.E. McCue, S. D. McKay, R.G. Mateescu, B.M. Murdoch, et al. 2019. A vision for development and utilization of high-throughput phenotyping and big data analytics in livestock. Front. Genet. 10:1197. doi:10.3389/fgene.2019.01197.

Li, B., P.M. VanRaden, E. Guduk, D.J. Null, E.E. Connor, M.J. VandeHaar, R.J. Tempelman, K.A. Weigel, and J.B. Cole. 2020. Genomic prediction of residual feed intake in US Holstein dairy cattle. J. Dairy Sci. (in press). doi:10.3168/jds.2019-17332.

Liang, D., H. Delgado, and V. Cabrera. 2018. A virtual dairy farm brain. In: Koutsouris, A., editor. Proceedings of the 13th European International Farming System Association Symposium; July 1 to 5, 2018; Wallingford (UK): International Journal of Animal Extension, CABI.

Lokhorst, C., R.M. de Mol, and C. Kamphuis. 2019. Invited review: big data in precision dairy farming. Animal 13:1519–1528. doi:10.1017/S1751731118003439.

Lush, J.L. 1994. The genetics of populations. Ames (IA): Iowa Agriculture and Home Economics Experiment Station, College of Agriculture, Iowa State University.

Martin, P., H.W. Barkema, L.F. Brito, S.G. Narayana, and F. Miglior. 2018. Symposium review: novel strategies to genetically improve mastitis resistance in dairy cattle. J. Dairy Sci. 101:2724–2736. doi:10.3168/jds.2017-13554.

Mir, R.R., M. Reynolds, F. Pinto, M.A. Khan, and M.A. Bhat. 2019. High-throughput phenotyping for crop improvement in the genomics era. Plant Sci. 282:60–72. doi:10.1016/j.plantsci.2019.01.007.

Mottet, A., C. Haan, A. Falcucci, G. Tempio, C. Opio, and P. Gerber. 2017. Livestock: on our plates or eating at our table? A new analysis of the feed/food debate. Glob. Food Sec. 14:1–8. doi:10.1016/j.gfs.2017.01.001.

NAV (Nordic Cattle Genetic Evaluation). 2017. NAV routine geneticevaluation of dairy cattle—Data and genetic models [accessed February 10, 2020]. http://www.nordicebv.info/wp-content/uploads/2017/03/NAV-routine-genetic-evaluation-122016_FINAL.pdf.

Poppe, M., H.A. Mulder, B. J. Ducro, and G. de Jong. 2019. Genetic analysis of udder conformation traits derived from automatic milking system recording in dairy cows. J. Dairy Sci. 102:1386–1396. doi:10.3168/jds.2018-14838.

Poppe, M., R.F. Veerkamp, M.L. Van Pelt, and H.A. Mulder. 2020. Exploration of variance, autocorrelation, and skewness of deviations from lactation curves as resilience indicators for breeding. J. Dairy Sci. 103:1667–1684. doi:10.3168/jds.2019-17290.

Pryce, J.E., T.T.T. Nguyen, M. Axford, G. Nieuwhof, and M. Shaffer. 2018. Symposium review: building a better cow—the Australian experience and future perspectives. J. Dairy Sci. 101:3702–3713. doi:10.3168/jds.2017-13377.

Rexroad, C., J. Vallet, L.K. Matukumalli, J. Reecy, D. Bickhart, H. Blackburn, M. Boggess, H. Cheng, A. Clutter, N. Cockett, et al. 2019. Genome to phenome: improving animal health, production, and well-being—a new USDA blueprint for animal genome research 2018-2027. Front. Genet. 10:327. doi:10.3389/fgene.2019.00327.

SION. 2015. Israeli Holstein bulls catalogue 2015 [accessed February 11, 2020]. http://www.sion-israel.com/articles/files/3635046369.pdf.

Song, X., E.A.M. Bokkers, S. van Mourik, P.W.G. Groot Koerkamp, and P.P.J. van der Tol. 2019. Automated body condition scoring of dairy cows using 3-dimensional feature extraction from multiple body regions. J. Dairy Sci. 102:4294–4308. doi:10.3168/jds.2018-15238.

Vanlierde, A., H. Soyeurt, N. Gengler, F.G. Colinet, E. Froidmont, M. Kreuzer, F. Grandl, M. Bell, P. Lund, D.W. Olijhoek, et al. 2018. Short communication: development of an equation for estimating methane emissions of dairy cows from milk Fourier transform mid-infrared spectra by using reference data obtained exclusively from respiration chambers. J. Dairy Sci. 101:7618–7624. doi:10.3168/jds.2018-14472.

VanRaden, P.M. 2017. AIP research report NM$6 (2-17). Net merit as a measure of lifetime profit: 2017 revision [accessed February 11, 2020]. https://www.aipl.arsusda.gov/reference/nmcalc-2017.htm.

VIT. 2017. Estimation of breeding values for milk production traits, somatic cell score, conformation, productive life and reproduction traits in German dairy cattle [accessed February 11, 2020]. https://www.vit.de/fileadmin/DE/Zuchtwertschaetzung/Zws_Bes_eng.pdf.