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Animal Frontiers is published quarterly by the American Society of Animal Science (ASAS), Canadian Society of Animal Science (CSAS), the European Federation of Animal Science (EAAP), and the American Meat Science Association (AMSA). This magazine synthesizes information, through applied reviews, from across disciplines within the animal sciences. Animal Frontiers is provided as a benefit to the members of these societies. The digital version of this magazine is online at www.animalsciencepublications.org/publications/af.
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Introduction

The impact of Animal Frontiers on the Canadian Society of Animal Science

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As the world’s fifth largest exporter of agricultural products (Agriculture and Agrifood Canada, 2018), and with a growing export market for animal genetic materials, the Canadian livestock industry is poised to help attain the 70% increase in world food demand expected by 2050. To do so, however, our scientists need to be aware of the trends and activities in global agriculture.

Animal Frontiers incorporates the perspectives and approaches employed by leading scientists and policy makers around the globe. In the past 10 yr, Animal Frontiers has provided its readership with comprehensive reviews of important themes within animal agriculture, including those related to genomics, reproduction, animal health, nutrition, and many more. Issues of Animal Frontiers that were organized by members of the Canadian Society of Animal Science have touched on many important topics which affect the future of our planet including climate change, water use, antibiotic resistance, and others. We look forward to continuing our collaboration with the American Society of Animal Science, the European Association of Animal Production, and the American Meat Science Association which aims to maintain a high-quality and factual information source for these important topics and themes to our readers.

The organizations responsible for publishing Animal Frontiers are dedicated to the advancement and dissemination of science-based knowledge concerning animal agriculture. Animal Frontiers provides a forum for innovative and timely perspectives that have relevance to understanding the complex dynamics at work through animal agriculture. The discussion and position papers that present international perspectives on the status of high-impact, global issues in animal agriculture explore themes of broad and current interest within animal science and animal agriculture.

The Canadian Society of Animal Science is proud to be a part of the editorial board of Animal Frontiers, and we look forward to both contributing to and learning from our global colleagues to ensure safe, ethical, and sustainable animal agriculture for many generations to come.

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**From the Editor**

**The Future of Phenomics**

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Advances in genomics have led to an improved understanding of genetic variation in livestock production traits. In this context, collection of high-throughput, accurate phenotypic data has become the limiting factor in livestock genomics and related fields. To improve understanding of the complex interactions and underlying biological and physiological systems within livestock species, improved trait definitions of specific, economically relevant phenotypes are required. Collecting both high-density phenotypic and environmental data is therefore a major challenge for livestock production research. Novel phenotypes of interest, from gene expression to animal product characteristics, need to be identified, standardized, and their collection automated in computable formats. Development of high-throughput data collection techniques from multiple research disciplines at different biological levels is required. Research networks between academia, government, and the private sector should enhance scientific collaboration and catalyze development of modern data sharing policies. New bioinformatics approaches and advanced data management, processing, and analysis methods have become essential for integrating and interpreting the large amounts of data generated by multiple sources. Such unprecedented advances should allow a better understanding of the phenome, as well as advances to economically important traits for livestock production systems.

Included in this issue of *Animal Frontiers* are seven review articles showcasing how phenomics will impact livestock production in the future (Figure 1). The contributions from Africa, Europe, Asia, and the Americas provide a global perspective of how livestock scientists view the automation of phenotype recording.

The first two reviews offer contributions from Kenya and South Africa. Dr Raphael Mrode from the International Livestock Research Institute (Kenya) and Scotland’s Rural College (United Kingdom) and his colleagues provide excellent insight into how digital technology could change livestock development in low-income countries by examining innovative applications of emerging trends (Mrode et al., 2020). Dr Carina Visser and her colleagues from the University of Pretoria describe phenomics for sustainable production in the South African beef and dairy cattle industry (Visser et al., 2020). We then move to Europe, where Mike Coffey from Scotland’s Rural College (United Kingdom) coined the phrase “in the age of the genotype, #PhenotypeIsKing”, a hashtag that has been widely spread throughout the genetics and genomics world (Coffey, 2020). Dr Anita Seidel and her colleagues from the Christian Albrecht University in Kiel, Germany provide insight into dealing with complexity in modern dairy cattle breeding (Seidel et al., 2020). Dr Yachun Wang and her colleagues from China Agricultural University describe future opportunities and their implications for genetic improvement of temperament traits in dairy cattle (Chang et al., 2020). From there, Dr John Cole of the United States Department of Agriculture and collaborators describe the future of phenomics in the American dairy production system.
cattle industry (Cole et al., 2020). The issue is completed with Dr Ricardo Ventura and his team’s description of the opportunities and challenges of phenomics applied to livestock and aquaculture breeding in South America (Ventura et al., 2020).

The overall goal of this issue of Animal Frontiers is to provide insight into emerging trends in livestock phenomics and to offer viewpoints from some of the leading researchers in the field on how to use phenomics in livestock agriculture. It is clear that the pressure to improve animal housing and breeding strategies will only increase in the future, so the need to critically evaluate new strategies at the farm level is imperative. The initial research findings showcased in this issue are exciting and suggest that the future of data collection using new approaches and technologies is a bright one. Precision phenomics will not come from one technology, but an integrated approach involving many different levels of farm management, public policy, and industry commitment. Are you ready for the future?

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Phenomics and its potential impact on livestock development in low-income countries: innovative applications of emerging related digital technology

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Key words: dairy cattle, emerging digital technologies, information and communications technology, novel traits

Introduction

Phenotypes play an important role in understanding the genetic basis of livestock performance and are vital in informing and ensuring effective herd and flock management. At the national level, capturing phenotypes is fundamental in national aggregates of production data that underlines government agricultural policies and projections. Therefore, phenomics is important at both the farm level for profitability and at the national level for effective government agricultural policies. Phenomics may be regarded as the application of technologies to enable the collection of phenotypes cheaply, easily, and in large volumes. This may be driven by the need for automation enabling high throughput collection of phenotypes or to enable indirect collection of phenotypes which are difficult and expensive to measure through affordable and high throughput innovations. In Sub-Saharan Africa, with agricultural systems based on subsistence farming and small holder systems, capturing phenotypes has always been a major challenge. This could be attributed to several factors including 1) production systems characterized with many small farms and few animals, therefore the inability of farmers to pay for the cost of recording phenotypes, 2) small farms that are highly dispersed making the logistics of recording very cost inefficient and unattractive to private investors, and 3) the lack of government support for such services (Chagunda et al., 2006; Kosgey and Okeyo, 2007; Visser and van Marle-Köster, 2017). Therefore, earlier attempts to capture phenotypes have mostly been restricted to the easy to measure traits such as body weight (either measured directly or predicted) and milk yield. However, fitness traits such as fertility, resilience to local environments, and survival have largely been ignored.

Examples of Historical Attempts to Capture Data in Some Developing Countries

Some early attempts to capture phenotypes have tended to mimic systems in developed countries, with less regard to the
fundamental differences between the two systems. These attempts often led to failures but these have been successful in some cases. A few of these early attempts to capture data are briefly summarized below.

Examples of recording activities in small ruminants

Some historical attempts to capture phenotypes for growth traits in sheep and goats in some countries (e.g., India and Kenya) have been associated with research projects aimed at implementing breed improvement programs. Examples include the goat improvement program involving 34 villages by the Nimbkar Agricultural Research Institute in 1991 in South-Central Maharashtra of India with the aim of improving productivity in goats through cross-breeding (Nimbka, 1999). The Sirohi bucks involved in the cross-breeding were selected using records on their individual growth rates and their mothers’ milk yields. However, the project collapsed after a few years including the performance recording due to lack of funds. Second, the Kenya Dual Purpose Goat Development Project which was started in 1980 with the aim of developing a synthetic breed of goat that combined the adaptability of the indigenous East African and Galla goats and the growth and milk producing abilities of the Toggenburg and Anglo-Nubian breeds (Ojango et al., 2010). The project ran for several years with on-station testing in a nucleus herd and on-farm testing by several farmers with milk yield recorded. However, at about 2005, there were only a few animals involved in the project mostly due to funding issues leading to termination of the project and recording activities.

However, in countries such as South Africa where several goat breed associations were established and in Kenya where the Meru goat breeder association was formed as part of the FARM-Africa dairy goat and animal healthcare project this has led to a more sustainable system of capturing various performance data for goats (Ahuya et al., 2009; Visser and Van Marle-Köster, 2017). A summary of the traits recorded by some of the goat breeders’ association in South Africa is presented in Table 1. For instance, the Angora Goat Breeders’ Society was established in 1892, the South African Boer Goat Association in 1959, and the South Africa Milch Goat Breeders’ Society was formed in 1958. The existence of these breed association meant that phenomics was not only restricted to “the easier to capture traits” such as growth but linear type traits were also recorded. In the case of Angora goat, traits such as fiber diameter and fleece weight were also captured and selected for (Visser and Van Marle-Köster, 2014).

Examples of performance recording in dairy cattle

Mrode (2019) presented a detailed historic perspective for the establishment of milk recording services in several African countries, India, and Brazil. In some African countries (Kenya and Zimbabwe) and in South American countries (Brazil and Argentina), phenomics aimed at capturing milk records in the dairy sector in the early 1900s were initiated by stud books or breed associations with government support and/or funding from international development agencies. Usually these milk recording activities were confined to large herds owned by settler farmers in these countries (Kosgey et al., 2011). The traits focused on were milk yield and milk solids (fat and protein percent). Most of these records were associated with far too complex institutional arrangements and high costs; hence most of these systems collapsed when project and government support were withdrawn (Kosgey et al., 2011) or they were able to transit successfully to schemes where farmers pay for such services usually accompanied with an initial drop in number of farms recorded as was the case in Kenya and Brazil (Trivedi, 1998; Costa et al., 2004). Currently, these systems are still operating in these two countries with farmers paying for the recording activities with little or no government support. Milk recording in India has, however, been based on a slightly different approach with the National Dairy Development Board working in collaboration with several developmental agencies and Non-Governmental Organizations such as the Bharatiya Agro Industries Foundation (BAIF) providing these services. However, as mentioned by Ducrocq et al. (2018), the recording is immature with a high percentage of the records of limited use due to poor quality such as unknown sire, animal identification errors, or transcription mismatches when entering information in the database.

Current or Modern Trends in Phenomics in Developing Countries

The production systems of small holder farmers characterized with small and dispersed herds in addition with associated high cost of performance recording constitute some of the bottlenecks to sustainable phenomics in developing countries. Therefore advances in mobile technology has prompted attempts to investigate information and communications technology (ICT) models for performance recording in small holder systems and for the feedback of management information to farmers to help them make informed decisions. A summary of some of the initiatives on the application of ICT and mobiles

Table 1. A summary of goat breed societies in South Africa and their recording activities

| Goat breed societies                  | Year formed | Examples of traits recorded                                      |
|--------------------------------------|-------------|------------------------------------------------------------------|
| Angora Goat Breeders’ Society        | 1892        | Fleece weight, fiber diameter, comfort factor (%) and spinning effective fineness |
| The South Africa Milch Goat Breeders’ Society | 1958        | Milk yield, milk composition and linear type traits               |
| South African Boer Goat Association  | 1959        | Birth weight, weaning weight, weaning rate, growth rate, kidding rate (kids born or does mated) and twining rate |
phones and other digital tools for data collection in some developing countries is presented in Table 2. Some of the projects applying modern technologies for data capture include the African Dairy Genetic Gain (ADGG) and the Private Public Partnership for AI Delivery (PAID) sponsored by the Bill and Melinda Gates Foundation in Tanzania and Ethiopia for the capture of performance records (milk yield), hearth girth for the prediction of body weight, body condition score, and insemination data for dairy cattle. The performance and fertility data were collected monthly by using a software based on the Open Data Kit, installed in tablets as well as on mobile phones employing the services of performance recording agents. Heart girth has been measured in animals using a tape (Figure 1) for the indirect prediction of body weight. Moreover, a technological platform called iCow (http://www.icow.co.ke/), owned by a private company called Green Dreams, was used as means of feeding back management information to farmers and for their training. The achievements of the project as of March 2018 are summarized at https://www.slideshare.net/ILRI/adgg-achievement and selected results presented in Table 3. The performance data collected from ADGG has enabled genomic prediction and selection of top young bulls for breeding (Mrode et al., 2019). Similarly, Ducrocq et al. (2018) examined the use of ICT for the collection of performance data on a large scale in India by the BAIF. The project consisted of 170 AI technicians equipped with multi-component software, installed first on dedicated “data loggers” and later on mobile phones. The outcome was a rapid collection of hundreds of thousands of good quality fertility records; however, the quality of milk production data was not as good.

In the case of small ruminants, the implementation of data collection in a group of farmers through the Community-Based Breeding Programs (CBBP) in Ethiopia and Malawi (Table 2) have resulted in successfully capture of performance data related to growth traits, twinning rate, and fleece weight (Haile et al., 2019). In addition, a digital system, AniCloud (https://anicloud.com/), which integrates with AniCapture, a smart device software designed for offline gathering of data in situations where connectivity is challenging has been employed for data collection. The CBBP underscores the importance of farmer participation and use of ICT tools in the successful collection of performance data.

Capturing fitness traits in small holder systems constitute a major challenge as it is more involving compared with measuring growth traits. However innovative approaches are emerging for the capture of novel phenotypes on fertility. Some of these approaches include estrus detection through the use of sensors to detect the different behavior patterns (time and duration) of the animal and generate farmer-useful information. This may involve the use of electronic rump-, neck-, or leg-mounted detectors that transmit data via either radio signal or ultra-wide band technology to a receiver or video cameras to supplement visual observations (Bruyere et al., 2012). An increasingly popular method for estrus detection is through measurement of activity through the use of pedometers. Cows in heat tend to be restless resulting in increased movement (Baxter et al., 1977) and the sensors, usually attached to the hind leg, record the number of steps made by the cow per unit of time. Measures of cow activity are then used to predict progesterone profile for individual cows. Application of such activity sensors have been attempted in small holder farms in Kenya. In a recent study involving a large scale farm in UK and Kenya, and small holder dairy farms in Kenya,

Table 2. Summary of digital tools that have been employed for capturing performance data in some developing countries

| Initiatives                                      | Livestock          | Tools                                                                 | Traits recorded                                      | Countries          |
|--------------------------------------------------|--------------------|----------------------------------------------------------------------|-----------------------------------------------------|--------------------|
| African Dairy Genetic Gains Project              | Dairy cattle       | Mobile phones and tablets, Open data kit, information, and technology Platform called iCow (http://www.icow.co.ke/) | Milk yield, body condition score, hearth girth and insemination details | Ethiopia, Tanzania, Kenya |
| Dairy Project Bharatiya Agro Industries Foundation (BAIF), India | Dairy cattle       | Data loggers and mobile phones                                        | Milk yield                                             | India              |
| Community-Based Breeding Program                 | Sheep and goats    | Digital system, anCloud (https://anicloud.com/), and software AniCapture | Birth weight, body weight at various ages and twinning rate | Ethiopia, Malawi   |
| Muasa (2020)                                     | Dairy cattle       | Pedometers                                                           | Cow activities for prediction progesterone profile (fertility) | Kenya              |

Figure 1. Tape for measuring heart girth of animals for the prediction of body weight.
Muasa (2020) demonstrated very comparable results in the sensitivity and specificity of three different estrus detection technologies (rapid progesterone, CowAlert, and Estrotect).

Future Perspective for Phenomics in Developing Countries

The widespread use of mobile phones and rapidly advancing ICT presents novel opportunities for innovative approaches to data capture. The ADGG and CBBP have demonstrated feasibility of such approaches. However, this emphasizes the need to design and develop simple, efficient, inexpensive, non-invasive, and sturdy phenotyping devices to support collection of a range of existing or new quantitative data relating to animal welfare, production, reproduction, product quality, feed efficiency, etc. on the farm. Most suitable technologies will be those that will support routine data collection and near to real-time transmission to agile databases, with robust analytics that enable meaningful feedback to be sent to users (researchers, producers, policy makers, etc.) as quickly as possible, and which can be easily incorporated into genetic improvement. However, reliable internet connectivity has been a challenge in the application of some of these digital tools for data capture in some countries shown in Table 2. Animal scientists will need to collaborate with an interdisciplinary team of scientists (software developers, engineers, programmers, etc.) capable of designing a variety of innovative technologies needed for innovative phenotypic data collection. A major emphasis will be technological systems that can work offline in data capture and transmission, as reliable internet connectivity is a challenge in many developing countries.

Preliminary attempts of innovative approaches to capture fertility traits have been described in a previous section. Such methods and other emerging cheap and innovative approaches such as the use of mid-infrared spectrum for indirect prediction of various economically important traits in dairy cattle will need to be calibrated and adapted for use in small holder systems. While measuring feed intake remains an expensive undertaking even in developing countries, the use of automatic systems to capture feed intake (e.g., the Insentec Roughage Intake Control system, the GrowSafe system, or the Calan Broadbent Feeding System), in a set up mimicking small holder systems to evaluate the impact of locally available feed resources on performance or to derive some predictive equations will not only provide useful guidelines to farmers, but may also be useful in providing approximate measures of feed intake, which might be better than the current situation with no information on feed intake.

Development and application of innovative and efficient methods of data collection will generate a large amount of data from herds or flocks located in different places, and if georeferenced will enable such data to be linked with related global meta-weather and soil data, thus further enriching the dataset. The amount of stored information will be substantial, so an important aspect of phenomics in developing countries is the need for efficient data infrastructure for permanent storage as well as software and web applications that allow easy access and analysis of these data by stakeholders. Designed data bases or platforms need to be secure and should be able to: 1) easily interface with other databases and 2) accommodate integrated compilation of phenotypic and genotypic data to support generation of substantial sample sizes needed for rigorous data analysis to inform management practices and optimize animal production systems. Increasing the volume of genomic and production data collected on individual animals across production environments will enhance the ability to select animals for desired performance traits suited to specific agro-ecological areas. Use of such data for management decisions by farmers might encourage them to undertake the expense and labor necessary to collect the needed data.

Currently, various government and international policies exist that govern the movement and use of germplasm across countries. However, with digital tools offering more opportunities to collect performance data from small holder systems (including farmers’ location), similar policies might be needed to govern the use of such data.

Conclusion

In summary, elaborate infrastructure, herds of small sizes which are widely dispersed plus the high cost of recording have been some of the bottlenecks to sustainable phenotyping systems in developing countries in Sub-Saharan Africa. In spite of these challenges, advances in technology and innovative use of ICT and mobile technologies to capture performance data have been demonstrated for dairy cattle and small ruminants. However, reliable internet connectivity continues to be the main challenge. To a small extent, use of digital sensors to indirectly capture “the not-too easy to capture” traits have been tested with promising prospects. Animal scientists will need to collaborate with an interdisciplinary team of scientists to design the next generation of innovative technologies which are cheap, robust, easy to use, and can function without internet connectivity for efficient capture of performance data in developing countries. Emerging and innovative approaches for measuring traits directly and indirectly need to be calibrated and adapted to the conditions prevailing in small holder systems. Application of

Table 3. Number of farmers and animals registered and monitored on the African Dairy Genetics Gains (ADGG) platform by October 2019

| Country | Registered Farmers | Registered Animals | Monitored Farms | Monitored Animals |
|---------|--------------------|--------------------|-----------------|------------------|
| Ethiopia |                    |                    |                 |                  |
| ADGG    | 12,576             | 36,042             | 6,559           | 19,658           |
| PAID    | 50,460             | 60,944             |                 |                  |
| Tanzania |                    |                    |                 |                  |
| ADGG    | 15,690             | 38,914             | 13,589          | 26,433           |
| PAID    | 18,585             | 23,170             |                 |                  |
| Total   | 97,311             | 159,070            | 20,148          | 46,091           |

PAID = Public private partnership for AI delivery.
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these technologies will be critical to attracting youth into agriculture in developing countries and thus ensuring sustainable phenomics platforms.

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Feature Article

Phenomics for sustainable production in the South African dairy and beef cattle industry

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Implications

• Phenotypic and pedigree recording of livestock remains a challenge in developing countries with informal agricultural sectors.
• Automated technologies would assist commercial farmers to become more efficient and productive, and to make full use of genomics.
• Farmers will benefit from the use of automated technologies in terms of improved animal welfare and economic sustainability in resource-poor areas.

Key words: smallholder, recording, sensors, welfare

Introduction

The impact of the rapidly growing human population on natural resources and in particular on food security has been well documented. As an example of the growth expected in Africa, the current South African human population of approximately 57.7 million people (Statistics South Africa, 2018) are expected to increase to 72.8 million people by 2050 (United Nations, 2017). Nutritional demand, specifically the demand for animal protein, would follow a similar pattern, and the responsibility of meeting this demand will place additional burdens on livestock producers. Climate change will add to this already demanding task, with extreme environmental changes expected for developing countries south of the equator.

Modern genetic improvement in livestock relies on the availability of genomic data (e.g., Single-Nucleotide Polymorphism genotyping and sequencing), as well as accurate recording of relevant phenotypes. The combination of the available phenotypes and genomic data have contributed to identification of specific genes and quantitative trait loci of economic importance and generation of genome-enhanced estimated breeding values for application in genomic selection. Although the field of molecular genetics has advanced rapidly over the past two decades, accurate phenotyping still remains a serious constraint, and has become the overriding bottleneck in improving livestock production and efficiency.

In South Africa, there are almost 14 million cattle which constitute 1.6 million dairy (604,781 cows in milk) and 12.5 million beef cattle. Of the latter, approximately 53% are kept in commercial systems and the remaining 47% in informal systems (DAFF, 2019). Phenotypic and pedigree recording of livestock in Africa faces constraints in terms of the extensive nature of the farming systems and the large informal livestock sector consisting of communal and small-holder farmers, which is characterized by a general lack of resources such as financial, infrastructural and extension support. Within the commercial sector, participation in collection of data from animal production systems ranges from compulsory participation (100% participation for stud breeders) to extremely poor (mainly within the informal and small-stock industry). Identifying breeding objectives across this wide spectrum of production levels is crucial, followed by the collection of relevant data to address the various issues.

Livestock phenomics is defined as obtaining high-dimensional phenotypic data on an animal-wide scale, which can capture missing heritability, break down composite traits into their components and transform hard-to-measure traits into easily measurable traits (Greenwood et al., 2016). Several state-of-the-art technologies (mostly making use of remote sensing techniques) to enhance phenotyping have been developed and are in various stages of incorporation within the crop production field (Mir et al., 2019). Plant phenomics have the distinct advantage of plants being stationary, and basic crops can be produced rapidly and artificially, with short generation intervals (Greenwood et al., 2016). Object tracking is more complicated in livestock than in either crops or humans, as similar colors and shapes between animals, as well as background clutter often lead to failures (Kim et al., 2017). The use of radio-frequency identification also has limitations, as the range of these sensors is quite restricted. There is a growing interest in low-cost sensor solutions and the use of mobile platforms to address these challenges.
This review aims to discuss the use of precision phenotyping in the beef and dairy cattle industries of South Africa, highlighting the challenges, limitations and possible contribution of these technologies towards the livestock sector.

**Advanced Technologies for Animal Sensing**

A key enabling technology for precision phenotyping is sensor networks. A sensor is a device that converts an observed property into an electrical signal. In wireless sensor networks, multiple sensors consolidate their observations wirelessly to provide fine-grained monitoring and automation in challenging environments. An important aspect in designing wireless sensor networks is in selecting suitable sensors, which is typically application driven. Sensors are classified as attached or nonattached. Attached sensors are composed of sensors inserted inside an animal, and wearable sensors that are fitted to the outside of an animal. Nonattached sensors are off-animal sensors which observe an animal, animal by-products, or the environment. Figure 1 provides an illustration of the general framework of a sensor network which could be applied in the South African dairy and beef industries for precision livestock farming.

Although a clear abundance of various sensors exists in the literature (corresponding to the physical/communication blocks in Figure 1), there is a lack of intelligence in sensor...
systems (which is provided through the cloud processing/local processing blocks in Figure 1), as sensor measurements are presented to farm personnel directly, or with minor processing, who are then required to draw their own conclusions (Rutten et al., 2013). However, this becomes problematic when there are a large number of animals producing excessive amounts of sensor data that must be interpreted by farm personnel; or when farm personnel do not have the required level of education to interpret sensor readings. This has led to poor adoption rates of intelligent systems by farmers. Poor adoption rates have also been attributed to exorbitant costs of solutions which are difficult to operate, and a lack of solutions that provide meaningful alerts. This is consistent with multiple farmer surveys on drivers of decision making which highlighted economic feasibility, and usability and technical support among others (Eckelkamp, 2019). In the context of Southern Africa, it was also found that technology adoption is linked to farmer’s participation with an innovation platform, which is described as a multisectoral and multi-institutional coalition of actors in specific value chain systems (Hanyani-Mlambo et al., 2017). These platforms provide greater access to agricultural advisory services and other support services.

**Precision Farming in the South African Dairy Industry**

Genetic progress in dairy cattle over the past three decades has been substantial compared to beef cattle or sheep. The extensive use of reproductive technologies in dairy cattle has given this industry an advantage in making genetic progress in production traits and more recently in traits with low heritability with the application of genomics (Miglior et al., 2017). Decades of selection pressure on milk yield has resulted in a number of unfavorable outcomes in fitness traits. DNA marker technology has solved many challenges regarding the identification of recessive genes using diagnostic tests, while genomic selection is contributing to genetic progress in fertility and feed efficiency (Miglior et al., 2017).

The trend worldwide is towards larger dairy farms with economics as the main driver (Rutten et al., 2013). A similar tendency is observed in South Africa where the number of milk producers decreased from 3,551 in 2009 to 1,253 in 2019 (Lacto Data, 2019), while herd sizes have increased. Pasture-based production accounts for up to 70% of dairy production in South Africa, and the remaining 30% are on total mixed ration systems (Meissner, personal communication). The larger dairy units have adopted automated milking systems, which require less labor and have the advantage of automated recording of a large number of phenotypes. The automated milking systems include Afifarm, DeLaval-Alpro and DeLaval-Delpro management systems as shown in Figure 2. Traditional milk recording schemes are used by less than 10% of South African dairy farmers (SA Stud book, http://www.sastudbook.co.za/p116/services/logix-milk.html).

Production, fitness, health, and workability traits have been included in genetic evaluations providing producers with estimated breeding values, genomic enhanced breeding values, and selection indices (Van Marle-Köster & Visser, 2018). Welfare traits in dairy cattle, which include claw health, lameness, mastitis, and other health traits are more difficult to improve due to limitations in effective routine recording, compared to production traits, as well as the low heritability of these traits. Precision or smart farming has presented advanced technologies for automated recording of a large range of welfare phenomes using automated monitoring systems (Hansen et al., 2018; Alsaaod et al., 2019), with the primary focus on early detection of a potential problem for timely interventions. Table 1 describes an array of sensors currently used in dairy farms.

The average herd size (in terms of cows in milk) in South Africa varies from 918 in the pasture-based provinces to as low as 119 in the drier regions (Lacto data, 2019). The larger operations making use of automated milking systems are primarily found in the coastal regions. Gresse (2018) demonstrated the use of data from automated milking systems for improved cow production, emphasizing the potential of the data for improving a range of dairy production traits. Implementation of precision dairy monitoring technologies in South Africa will be dictated by herd size and feasibility of automated milking systems.

Improvement of fertility relies largely on sound reproductive management and accurate record keeping. Estrus detection is often a primary constraint and various studies have shown that pedometers can improve detection compared to using only observations by herdsmen. The reliability of pedometers, however, has been shown to vary and can therefore not yet be implemented as a fool-proof method (Mottram, 2016). Rutten et al. (2017) explored the automatic behavior detection of calving, where each cow was fitted with an ear tag device consisting of sensors which monitored cumulative activity, rumination activity, feeding activity, and temperature on an hourly basis. Based on the sensor data, a predictive model predicted 43.5% of the calving events with 1% false positive alerts. A range of precision dairy monitoring technologies were tested with...
Table 1. Nonexhaustive list of sensors used for dairy cattle health management (Adapted from Rutten et al., 2013 and Mottram, 2016)

| Animal-health management | Attached sensors                                                                 | Nonattached sensors                        |
|--------------------------|----------------------------------------------------------------------------------|--------------------------------------------|
| Mastitis                 | • Reticular bolus temperature sensors                                             | • Electrical conductivity                  |
|                          | • Pedometer and 3 dimensional accelerometers (activity sensing)                    | • Milk color sensors                        |
|                          | • Pressure pads on cows’ back (mounting behavior sensing)                          | • Biosensors able to detect enzymes of interest|
|                          | • Temperature transducers                                                          | • Somatic cell count sensors               |
| Locomotion               | • Pedometer and 3 dimensional accelerometers (activity sensing)                    | • Video camera (mounting behavior sensing)  |
|                          | • Pressure pads on cows’ back (mounting behavior sensing)                          | • Microphone (cow vocalization sensing)     |
| Metabolism               | • Radiotelemetric rumen bolus (pH and temperature of rumen fluid sensing)          | • Biosensors able to measure progesterone  |
|                          | • Pedometer and three-dimensional accelerometers (activity sensing)                | • Video camera (walking behavior sensing)    |
|                          |                                                                                   | • Balance-weighing floors (weight distribution sensing) |

against the reference gold standard (progesterone patterns) and the accuracy of estrus detection was improved by between 15% and 35% compared to human observations (Mayo et al., 2019). The sensors in this study ranged from attachments to the front or rear legs, the ear or neck or a bolus in the reticulorumen, which all monitored activity, eating, ruminating and lying times. A primary advantage of precision dairy monitoring technologies is the continuous measurement of these activities which have been linked to health and metabolic disturbances (King et al., 2018). These measurements hold the potential for early detection of estrus and enhanced management as dairy units become larger and the farmer has less time available to inspect the herd.

Development of tri-axial accelerometers and sensors attached to ear tags also holds potential for more effective recognition of other cow activities which include behavioral changes, eating patterns, and locomotion (Mottram, 2016). Rahman et al. (2018) placed accelerometers on a neck collar at the back of the head, on a halter position at the side of the head behind the mouth, and on the ear using a tag. The data were used to train a machine learning-based model to classify three animal behaviors (grazing, standing, or ruminating), and attained accuracies of approximately 90%. In South Africa, collars and pedometers are used for detection of ruminating and eating patterns, activity, and estrus, while milk meters and analyzers are popular for milk traits such as milk flow, conductivity and composition. Substantial data are generated in automated milking systems in South Africa, but the data are primarily used for short-term management and economic decisions (Gresse, 2018). Somatic cell counts are used as an indicator trait for incidence of mastitis. An animal with a cell count of less than 50,000 cells/mL is regarded as a noninfected animal (Seegers et al., 2003). Mastitis being a complex trait and influenced by several factors, individual herd data are not available. The Milk Producers’ Organization (MPO) of South Africa estimated a loss of 1 billion ZAR for 2019 due to suboptimal udder health (Chris van Dijk, MPO, personal communication, https://www.mpo.co.za).

The consequences of lameness in dairy cows have been well documented, including adversely affecting genetic improvement, welfare, and farm profitability. Visual inspections and scorings are both time consuming and subjective. Automated methods for lameness detection include kinematic sensors (on the legs and feet) for monitoring body movement with three-dimensional video analyses or accelerometers and pressure-sensitive walkways. There are also kinetic methods using walkways with pressure plates based on ground force reaction (Alsaaod et al., 2019). Walkways with pressure sensors can distinguish between lame and non-lame cows and provide an indication of potential claw lesions (Volkman et al., 2019).

Lameness cannot be considered without recognizing the role of claw quality and health, which are both influenced by housing and environmental factors. Literature indicates that claw traits should be considered for improvement of lameness and moderate genetic correlations were reported between claw health and lameness. However, accurate scoring of claw traits and lameness remains the main challenge. In South Africa, claw data are limited to producers who make use of private hoof trimmers, who record the claw lesions on paper and the data is not necessarily captured in an electronic recording system (Mhlongo, 2019). Claw quality and health are not included in goal driven selection and available data have not been explored in research for lameness in South African dairy cattle.

**Precision Farming in the South African Beef Industry**

Widespread regions of South Africa are experiencing a state of drought, which is the result of the strong El Niño event that occurred in 2015 to 2016 (South African Weather Service, 2016). The shortage of water in the country has raised concerns, among other things, about the amount of water it takes to finish cattle in feedlots (Meissner et al., 2013). Approximately 68.6% of South African land is available for grazing, which is an ideal situation for extensive livestock production systems that rely on natural veld as a feed source. Global warming, however, will be
Responsible for fluctuations in the nutritional value of the natural veld (Scholtz et al., 2014).

There is pressure from consumers to produce beef with less greenhouse-gas emissions and limited exploitation of natural resources, while considering the health and well-being of the livestock. Most of the traits relevant to these objectives are difficult and expensive to measure, expressed late in life, and for some new equipment are still being developed. Phenomics aims to make use of advanced technologies and management systems to develop labor saving automated data collection. This would result in the collection of large amounts of phenotypic data, which could be used for genomic prediction and faster genetic improvement.

The level at which phenotypes could be measured varies between traits (i.e., behavioral vs. physiological), and systems (i.e., in-field walk-over vs. animal-attached collars). Traits that are routinely recorded by South African beef breeders commonly reflect easily measured traits that can be measured on farm with no additional financial burden, such as live weights (birth weight to mature weight), growth (average daily gain and Kleiber Ratio) and a smattering of reproduction traits (scrotal circumference, age at first calving and inter calf period), as suggested by Van Marle-Köster & Visser (2018). Traits such as feed conversion ratio, residual feed efficiency and disease resistance are extremely difficult to measure in extensive production systems. Pasture intake is the limiting phenotype for many efficiency parameters, and the measurement of selectivity of pasture would also be important as a variable influencing performance. Chemical markers and $n$-alkanes have been used for this purpose, but have limitations in terms of applying them over long periods of time. In-field walk-over weighing units, as well as on-body sensors to estimate grazing behavior have been developed to overcome this problem, but vary in terms of accuracy. Greenwood et al. (2018) acknowledges that the number of variables that can be measured is limited, and this poses a challenge with regard to developing a single phenotyping approach across systems.

A small number of individual breeders representing only seven beef cattle breeds perform real-time ultrasound scanning for carcass traits. This methodology is not readily available to all farmers (and comes at an additional cost), and farmers should have an economic incentive to pursue such additional phenotyping. South Africa has a meat classification system, which includes the age of the animal, fat content, conformation of the carcass and any damage to the carcass (Soji & Muchenje, 2017). It includes a visual assessment of the subcutaneous carcass fat content and fat distribution and does not make provision for grading of carcasses based on marbling. However, the Wagyu breed has recently entered the South African beef industry, and in this breed marbling score is highly correlated with the price paid for the carcass. A reliable measure of marbling is the use of a carcass camera. The MIJ-30 Digital Carcase camera used by Wagyu SA (http://wagyu.org.za/) allows objective measurement of marbling score, marbling fineness, marbling percentage, and eye muscle area (as shown in Figure 3), and will also be used to score fat and meat color.

Very few automated interventions have been introduced to the South African beef industry. One of the easiest to implement would be in-field walk-over weighing systems, such as those used in the Australian BreedPlan system (Greenwood et al., 2016). Wireless sensor data could also be used for deeper phenotyping and estimation of feed intake on pasture, as well as normal and aberrant behavior data.

Measuring physiological parameters such as temperature, rumen function, heart rate and metabolites would be the ultimate application of phenomics. These presently require invasive sampling such as tissue or blood collection, but could become more accessible if the sample used for genotyping could be applied for phenotyping as well. This would assist extensive commercial farmers in becoming more competitive and profitable, as precision phenotyping would be done without any additional costs to the farmer. A graphical illustration of some deep phenotyping interventions is given in Figure 4.

Figure 3. Scoring of carcass quality using the MIJ-30 (photo courtesy of the SA Wagyu breed society).

Figure 4. A summary of some traits that would benefit from precision phenotyping in both beef and dairy cattle in South Africa.
Automated, precision phenotyping would also improve animal health and welfare in resource-poor areas by early diagnosing subclinically ill animals, and even preventing antimicrobial resistance (Ramírez et al., 2019). Additionally, it could have a downstream impact on rural economies by creating jobs and sustaining businesses. Unfortunately, even if the technologies were commonly available, several challenges in terms of internet connectivity and signal quality would have to be overcome before this could become a reality.

**Opportunities Within the South African Framework**

The fourth industrial revolution (4IR) inaugurates a new chapter in human development, where technological advances of the past few decades are harnessed to change and improve the way we live and work (World Economic Forum, 2019). It involves the merging of the physical, digital and biological, and it is set to disrupt the largest global industries. The advent of high speed communication networks, Artificial Intelligence and Machine Learning, combined with a myriad of available sensors, will pave the way for improving the efficiency and productivity of the agricultural sector. These technologies will enable critical information to be available to the farmer in real-time and automation of key farming processes, which will lead to increased efficiency and productivity, while reducing the cost of production. The 4IR will be key in affecting social upliftment and empowerment of small and emerging farmers, enabling sustainable businesses and social change.

Development of real-time intelligent cattle monitoring and behavior modeling systems will enable identification and tracking of individual cattle in the kraal, as well as measuring vital parameters and predicting various future occurrences. For instance, one can measure the activity level, temperature, and weight of an individual animal over time, in order to detect sickness before it exacerbates to the point of death. Weight measurement is especially useful in the developing sector where infrastructure is not available. It could provide insight into the nutritional needs of the livestock, timing of the mating period, the possibility of disease, or internal and external parasites. Temperature measurement would be helpful to detect the onset of estrus, which could help improve the success of artificial insemination and therefore higher production rates and the rate of genetic improvement. Such monitoring systems would typically make use of high definition cameras installed above the kraal to provide a real-time video stream of the cattle. Radio-frequency identification scanners at the gate of the kraal could identify individual animals entering/exitng through the gate. The data extracted and information gathered from this system could be sent to a centralized system, using various wireless communication technologies, from where total farm surveillance would be possible.

Active livestock monitoring and behavior modeling offers a number of opportunities for commercial and especially emerging farmers to monitor the health of their animals, giving them real-time information which can be used to make critical decisions to

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**Prof Este van Marle-Köster** joined the Department of Animal & Wildlife Sciences, University of Pretoria in 1995 as a lecturer after working in the agricultural industry for 7 years. For her PhD research, she applied microsatellite markers for the first South African study on genetic characterization of native fowl. Locally developed and indigenous breeds used in Southern Africa have been included in her genetic diversity studies and in other projects. Her current research interest is on the application of genomic technology for genetic improvement of livestock with a preference for beef and dairy cattle in South Africa. She has interest in genomics to improve our understanding of the underlying genetic mechanisms governing traits of economic importance and gives priority to traits associated with animal welfare and sustainable production in a South African context.

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help ensure sustainability and improve productivity. This would empower emerging farmers to optimize productivity by providing critical information to the farmer at any given time. Such systems could be extended to any number of farms for large scale surveillance and farming operation optimization.

Evidently, there are a number of problems in need of solving in the cattle farming industry with the potential to greatly increase productivity and empower emerging farmers. The social impact that such a system could have is enormous, especially if it is provided at scale. New and emerging farmers will be able to participate in the agriculture economy, which will have a lasting effect of upliftment and empowerment on their generation and also contribute to the country’s agriculture output and its gross domestic product.

**Conclusion**

The use of automated, objective measurement technologies would assist South African commercial producers to become more efficient and meet market specifications, thus increasing profitability. Choosing objective, relevant phenotypes will enable the construction of comprehensive databases, which will assist in making full use of genomic tools. On the other side of the spectrum, it could assist in improving animal welfare and productivity of small holder farmers, as well as contributing to economic sustainability in rural areas.

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Dairy cows: in the age of the genotype, #phenotypeisking

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Introduction

Estimated breeding values (EBVs) have historically been calculated by national evaluation centers from phenotypes available in large quantities from national recording organizations, usually if not exclusively made available for no charge. The usual deal is that there is no charge then made to phenotype contributors for them to use EBVs. Most countries have an extensive range of EBVs for traits of economic importance and many countries participate in Interbull whereby local evaluations are merged with all others internationally for the same bull and an evaluation produced on a local scale containing information for all bulls internationally even when that bull has no offspring in the local country.

Prior to the widespread deployment of genomic selection in dairy cattle, the priority for global breeding companies was to collect enough genotypes on older bulls to create an informative reference population. The reason for this was that the phenotype available to them was the Interbull proof or national proof for the bull for the range of traits recorded in that country. This meant that phenotypes were not a limiting factor and that genotypes were the limiting factor since they were expensive at the time and large numbers (~20,000) were needed for a reference population producing genomic breeding values (gEBVs) at sufficient accuracy. However, DNA is easily extracted from frozen semen and many stores of old semen existed. The availability of Interbull proofs from all over the world meant that any bull from any country could contribute to a national reference population, even if that bull had never been used in a particular country. This was how national reference populations have been created. However, once all old bulls have been genotyped that have phenotypes (progeny proofs or Interbull proofs), the limiting factor for future evaluations has become unavailable genotypes or phenotypes.

The rapid fall in price per genotype means that many young females and nearly all new (young) candidate bulls are routinely genotyped and genotypes are no longer limiting. It seems the limiting factor for future evaluations of new traits of economic importance is now phenotypes. You might paraphrase all that with “In the age of the genotype, #phenotypeisking.”

The benefits of genomic selection have been highlighted especially for those traits that are available only late in life (lifespan), are difficult (expensive) to measure (e.g., feed intake) or are not yet measurable in large volumes or at sufficient accuracy (e.g., methane emissions). These difficult to measure phenotypes are coincidentally for those traits that are of current global importance in respect of climate change and are required right now to enable farmers to make socially important selection decisions (i.e., cattle that produce food with less resource use and that have a lower environmental impact). Genomics is an ideal technology to be used to spread the value of those phenotypes throughout the population since young animals with no phenotypes but that have been genotyped can have a prediction for the important trait made from the reference population. A really good review of genomic selection and phenotypes is given by Cole and VanRaden (2018).

Future Directions

So how will these difficult traits be measured? And by whom? Who will pay? And who will benefit?

Historically, genetic evaluations have been a by-product of national recording programs. The phenotypes collected for on-farm management were made available to national...
evaluation centers for processing into breeding values and were then passed back to farmers that recorded the phenotypes notionally for no charge for the breeding value (in essence a quid pro quo). Each country had a mechanism to pass the evaluations back to nonrecording farmers also which essentially meant every farmer had access to the breeding value for every trait. However, this model is set to change.

Take the example of feed intake in dairy cows. If we need feed intake for national evaluations, do we ask every farmer with milk records to install equipment and record feed intake? Impossible! Thus, we have to work out how to get enough phenotypes on informative animals that have been genotyped. This seems to suggest some form of nucleus. In some countries, this is organized by breeding companies (NLD, USA) and in other countries, it is an outcome of research facilities recording feed intake for research projects. The gDMI (global dry matter initiative) pooled records to produce an international dataset of genotypes from 6,000 cows with 10,000 phenotypes. This has created an international SNP key (set of equations based on the genotypes and phenotypes of the reference population) and genomic breeding values (gEBVs) for feed intake. The value of pooling records is described in Banos et al. (2012) and the benefits of so doing in de Haas et al. (2012). In Australia, the Dairy Information Nucleus (DIN) is an effort to gather feed intake (and other) records for genomic selection indices from contracted farms that genotype their cows (Pryce et al., 2018).

Examples of feed intake recording equipment for cattle are shown in Figures 1–3. One type of equipment has a gate that is activated as the cow approaches allowing some cows to be restricted to some gates (Figure 1). Another type of equipment that measures feed intake allows all cows to eat at each gate (Figure 2). Figure 3 shows equipment with hoods added to allow capture of methane emissions from individual cows.

For future recording the questions arises as to what animals would be recorded? The value of each incremental feed intake record for a bull’s daughters declines once sufficient records have been obtained for a reasonably accurate EBV. Each new bulls’ first records have much higher value and each incremental record has less value. Gonzalez-Recio et al. (2014) attempted to calculate the value of incremental records which could be used as a framework to pay for future recording schemes. If the recording scheme is organized specifically for the purpose of creating phenotypes for genomic selection, those animals for recording will be identified as having the greatest information contribution to the existing dataset. If records are gathered for some other (research) purpose, then the information content may not be optimal for genomic evaluations but this information would be better than having no information.

**How will animals become part of the nucleus?**

A nucleus can be a single large farm that genotypes all cows and records all available phenotypes of interest. In dairy farming, some single farms are sufficiently big to create their own nucleus. However, the general trend appears to be groups of farms being contracted to either a breeding company or a research project to become a distributed nucleus all recording to some predefined protocol allowing records to be merged and analyzed together. The DIN in Australia or the Langhill herd in United Kingdom are examples of farms that create large collections of phenotypes for genotyped cows. Some breeding companies have their own farms where data is recorded on daughters of their own bulls to be merged with data from other participating farms. It is easy to imagine a wide range of solutions that are driven by the circumstances prevalent in each country ranging from breeding company nuclei through to farmer coops.

**Who pays?**

For breeding companies, the availability of information for breeding values cannot be left to chance. As such, many are seeking to secure datasets for breeding value estimation for traits that will provide a competitive advantage. An example is Immunity Plus marketed by Semex and Wellbeing from Zoetis. These indices will be by definition, proprietary, and will not be comparable across companies. In these situations, farmers will have to make decisions about which company they deal with on the basis of available breeding values. Some companies are now establishing their own network of phenotype providers. These are a mixture of their own farms that collect data specifically for them and contracted farms that have some commercial arrangement with them. These “phenotype farms” collect data that may have a value greater than the agricultural product they coincidentally produce.
In some countries, if farmers can be paid the value of the phenotype they collect this may provide an attractive route into farming for new entrants. Borrowing against a secure and predictable income stream such as sale of phenotypes under contract may enable greater borrowing potential and may increase the penetration of younger farmers into modern agriculture. Records for traits that are expensive to measure may be paid for by whomever contracts with the farmer. In some cases, it could be national evaluation centers; in other cases, it could be breeding companies. In countries that have well-integrated recording, evaluation, and breeding centers such as NLD and NZ, these issues are simply internal accounting procedures. In countries that are less integrated (e.g., United States, United Kingdom, AUS), there may be competition to procure phenotypes on important traits such as feed intake and disease traits but for other traits that are for notifiable diseases such as bovine tuberculosis; these phenotypes may not be available to commercial companies.

**Who benefits?**

Clearly, everybody benefits from more efficient and healthy cows. The farmer will be the first to benefit but benefits spread through to consumer and society as a whole. This is especially true for efficiency-based traits and greenhouse gas (GHG) emissions. At present, no known system exists for rewarding farmers for reduced GHG emissions and so, farmers do not currently benefit directly. Once mechanisms are available to accurately record GHG emissions, it is anticipated that farmers will benefit for reducing GHG emissions from their dairy cattle.

For farmers to be able to breed more efficient cows that produce less GHGs, they need access to a SNP key at a price that...
makes selection beneficial. The SNP key therefore becomes the route by which the benefit is created for whole populations based on a small part of the population investing in it. The main difficulty will be in ensuring equitable distribution of benefits and costs across the supply chain. Will society get the benefits of more environmentally friendly dairy cows? Yes. Will they pay directly to farmers for that benefit? No. There are many actors in the chain required to create that benefit and the creation of those value chains for new and difficult to measure traits is still in its infancy.

Conclusion

If I were a dairy or beef farmer, I would genotype all my animals and farm phenotypes for sale. Those phenotypes would be based around efficiency, resource use, disease, and product quality. #phenotypeisking

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Dealing with complexity of new phenotypes in modern dairy cattle breeding

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Introduction

Worldwide, animal breeding has played and still plays an important role in increasing the production efficiency of animals, e.g., dairy cattle. The development of low-cost genotyping strategies such as single nucleotide polymorphisms (SNPs) and genotyping-by-sequencing (Elshire et al., 2011; Kumar et al., 2012) has made genomic evaluations indispensable for modern dairy cattle breeding methods (Meuwissen et al., 2001; de los Campos et al., 2013; Gianola, 2013) and programs (Schaeffer, 2006; Lillehammer et al., 2011; Pryce and Daetwyler, 2011) and represented a quantum leap—often compared to the successful implementation of artificial insemination. However, the quality of any genomic breeding value estimation strongly depends on the number of phenotyped animals and the observed heritability of the used phenotypes (Daetwyler et al., 2008). The success of animal breeding is still mainly based on phenotypic animal observations and the tremendous progress made is largely due to appropriate trait definitions and comprehensive performance tests.

Animal breeding companies as well as dairy farmers face several challenges concerning the sustainability of the entire dairy production system. This includes the impact of livestock on the environment and climate, the concern of increasing scarcity of natural resources (including genetic diversity) and feed, or concerns about animal welfare and health, and antimicrobial resistance. In the era of phenomics, the availability of robust phenotypes for these new issues is important. The technical revolution and the availability and processing of high amounts of data play a key role in this context. New phenotypes are based on large-scale or advanced measuring technologies. Sensor recordings play an increasingly important role for a wide range of traits (e.g., methane emissions, rumen microbiome characterization, mid-infrared spectra from milk samples, and behavioral traits).

Especially in the initial phase of recording, when the use of novel phenotypes is often not yet or insufficiently validated by research, pooling of data across different research partners within and across countries can be very helpful. It allows for a faster and sound implementation in breeding programs. Nevertheless, data pooling can get complicated if data are measured using different protocols or sensor technologies or if data processing is handled differently or not transparently.

All phenotypes have an inherent value that can be estimated as the contribution of an additional record to the genetic gain within a modern breeding goal (González-Recio et al., 2014). However, integrating a variety of new phenotypes into existing breeding programs is challenging due to the increasing complexity and unknown or potentially undesirable genetic correlations between different traits in the breeding goal.

Our goal here is to give a brief overview about the development and use of new phenotypes in the era of phenomics as well as to show constraints when implementing them in modern dairy cattle breeding programs.

Evolving new phenotypes in the era of phenomics

The definition of the phenotype of an organism can be broad; in general, it refers to a set of traits of an organism and includes morphological and physiological characteristics as...
well as behavioral patterns. Traits are identifiable characteristics of animals which differ from each other, and which can be measured and analyzed as statistical quantities. In the context of animal breeding, important traits are those that have a considerable genetic determination and which either have an immediate economic, social, or environmental value.

Mike Coffey’s often quoted statement “In the age of the genotype [genomics], phenotype is king” points out that measuring and recording of appropriate phenotypes is critical for genomic selection to function accurately. In the era of phenomics, the phenotype is even more in the spotlight of research. Difficult-to-measure phenotypes and complex interactions between old and novel breeding goal traits have become increasingly important. Currently, three main trait complexes are considered meaningful in the future: on the one hand, efficiencies of energy, nutrients, and environmental resources, on the other hand, health and resistance characteristics as well as animal well-being (Boichard and Brochard, 2012). This results in the challenge of obtaining precise and comprehensive information for these traits.

Recent engineering advances and the decreasing cost of electronic technologies have allowed the development of sensing solutions supporting precision farming that automatically collect data, such as physiological parameters, new production measures, and behavioral traits. One of the current target values is sensor-derived activity patterns (e.g., from pedometers, transponders, bolus, and camera systems) from which characteristics of specific animal behavior can be derived. In addition, conclusions regarding health, fertility, or well-being can be drawn from individual deviations from such animal-specific patterns. Furthermore, animal interactions and social behavioral characteristics (aggressive vs. tolerant animals) as well as social networks within a herd can be derived (Foris et al., 2019; Salau et al., 2019).

Moreover, in dairy science mid-infrared spectroscopy has been pointed out as a potential tool to collect data at the population level for phenotypic and genetic purposes, and, thus, is an evolving research topic. Commonly, mid-infrared spectroscopy is used to predict quality traits in milk samples. In addition to traditional traits (e.g., protein, fat, lactose, and urea contents), also milk characteristics like fatty acid, protein and mineral composition, milk coagulation, milk acidity, melamine content, and ketone bodies can be predicted and used to estimate, e.g., body energy status and methane emissions (de Marchi et al., 2014).

Beyond this, research in the world of “omics” has led to different levels of phenotypes. The study of the omics cascade includes investigations based on metabolomes, proteomes, transcriptomes, and genomes (Figure 1). Metabolomics applied to animal breeding might become a cornerstone of the next generation of phenotyping approaches that are needed to refine and improve trait description and, in turn, to set up innovative breeding value estimations (Fontanesi, 2016). Knowledge of the biological background and genetic architecture of new and conventional traits can be enlarged using metabolomic information, thereby opening opportunities for novel applications in animal breeding. For example, biomarkers for particular physiological states or predispositions of animals can be used to breed more robust animals, as pointed out by Klein et al. (2012) who revealed that the level of glycerophosphocholine in milk samples is a suitable biomarker for the risk of ketosis, and, furthermore, allows selection for metabolically stable cows.

Figure 1. The omics cascade in systems biology approach is linking several levels of biological information of a certain phenotype. Adapted from Schwerin, unpublished.
Based on these findings, Ehret et al. (2015) combined SNP information, routine milk recording data, and, among other metabolites, the concentration of glycerophosphocholine in individual milk samples to predict the cow’s individual ketosis risk by machine learning techniques (Figure 2), and, thereby first showed the potential of these approaches.

Recently, effects of animal production on climate (e.g., emission of methane) have become an important topic, at least in the scientific community, whereas no concrete efforts to include greenhouse gas emissions in breeding goals are currently in progress; however, given that greenhouse gas emissions are a much-debated political topic, studies to include this trait in breeding goals may be conducted in the near future. A series of studies revealed a moderate heritability of methane emissions showing that selective breeding for lower- emitting animals is possible (de Haas et al., 2011; Hayes et al., 2013; Bell et al., 2014). However, many direct phenotyping methods currently available are expensive and time-consuming, and therefore, the number of possible measurements is limited to a few animals. In addition, the gold standard method (respiration chambers) has the disadvantage that animals are measured in an artificial environment. Other methods that can be used in production situations (pasture, feedlot, or dairy feeding station) allow collection of methane samples for only a part of a day and require repeated measurements (Pickering et al., 2015). Given that direct phenotyping techniques are difficult and expensive, it can be assumed that recording on a large scale is only feasible using a proxy or, most likely, a combination of different proxies (i.e., indicators or indirect traits) which are sufficiently correlated to methane output, easily accessible, inexpensive to record, and, if more than one proxy is used, reflect independent sources of variation in methane emission. Currently, methane emission is measured or estimated using a large number of different methods (rarely on the same individuals) and there is lacking knowledge about how these data can be combined to enable genomic selection of cows with lower methane emissions (de Haas et al., 2017). Furthermore, there is no consensus on which phenotype to use for selection purposes: methane in liters per day or grams per day, methane in liters per kilogram of energy-corrected milk or dry matter intake, or a residual methane phenotype, where methane production is corrected for milk production and live weight (de Haas et al., 2017).

Feed intake, a major determinant of methane production (Knapp et al., 2014), is currently discussed as an important new breeding goal trait, and, in contrast to methane, implementation of this trait into modern breeding goals is underway, yet, this is not trivial. Selection for dry matter intake has to be seen in the context of conflictive requirements regarding animal fitness and efficiency (Tetens et al., 2014). Simultaneous selection for low dry matter intake and high milk yield might improve feed efficiency but bears the risk of aggravating the energy deficit postpartum and related health problems (Tetens et al., 2014). Based on longitudinal and multivariate analyses of energy balance, dry matter intake, and energy-corrected milk yield across days in milk, Krattenmacher et al. (2019) were able to demonstrate a clearly lactation stage-specific genetic architecture of energy homeostasis with heritability estimates and genetic correlations that varied in the course of lactation and lactation stage-dependent association signals and concluded that it seems possible to optimize the lactation trajectory of dry matter intake in order to improve animal health in early lactation and feed efficiency in later lactation. This example illustrates that repeatedly recording phenotypes at different production phases, as well as knowledge on genetic correlations among all traits of interest across days in milk, is an important prerequisite for designing balanced breeding goals aiming to fine-tune dairy cattle in a proper way. With more traits, especially more complex traits, setting up reasonable breeding goals is much more sophisticated and often requires innovative approaches.

Need and prerequisites for data pooling and joint research

Breeding programs are often similar across countries, at least with respect to the traits included in the breeding goal. Even for novel traits with predominantly environmental or societal (instead of economical) relevance, efforts to implement these new traits into breeding goals are usually not limited to a single country. When dealing with traits which are difficult or costly to measure (e.g., feed intake/efficiency), in most cases, phenotypes are scarce. In such situations, interdisciplinary and across-country data pooling and research is often the best guarantee to ensure a fast and adequate implementation in breeding programs. However, such initiatives can be hindered...
by different production systems, the use of different protocols or methods for measuring, IP issues, and finally, if breeding companies are involved, by competition between countries. Likewise, setting up suitable agreements for data sharing and usability of the information derived through the analysis of pooled data is often a complicated and time-consuming task.

Shortly after the successful implementation of genomic selection for routinely measured traits, the world’s largest collection of data for feed intake on genotyped dairy cattle has been created within the framework of the global Dry Matter Initiative (gDMI). de Haas et al. (2015) for the first time demonstrated that, provided a multi-trait approach is used, combining similar phenotypes across populations can increase the accuracy of genomic breeding values for important, but rare traits, such as dry matter intake. In the meantime, similar projects combining feed intake data were set up, e.g., the German project optiKuh which has been described in detail by Harder et al. (2019). The optiKuh data set consisted of data from different research farms that agreed to record as homogeneous data as possible over a 2-yr period. Using these data for genomic breeding value estimation, Harder et al. (accepted) observed comparably high reliabilities. This highlights the importance of standardized protocols for data recording, which is also considered relevant for other novel traits such as greenhouse gas emissions. Thus, the development of universal guidelines for recording difficult-to-measure traits is a crucial step toward implementation in breeding programs.

Need for collaborations of different scientific fields

New phenotypes from different sources, the technical revolution, and the need for detailed data on individual animals for precise dairy farming management have led to a dramatic increase in data volume (Figure 3). In the past, the rapidly growing number of genotyped and sequenced animals has already provoked geneticists to strengthen the scientific cooperation with experts from several other disciplines, such as computer science, bioinformatics, mathematics, and statistics. This newly evolved field of interdisciplinary research focuses on estimating more accurate predictive values of phenotypes by using predictive modeling methods such as machine learning (González-Camacho et al., 2018). The field of machine learning offers many flexible algorithms that are suitable for analysis of large, mainly complex data sets. Conventional statistical methods, such as regression, require the assumption of a specific parametric function (e.g., linear, quadratic, etc.), and large quantities of data must be discarded if one or more explanatory variables are missing. Machine learning algorithms, on the other hand, can accommodate complex dependencies among explanatory variables and can function effectively in the presence of missing values for some variables (Caraviello et al., 2006). In addition, network reconstruction methodologies based on systems biology concepts have been applied to disentangle the complexity of different levels of phenotypic information and linking metabolomics with other omics data (Fontanesi, 2016).

Challenges in defining modern breeding goals in dairy cattle

The essence of achieving a breeding goal through elaborated genetic improvement programs is the collection of accurate and comprehensive phenotypic data. The main factors determining the immediate merit of a phenotype are the number of phenotypic records available, the heritability, and the economic value of the trait. Furthermore, the usefulness of a phenotype is affected by several other factors, including the costs of establishing an adapted breeding program as well as the costs for phenotyping and genotyping (Gonzalez-Recio et al., 2014). In this context it is especially challenging to include traits which are related to public goods and, therefore, are of social relevance rather than of direct economic impact for farmers or hard-to-measure traits (e.g., addressing efficiency). In some instances, contingent valuation could serve as a tool to incorporate nonmarketed goods in the breeding goal. With respect to feed efficiency breeding goals have to be treated with some care. It is intuitive to propose saving feed costs by selecting on residual feed intake (Pryce et al., 2015); however, it well might be counterproductive at the sensitive early stage of lactation, when cows experience a negative energy balance and are prone to production diseases. Genetic correlations for feed intake and energy balance on the trajectory of days in milk now allow to select for these lactation stage-specific traits but the according economic weights have to be derived to make full use of these characteristics (Harder et al., 2019; Krattenmacher et al, 2019). To accomplish a broader view next to the monetary outcome on the farm level, the impact on the sector level should be considered and incorporated. Further unsolved problems are interdependencies and causality between traits. For example, on the one hand, high yield in dairy cows may increase susceptibility to certain diseases and, on the other hand, the incidence of a disease may affect yield negative (Rosa et al., 2011). The use of structural equation models can be extremely useful in this context (Wu et al., 2010).

Genomic selection enables efficient selection for hard-to-measure traits, which was previously a limitation. Apart from

Figure 3. Data sources and volumes are steadily increasing, and, as a result, analysis techniques are also getting more complex.
the increased rate of genetic progress for production and quality traits, which allows faster reaction to changes in production circumstances, the huge benefit of this methodology lies in the improvement of expensive-to-measure traits (e.g., methane emission) by transferring genomic knowledge from estimates within comparatively small reference populations to the population level.

Conclusion

Modern dairy cow breeding programs aim to achieve an efficiency optimum in production under several constraints such as the best possible standards of animal health and welfare, together with minimal environmental impact (Figure 4). In the era of phenomics, both research and practical developments are focused on new phenotypes for animal breeding purposes that face these new challenges. It should be noted that there are still large gaps in understanding the biological background and genetic architecture of novel traits. Particularly for poorly defined phenotypes that are difficult or expensive to measure, the relationship between genome and phenotype is far from being understood. Therefore, a strong interdisciplinary collaboration is necessary, both in the development of suitable measuring technologies, operation protocols, and evaluation methods as well as for the analysis of interactions between relevant (possibly unwantedly correlated) traits. Some of the traits which are currently studied might turn out to be not suitable for breeding but can still be useful for management purposes. With increasing number and complexity of breeding goal traits, the design of balanced breeding goals has become more complicated than in the past. However, problems and target directions are similar across different countries, and, thus, pooling of data (e.g., to create sufficiently large reference populations for genomic selection) still enables rapid progress.

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Nina Krattenmacher (née Buttcheret) is a research assistant with Dr Georg Thaller’s group at Kiel University, Germany. During her PhD, she worked on metabolomic and genomic analyses of milk for dairy cattle health. In the framework of a research visit at Scotland’s Rural College, she was also involved in the project “Genetic regulation and genomic selection of energy balance traits in dairy cattle” under Dr Mike Coffey’s supervision. Her research focuses on genetic improvement of difficult-to-measure traits and the use of genomic information for this purpose. She has participated in “gDMI” which was initiated by Dr Rod Veerkamp in 2011 to build the world’s largest reference population for feed intake thereby enabling genomic selection for this trait in dairy cattle. She is a member of the ICAR Feed & Gas Working Group aiming to facilitate proper implementation of dry matter intake and methane output in modern breeding programs.

Georg Thaller is Professor of Animal Breeding at Kiel University, Germany. He did his PhD at the Technical University Munich-Weihenstephan (TUM) under the supervision of Dr Leo Dempke. He was a Postdoctoral Fellow with Dr Ina Hoeschele’s group in the Department of Dairy Science at the Virginia Polytechnic Institute & State University in Blacksburg, Virginia (United States) and was among the first to apply Bayesian methodology for QTL mapping. At TUM he was research assistant with Dr Ruedi Fries at the Animal Breeding Institute implementing statistical approaches to utilize molecular genetic markers in livestock. He has made major contributions to the understanding of complex traits and, more lately, to the successful implementation of genomic selection in Germany. His current research focuses on exploiting high-density panels to unravel the genetic architecture and genomic phenomena in major livestock species and on the improvement of functional traits, especially in dairy cattle.
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Feature Article

Incorporating temperament traits in dairy cattle breeding programs: challenges and opportunities in the phenomics era

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Introduction

Since domestication, cattle populations have been intensively selected for various behavioral traits based on phenotypic characteristics, especially those related to handling ease.

Implications

• Cattle temperament can be described based on reactivity to human handling, novel objects, or stressful situations. Despite its economic and welfare implications, there is a lack of objective indicator traits and limited incorporation of temperament in dairy cattle breeding programs.
• The increased intensification of dairy production systems, including the adoption of robotic milking machines and automatic feeders, is contributing to a growing interest to selectively breed for improved temperament and milking efficiency.
• The main challenges for wider incorporation of temperament in dairy breeding programs are the definition of indicator traits, large-scale phenotyping, lack of understanding of the genetic background of the traits, and availability of the economic values of temperament.
• Genomics combined with high-throughput phenotyping will be essential to optimize selection for improved temperament traits in dairy cattle.

Indicators of Dairy Cattle Temperament

Temperament can be defined based on the animal’s reactivity to human handling and response to novel objects or stressful situations. The assessment of cattle temperament can provide important information on the physical, physiological, and psychological state of the animal, including immunity, stress level, and metabolic processes. For instance, milking temperament has been associated with udder health (Santos et al., 2018), survival (Cue et al., 1996), rectal temperature and milk yield (Chang et al., 2019), reproductive performance (Sewalem et al., 2011), milking speed (Kramer et al., 2013), performance in automated milking system (AMS, Wethal and Heringstad, 2019), and conformation traits (Cue et al., 1996; Sewalem et al., 2011).

Understanding the genetic relationship between temperament and other important traits in dairy cattle has been a
research focus for a very long time. Based on a detailed literature search, “production,” “physiological parameters,” and “genetic parameters” were the main terms associated with research in the area of dairy cattle temperament (Figure 1).

In general, inclusion of a novel trait in a breeding program (e.g., temperament) requires several steps: 1) the breeding goal needs to be defined, which can be done by any component of the dairy industry (e.g., farmer, retailer, and consumer); 2) an indicator trait needs to be chosen (e.g., milking temperament score on a scale from 1 to 5) based on the practically and economic feasibility of phenotypic recording; 3) the heritability and genetic correlations with traits already under selection need to be accurately estimated; and 4) the economic value of the trait and selection index weighting needs to be determined. This process is not static and depends on the availability of novel technologies to better measure indicator traits, advanced statistical and bioinformatic tools and methods, and refinement of breeding goals by the industry.

**Behavioral tests**

Behavioral reactions that are indicators of temperament can be measured during stressful handling procedures and human–animal interactions. In general, fear of humans, curiosity to novelty, and adaptability to handling are the main variables considered in behavioral tests. For instance, flight distance can be assessed by measuring the distance that a human can approach a stationary cow before she moves away. This distance can also be converted to speed by measuring distance and time, that is, flight speed. A large flight distance or high flight speed indicates a poorer temperament or “fearful” animal. Furthermore, the closest distance that a cow voluntarily approaches a stationary human has been described as approach distance. This indicates the animal’s confidence in the human as well as the animal’s exploratory ability. Tilbrook et al. (1989) also measured the time and number of interactions with humans in an approach test. In addition to a novel human test, novel areas, or object tests have been used to evaluate the animal’s neophobia (Foris et al., 2018). These temperament tests are more suitable for small-scale applications (e.g., research or small farms). However, they are labor intensive in large dairy cattle operations. Usually, temperament metrics based on restraining the cows during weighing, feeding or milking, crush score (Gibbons et al., 2011), milking temperament score or flinching, stepping, and/or kicking score are often recorded on a subjective matter (e.g., scales from 1 to 3, 1 to 4, 1 to 5, 1 to 9, or 1 to 50; Sewalem et al., 2010; Sutherland and Dowling, 2014; Stephansen et al., 2018). For instance, Chang et al. (2019) evaluated the response of Chinese Holstein cattle on a 3-point scale (1: calm, 2: intermediate, and 3: temperamental) when measuring cows’ rectal temperature in a restraint test. These tests are reasonably safe, quick, and simple to implement on-farm, but subjective (i.e., dependent on the training of farmers or technicians).

**Milking temperament based on AMS**

AMS or milking robots are becoming popular around the world. There are over 38,000 AMS operating in worldwide dairy farms (Sandgren and Emanuelson, 2017), with the greatest proportion located in Northern Europe (Barkema et al., 2015) and North America. There are countries (e.g.,

Figure 1. Frequency of (a) topics and (b) indicator variables associated with dairy cattle temperament, based on scientific reports published between 1966 and 2019. Consistency: repeatability across time and events in temperament traits. GWAS, genome-wide association study; AMS, automatic milking system.
the Netherlands and Norway) with 30–45% of cows milked through AMS and this is predicted to increase up to 50% in the next few years (Tine, 2017). In the United States and Canada, there are over 3,000 AMS stations. A significantly growing number of AMS in Canada was reported (Barkema et al., 2015), and more than 11% of milk recorded herds used AMS in 2018. In China, the adoption of AMS is low due to the large average herd size (~851 cows; DAC, 2019) and relatively low labor costs.

With the increasing use of AMS, the accuracy of traditional milking temperament scoring might decrease due to a reduced interaction between animals and farmers (Stephansen et al., 2018) and therefore, better indicators of temperament are needed. Unsuccessful milking and poor milkability influence the capacity and efficiency of AMS and consequently, the farmers’ profitability. The number of rejected and incomplete milking, kickoffs, and teats not found are promising indicators of temperament in AMS (Wethal and Heringstad, 2019). There are several advantages of assessing temperament based on AMS information: 1) it does not interfere with the farm routine activities and no additional labor is required; 2) it generates standardized (and objective) measures across individuals and large amount of repeated records per animal, which are crucial for more accurate genetic analysis; and 3) it has greater phenotypic variability when compared with subjective scoring systems. Therefore, variables collected in AMS are promising indicator traits to improve milking temperament.

**Additional Data Sources**

The use of novel technologies and data sources is essential to standardize temperament assessment across farms, and thus improve genetic progress for dairy cattle temperament. This includes technological devices such as video-imaging, activity-collars (Figure 2a), pedometers (Figure 2b), and metabolite profiling.

**Activity monitors**

Activity monitors (e.g., pedometers, collars, and microchip sensors) can be used to detected many behavioral and physiological activities (e.g., reproduction and feeding behavior). For instance, activity-collars infer animals’ movement through an accelerometer usually placed on the animal’s neck. Another example of activity sensor is a molded microchip coupled to an identification ear tag, which assesses ear temperature, rumination activity, eating behavior, and cow activity. Another example is a sensor node installed on the animal’s neck to capture body temperature, respiration rate, and movement. Temperament can be assessed through regression of animal locomotion (e.g., active or resting), blood pressure, temperature, respiration rate, and other variables already accessed from activity monitors. In this context, developing algorithms to predict temperament based on high-throughput phenotypes (e.g., pedometers, activity-collars, and microchip sensors) are an emerging area of research.

**Video-imaging**

The cost-effectiveness and accessibility of video technology and computer image processing methods have created opportunities to better measure dairy cattle temperament. Video-imaging analysis has been used for several purposes in cattle, including lameness detection and carcass traits. This is an emerging research area that is expected to grow substantially over the next few years, especially in line with the development of machine learning methods.

**Physiological biomarkers**

Biomarkers are also another group of variables that can be used to indicate cattle temperament. For instance, biomarkers linked to stress level (e.g., heart rate, eye temperature, and cortisol levels) have been correlated with temperament traits (e.g., chute test, separation, and restraint test) in German Simmental and Charolais cattle (Geburt et al., 2015). More reactive dairy animals have been shown to have increased plasma and salivary cortisol concentrations and higher cardiac autonomic responsiveness to transrectal examination than less reactive cows (Kovács et al., 2016). Metabolite profiling (e.g., serum) is also another important method to identify novel indicators of temperament. For instance, physiological parameters of cows with

![Figure 2. Technological devices such as (a) activity-collars and (b) pedometers.](image)
divergent temperament have been shown to differ, including hormones, neurotransmitters, neuromodulators (Réale et al., 2007), and concentration of prefrontal cortex and serum metabolites (Brand et al., 2015). Furthermore, temperamental dairy cows have been reported to have elevated cortisol concentrations and endogenous opioids in plasma, reduced oxytocin concentrations, and increased heart rate in unfamiliar milking surroundings. Furthermore, Chang et al. (2019) reported a moderate genetic correlation between temperament score and rectal temperature.

**Statistical Approaches to Analyze Temperament Traits**

Temperament traits are usually measured in categorical levels (discrete or noncontinuous variables). Some alternatives to analyze these traits are: 1) to assume that the categories follow a continuous distribution when phenotypic records are well distributed across four or more categories and then use the traditional mixed model equations (MME); 2) to convert categorical numbers to scaled values (e.g., probabilities), which can then be considered as a continuous trait and analyzed through the traditional MME; 3) to use a Bayesian threshold model, which is the most recommended alternative for analyzing categorical traits; and 4) to fit a multiple trait model and each phenotypic category is considered as a different trait. In addition, continuous phenotypes (e.g., flight speed) can be analyzed using the traditional MME. High-throughput phenotypes from precision technologies (e.g., milking robots) and video-imaging can be analyzed using more sophisticated machine learning approaches such as deep learning and neural networks.

**Genetic Background of Temperament Traits**

In general, dairy cattle temperament is a moderately heritable trait with a wide variation in heritability estimates depending on the indicator trait (0.002–0.47). Figure 3 presents 42 heritability estimates published between 1960 and 2019. Continuous phenotypes usually have higher heritability compared with subjective scores (Stephansen et al., 2018). In addition, phenotypes categorized in a smaller number of levels, such as 1–3, also have lower heritability than 1–5 or 1–9 subjective assessments. The method used for the analyses can also yield different estimates. For instance, general temperament scores (scale from 1 to 3, assessed during rectal temperature measurements) in 6,586 Chinese Holstein had a heritability of 0.024 based on a linear model using AI-REML, 0.033 when fitting a Generalized Linear Mixed Model, and 0.046 when using a threshold model in a Bayesian approach (unpublished data).

The most important characteristics of temperament phenotypes are situational and temporal repeatability. Consistency or repeatability indicates that variation among and within individuals is largely maintained across repeated measurements, which can be evaluated based on repeatability estimates (Figure 4) and intraclass correlation coefficients. With the exception from AMS-derived-traits, the interval between phenotypic recording varies from 1 mo to 1 yr. The repeatability estimates of temperament are mostly moderate, but with a wide range (0.04–0.56). Compared with other temperament trait groups, the repeatability of three farmer-assessed temperament traits were relatively high (0.32–0.56; Erf et al., 1992; Kramer et al., 2013). Wethal and Heringstad (2019) revealed that the repeatability of milking temperament (incomplete milking, teats not found, rejected milkings, and kickoffs) in AMS range from 0.25 to 0.43 in Holstein, which indicates the value of repeated measures for genetic evaluation of temperament traits.

Some factors influencing or linked with repeatability estimates are: breed, age, environment, habituation, learning ability, and evaluator. Cattle temperament measurements at 6–8 mo of age have been reported to be quite stable over time (Lansade et al., 2008). However, animals may become less responsive or more sensitive to the stimulation if measured repeatedly. Therefore, habituation should be avoided in novel tests.

Understanding the genetic association between temperament and other important traits is paramount for sustainable long-term selection. The average absolute values of genetic correlation between temperament and six other traits (i.e., health, production, reproduction, growth, milkability, and conformation) were calculated based on 15 dairy cattle studies published between 1960 and 2019 (Figure 5). In summary, temperament was observed to be favorably correlated with longevity (Sewalem et al., 2010). The genetic correlation between
calving-to-first service and temperament was close to zero (Chang et al., 2019), whereas a strong favorable genetic correlation between calving ease (0.48 ± 0.18) and number of services (0.56 ± 0.50) with temperament score was observed (Chang et al., 2019).

Regarding production traits, it is plausible that calm cows take less time to be milked, which agrees with the genetic correlations between milk speed and general or milking temperament ranging from 0.23 (Cue et al., 1996) to 0.57 (Visscher and Goddard, 1995). A moderate and favorable genetic correlation (~0.4) between fat-corrected milk yield and temperament was observed (Erf et al., 1992). However, a weak positive relationship between temperament score and milk yield has also been reported (Erf et al., 1992; Chang et al., 2019). There could be a competitive relationship for allocation of resources between production and temperament traits. Hence, more studies are needed to better understand the genetic relationships and underlying biological mechanisms of temperament and other relevant traits.

The majority of molecular genetic studies of behavioral traits have been focused on mice, drosophila, and humans. There are relatively few studies detecting candidate genes and Quantitative Trait Loci (QTL) in dairy cattle. This includes 115 QTLs for 15 cattle behavior traits (AnimalQTLdb, 2019), including 14 QTLs (Table 1) identified in Holstein (Hiendleder, 2003; Kolbehdari et al., 2008) and 71 QTLs in Holstein and Charolais crossbred animals (Gutierrez-Gil et al., 2008; Friedrich et al., 2016). The largest number of QTLs significantly associated with temperament was observed on BTA29 and overlapping QTLs were found on BTA10 and BTA29 for different behavioral tests (Gutierrez-Gil et al., 2008; Friedrich et al., 2016). Genome-wide association studies and functional validation of candidate genes using large genomic and phenotypic datasets are still needed.

**Incorporation of Temperament Traits in Breeding Programs**

Over the past decades, milk production and conformation have been the main breeding goals in Chinese dairy cattle. Milk yield, fat yield, protein yield, type, foot and leg, mammary system, and somatic cell score are the traits currently included in the China performance index (CPI). However, temperament is still not part of the national genetic evaluation system in China. In Australia and Nordic countries, milking temperament is already integrated into selection indexes (Table 2). The relative economic weight for temperament in the Australian
There are various reasons limiting the incorporation of temperament into selection indexes in dairy cattle, including difficulties to collect large-scale and standardized phenotypes and precise estimation of economic value for the trait. A more objective indicator of temperament is still required. In national genetic evaluations, subjective scoring milking temperament is still the most common indicator of temperament. In this context, Réale et al. (2007) categorized temperament traits into the following groups: shyness–boldness, exploration, avoidance, activity, sociability, and aggressiveness. Moreover, the correlation between different indicator traits has been reported to be low and some of them are even negative (Sutherland and Dowling, 2014). For instance, Purcell et al. (1988) reported a low genetic correlation (0.12) between milking temperament and flight distance and Kramer et al. (2013) reported a Pearson correlation between milking temperament and aggressiveness’s EBVs equal to 0.28. Consequently, a composite index that encompasses several temperament traits may be more appropriate than a single-trait. Analogous to overall type, one can put different weight on traits such as milking temperament, human–animal interaction, aggressiveness, and neophobia, according to their importance to specific production systems. In addition to developing selection indexes based on economic values of temperament, one could use the approach of desired gains.

As previously mentioned, technological equipment will help in the definition of more precise temperament phenotypes. It is also worth highlighting that there should be no collinearity between selected traits. However, the use of different temperament sources might not be feasible in Chinese dairy farms at the moment due to the large average herd sizes and low labor costs. The three most common types of milking parlors in China are herringbone parlors, parallel parlors, and rotary parlors, instead of AMS, so milkers are usually very familiar with cows. Type appraisers can also be in charge of the assessment of temperament.

Another challenge for including temperament in dairy breeding programs is the variety of environmental factors across production systems. Therefore, genotype-by-environment (G × E) interactions should not be ignored. There are a lack of reports on G × E for temperament in AMS vs. conventional milking systems, grazing vs. confinement, and small-holders vs. intensive and large-scale farms. However, Van der Laak et al. (2016) reported no G × E for milking temperament between farms with grazing or indoor production systems in the Netherlands.

Selection indexes are usually derived based on economic values, which are considered as the marginal value of one unit change in the respective trait. Economic values are calculated based on a bioeconomic model by computing the production profit. The main economic and welfare losses of temperamental cows are a reduction in management efficiency (increased labor) and injuring themselves or human

### Table 1. Genomic regions associated with temperament traits in Holstein cattle

| Chromosome | Position | Candidate gene | Reference |
|------------|----------|----------------|-----------|
| BTA4       | 40,499,442 bp | NRCAM | Kolbehdari et al. (2008) |
| BTA5       | 136 cM    |                  | Hiendleder (2003) |
| BTA13      | 60,045,226 bp | CSTF1 | Kolbehdari et al. (2008) |
| BTA18      | 105 cM    |                  | Hiendleder (2003) |
| BTA19      | 37,837,691 bp | CACNA1G | Kolbehdari et al. (2008) |
| BTA22      | 46,425,659 bp | CACNA1D | Kolbehdari et al. (2008) |
| BTA23      | 13,897,540 bp | BYSL | Kolbehdari et al. (2008) |
| BTA26      | 34,495,734 bp | SLC18A2 | Kolbehdari et al. (2008) |
| BTA29      | 20 cM     |                  | Hiendleder (2003) |
| BTA29      | 23,068,761 bp | LOC782544 | Kolbehdari et al. (2008) |
| BTA29      | 30,954,390 bp | NTM | Kolbehdari et al. (2008) |
| BTA29      | 36,737,805 bp | CCDC88B | Kolbehdari et al. (2008) |
| BTA29      | 38,944,167 bp | DPP3 | Kolbehdari et al. (2008) |
| BTAX       | 9 cM      |                  | Hiendleder (2003) |

### Table 2. Description of the national genetic evaluation for dairy cattle temperament in different countries

| Countries | Indicator trait | Breed(s) | Start time | Economic weight in total merit index |
|-----------|----------------|----------|------------|-------------------------------------|
| Australia | Scored on a 1–5 scale: the middle value is optimal | HOL, JER, GUE, RDC | 1985 | 3.51 (8.72%) |
| Canada    | Scored on a 1–5 scale: nervous to calm | HOL, AYR, GUE, JER, BS, CAN, MS | – | 0 |
| Denmark, Sweden, and Finland | Scored on a 1–9 scale | HOL, JER, RDC | 1988 | HOL: 0.04 (1.33%) RDC: 0.03 (1.08%) JER: 0.03 (1.06%) |
| France    | Scored on a 1–5 scale | HOL, MON, NOR, BS | 1996 | 0 |
| United Kingdom | Ease of milking | HOL | 1993 | 0 |
| New Zealand | Scored on a 1–5 scale: vicious to placid | HOL, JER, RDC | 1987 | 0 |
| Norway    | Scored on a 1–3 scale: easy to uneasy | NR | 1987 | 0.42% |
| The Netherlands | Scored on a 1–9 scale | – | 1994 | 0 |

HOL, Holstein; JER, Jersey; GUE, Guernsey; RDC, Red Dairy cattle; AYR, Ayrshire; BS, Brown Swiss; CAN, Canadienne; MS, Milking Shorthorn; MON, Montbéliarde; NOR= Normande; and NR, Norwegian Red.
Temperament in dairy cattle is moderately heritable and genetically correlated with milkability, health, longevity, and reproduction traits. The currently collected phenotypes are moderately repeatable, indicating the need to collect multiple records on each individual. It is still challenging to estimate the economic value of temperament and therefore, its inclusion in breeding programs. There is ongoing research in the area of temperament phenomics and various new measurement alternatives are being investigated, including video-imaging, pedometers, activity-collars, and AMS-derived traits. We expect that over the next few decades, there will be a greater focus on genomic selection for functional traits and temperament based on refined phenotypes will be a major one.

**Conclusions**

Temperament in dairy cattle is moderately heritable and genetically correlated with milkability, health, longevity, and reproduction traits. The currently collected phenotypes are moderately repeatable, indicating the need to collect multiple records on each individual. It is still challenging to estimate the economic value of temperament and therefore, its inclusion in breeding programs. There is ongoing research in the area of temperament phenomics and various new measurement alternatives are being investigated, including video-imaging, pedometers, activity-collars, and AMS-derived traits. We expect that over the next few decades, there will be a greater focus on genomic selection for functional traits and temperament based on refined phenotypes will be a major one.

**Supplementary Data**

Supplementary data are available at *Animal Frontiers* online.

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*Conflict of interest statement.* The authors declare that they have no competing interests.

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The future of phenomics in dairy cattle breeding

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Abstract

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 et 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.

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).

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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...
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...
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 of this new information?”
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.uscdb.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.

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Opportunities and challenges of phenomics applied to livestock and aquaculture breeding in South America

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Introduction

The world population is expected to reach 9.1 billion people by 2050 (FAO, 2019) and the largest area of populational growth is projected to occur in developing countries. Consequently, there is an urgent need to increase food production in these regions based on an efficient exploitation of a wide range of genetic resources (species, breeds) and production systems. In this context, South America is one of the major livestock and aquaculture producers in the world, especially beef, pork, poultry, South American camelids, tilapia, and salmon. As in other developing regions, the great productivity is accompanied by a large diversity of production systems (e.g., intensive, pasture-based, mountainous regions, and small holders), climatic and geographical conditions, availability of natural resources (e.g., water and forage), and genetic resources (numerous species, breeds, and populations). In order to meet the growing food demand and be competitive on a global scale, there is a need to increase production efficiency and therefore, long-term sustainability. This can be achieved through selective breeding by identifying animals with greater genetic merit for the traits of interest. Sustainable genetic improvement can only be achieved through accurate, routine recording, and proper use of at least phenotypic and pedigree information.

The success of selective breeding is highly dependent on the quality of the phenotypes recorded and their degree of representation of the biological and physiological mechanisms underlying the breeding goals of interest. Development of equipment and efficient measurement protocols (e.g., automatic milking systems, visual computing, infrared spectroscopy, biosensors and external sensors, and satellite-based images), the availability of new “-omics” technologies (e.g., genomics, metabolomics, proteomics, transcriptomics), and new statistical and bioinformatic tools, have enabled the livestock and aquaculture industries to speed up the rates of genetic progress per unit of time.

High-throughput phenotyping is a reality in livestock and aquaculture production systems in developed countries

Implications

• South America is a major food producer in the world, but there is still a large potential to optimize production efficiency and the industries’ long-term sustainability through the incorporation of modern phenotyping technologies, advanced breeding schemes, and better management strategies.
• There is a great diversity of livestock production systems (e.g., pasture-based, mountainous regions, feedlots) in South America, which makes it more challenging to collect certain phenotypes and also requires accounting for genotype-by-environment interactions in genetic evaluation models.
• There is a lack of large-scale and well-structured breeding programs for the majority of livestock and aquaculture species, mainly due to the low investments in pedigree recording, genotyping, and high-throughput phenotyping in commercial and small holder farms.
• As phenotype and pedigree recording and genotyping are still challenging in South America, data sharing across breeding associations and research institutions is paramount, especially for building training populations for genomic selection.

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Breeding program). However, numerous attempts to establish representative large-scale phenotype recording systems applied to breeding programs in South American countries have failed for various reasons. This includes poorly structured data collection systems, temporal discontinuity of data recording, extensive or small holder farms (more difficult to collect phenotypes), and disinterest or lack of financial resources from the industry to invest in large-scale and continuous phenotyping projects. Furthermore, the existence of genotype-by-environment interactions (GxE) plays a major role in the successful use of genetic material developed in other countries, which then requires the implementation of regional breeding programs. The main objectives of this paper are: 1) to succinctly review the current phenotypic collection systems coupled to breeding programs in South America, with a greater emphasis on Brazilian beef cattle and Chilean aquaculture; and 2) to present the opportunities and challenges in the area of phenomics to advance genetic improvement in livestock and aquaculture in South American countries.

**Beef Cattle**

South America is a major beef cattle producer, with approximately 25% of the worldwide cattle population (FAOSTAT, 2017). The cattle industry is based on a plethora of systems varying from small-holder farmers with low-productivity levels, basic management issues (e.g., nutritional, disease control) and minimal use of technology, to very large producers with intensive adoption of precision livestock technologies. These production systems include divergent genetic resources, with a predominance of Zebu cattle (Bos taurus indicus) in tropical regions (e.g., Brazil, Paraguay, Colombia, Venezuela, Peru, and Bolivia) and Taurine breeds or crosses in sub-tropical regions (e.g., South of Brazil, Uruguay, Argentina, and Chile). The three main beef cattle producers in South America are Brazil, Argentina, and Uruguay. Beef cattle production is pasture-based, with certain regions also finishing animals in feedlots. Nellore (Zebu cattle) is the main beef breed raised in South America.

The main current breeding goals, according to its relative importance on economic indexes, are: growth (particularly growth rate and cow maturity weight) and reproduction. New initiatives are evaluating the inclusion of feed efficiency and meat/carcass quality (ultrasound-based carcass measurements) as index components. In order to meet such goals, there are around 10 Nellore breeding programs currently established in Brazil, evaluating over 0.5 million cows per year (Carvalheiro et al., 2014). There are breeding program initiatives for other breeds as well (e.g., Angus, Montana Tropical Composite, Braford, and Hereford). The data collection system in most breeding programs is mainly performed by technicians that periodically visit herds spread out across the country (mainly to evaluate animals by visual scoring), in addition to data transfer uploaded into independent databases (owned by each breeding program).

**Undergoing research in the area of beef cattle phenomics**

As previously mentioned, improved feed efficiency is a key breeding goal. However, the cost and difficulty to quantify individual feed intake, especially in pasture-based systems, have limited the inclusion of this trait in breeding programs. Over the past decade, various research groups in South America have concentrated efforts on identifying the best indicator variables of feed efficiency, unveiling the genetic relationship with traits already evaluated, and investigating the feasibility of developing a training population for genomic selection (Santana et al., 2014; Silva et al., 2016). Recent studies have shown that a 35-d test with automatic tools for weight collection can attain sufficient phenotyping precision for traits considered in the Brazilian genetic evaluation of Nellore cattle (Torres-Junior et al., 2018).

Automated feeding systems have been implemented mainly in feedlots or research farms (www.intergado.com.br/intergado-efficiency/; https://growsafe.com/about/). For instance, data from experimental farms have been used to derive feed efficiency-related traits, such as RFI, feed conversion ratio, average daily gain, and dry-matter intake (Silva et al., 2016). Furthermore, these systems are usually coupled with other innovative tools (e.g., sensors and scan cameras) to measure (or predict) additional variables to be potentially included in breeding programs. These traits include in vivo carcass yield, body condition score, meat quality (Gomes et al., 2016), and behavioral traits (e.g., feeding behavior, temperament, and social dominance).

Over the past years, various studies have focused on identifying more specialized phenotypes related to reproductive traits. For instance, the number of antral follicles influences heifer pregnancy rate and the success of reproductive technologies (ovum pick-up, in vitro fertilization), which are widely used in Brazil (Oliveira-Junior et al., 2017). Testicular hypoplasia, a disorder attributed to incomplete development of the germinal epithelium of the seminiferous tubules has also been studied, which enabled the identification of important genomic regions affecting this reproductive disorder (Neves et al., 2019).

Animal resilience and adaptation is paramount in South American livestock production systems. For instance, tick infestation causes large economic losses and welfare issues, especially in Taurine populations. Therefore, infrared thermography was investigated as a potential tool to quantify the number of ticks in the body surface of Brangus cattle (Barbedo et al., 2017). However, the results were not satisfactory as the suggested approach only captured a small contrast between ticks and the animal hair coat. Alternative adaptation traits include scoring (subjective) protocols for traits such as prepuce (navel) length, hair length, ocular pigmentation, and tick resistance (based on tick count in one side of the animal body). These indicator traits were shown to be heritable and can be implemented in genomic selection schemes (Piccoli et al., 2019).
Zebu breeds are known for having lower meat quality (marbling and tenderness) compared to Taurine animals. However, there is enough genetic variability to enable selective breeding (Magalhaes et al., 2018). As meat quality traits are usually difficult to measure (slaughter of potential selection candidates), genomic selection will play an important role. Furthermore, near-infrared reflectance spectroscopy (NIRS) has been investigated as a non-destructive alternative to predict meat quality traits in Nellore cattle (Magalhaes et al., 2018). NIRS was shown to be useful to predict tenderness and meat color, but not indicated for subjective traits such as marbling. The genomic background of meat fatty acid profiling has also been investigated as an additional breeding goal in Nellore (Lemos et al., 2016; Feitosa et al., 2019).

Better assessments of carcass yield and meat quality traits are still needed. Another potential alternative could be through collaborations with commercial slaughterhouses. However, there is limited interest from the beef industry on sharing and using such data for breeding purposes. In this context, image analysis and visual computing could be promising tools to predict carcass yield in different ages. Sensors (e.g., Microsoft Kinect—MK) can be applied for this purpose. MK can minimize imaging interferences due to the ambient light through deep mapping image technology (Gomes et al., 2016). Subsequently, as shown in Figure 1, these image sections from the width of chest, thorax, and abdomen; body length; and, dorsal height can be used to predict carcass yield in cattle (as in Nellore, Gomes et al., 2016).

A common challenge associated with pasture-based production systems is the long period of food scarcity caused by the seasonal patterns of rainfall, and high temperature and humidity. In this context, genetic selection for improved animal resilience and adaptation in such environments is gaining importance (Carvalheiro et al., 2019). Another major issue is GxE, especially because of the outdoor production systems (pasture- or feedlot-based). Additionally, the feasibility of using datasets recorded in a particular environment to improve the genomic predictive performance and subsequent selection of breeding bulls in untested environments has become an important topic of research (Cappa et al., 2017). For instance, one could be interested in using proven bulls from Argentina to breed (through artificial insemination—AI) with cows raised in harsh environmental conditions in Brazil. Environmental covariables can be used to predict the performance of individuals in untested locations. This can be achieved through the use of geographical information systems (GIS) as environmental index in GxE models. In our conceptualization of GxE based on environmental index obtained from GIS, a particular geographical area is considered as a geoprocessing environment corresponding to a grid of pixels, and for any single environmental variable, a value can be assigned to each pixel. The value distribution of a particular environmental variable in this set of pixels is termed “envirotype” for each geographical area (van Eeuwijk et al., 2019).

Challenges and opportunities in beef cattle phenomics

There are several challenges for wider adoption of phenotyping tools in beef cattle, but at the same time, modern technologies are becoming more accessible and producers more interested in their adoption. For instance, Baruselli et al. (2017a) suggested a more aggressive strategy including the concentration of pregnancies early in the breeding season to improve reproductive efficiency. These authors and other research groups (e.g. Pugliesi et al., 2019) recommended the use of AI in all females at the beginning of the breeding season, and an early identification of non-pregnant cows, using color Doppler ultrasonography with subsequent AI.

The DNA pooling technique (Bell et al., 2017) is another technology that could be used to build a training population for genomic selection and to identify genomic regions affecting fertility traits in beef cattle. This strategy requires the identification of animals with divergent phenotypes (e.g. females pregnant at the first compared to those nonpregnant after three rounds of AI) and the genotyping of pooled biological samples of females clustered in the same phenotypic group, instead of genotyping each single female. The DNA pooling strategy could be also applied for other purposes, such as in

![Figure 1. An example of body measurements taken from a Nellore calf using the Microsoft Kinect tool.](image1)

![Figure 2. A scheme illustrating the phenotypic clustering of animals based on average daily gain. Biological samples from each group would be pooled together and genotyped as a single sample.](image2)
feedlot systems (phenotype extremes defined based on high or low growth rate; Figure 2). Furthermore, Brazilian start-up companies have recently been granted funding for the development of 3D cameras to predict cattle live weight, and to install automated scales and image analysis in feedlot operations to determine the optimal slaughter time (https://olhododono.agr.br/; https://techagr.com/). This could be used to identify the selection candidates (e.g., sires) more related to each DNA pool, assuming that all selection candidates are individually genotyped. Through this approach, phenotypes from commercial farms (or slaughter plants) could contribute to improve the performance of genomic evaluation for certain traits, as shown in Figure 2.

As there are limited financial resources and infrastructure for collecting phenotypes and individual genotyping in developing countries, the establishment of collaborations for data sharing is of utmost value. For instance, recent efforts in Brazil have been made to join existing genomic datasets for imputation purposes (https://bv.fapesp.br/pt/auxilios/97280). This will substantially reduce genotyping costs.

Dairy Species

Dairy cattle are the main milk producing species in South America, but sheep, goats, and buffaloes are also raised for similar purposes. Milk production in South American countries are mainly characterized by pasture-based production systems. However, an intensification trend has been observed after the inclusion of several large dairy operations, characterized by advances in nutrition and management practices. Girolando, a composite dairy breed developed in Brazil by crossing Holstein and Gyr cattle, is the main genetic resource used for milk production in the tropical regions of Brazil (Canaza-Cayo et al., 2018). Dairy goats (especially Alpine and Saanen breeds; Figure 3) have, to a lesser extent, economic importance in certain regions of South America, including the Northeast and Southeast of Brazil. Buffaloes are also raised for milk production (and cheese-making), especially in the Southeast and North of Brazil, Bolivia and Colombia. There are some dairy sheep producers, mainly in Argentina, Uruguay, Chile, and Brazil. However, these are usually small-holder farmers with no routine recording of phenotypes, with exception of a few research flocks.

Over the past decades, selection for improved milk production (total yield) was the main breeding goal, as the large majority of producers were paid only based on milk volume. Genetic improvement for additional traits was also achieved by importing semen from bulls (or other dairy species males) selected for additional traits including milk composition, conformation, health, and reproductive ability. In the past two decades, the breeding goals in South America have been redefined to include other traits. Currently, the main trait categories are as follows: milk production and composition (especially fat and protein), udder health (based on somatic cell count), fertility and reproduction (e.g., age at first parity and interval between parities), workability (especially milking temperament in dairy cattle populations with genetic contribution from Zebu breeds), and conformation traits. For instance, the Brazilian Girolando and Gyr national breeding programs currently report breeding values for milking ease and temperament, 305-d milk yield and composition (fat, protein, and total solids), age at first calving and conformation. Adaptation and environmental resilience are also key breeding goals in dairy species raised in the tropical regions. The main indicator traits are heat tolerance, survival, and resistance to endo- and ectoparasites. However, genetic selection for these traits is still incipient.

Even though the breeding goals for dairy goats are similar to those described above, phenotypic selection for morphological traits was heavily weighted as there were no production or reproduction records and pedigree information. In Brazil, milk recording in dairy goats started only in 2005 (Facó et al., 2011). In addition to milk yield, other breeding goals include lactation length and reproductive traits (e.g., kidding interval and age at first kidding). The high adaptability of buffaloes to tropical regions has contributed to the population expansion in South America, especially in the Amazon region and Southern Brazil (>3 million animals). There are also some incipient breeding programs for buffaloes and the main breeding focus is milk yield, lactation persistency and milk composition.

Research challenges and opportunities in dairy cattle phenomics

The dairy industry payment system is an important challenge for dairy improvement. For instance, mastitis (clinical and subclinical) is a great welfare and economic issue in South America (Goncalves et al., 2018) as producers are usually paid only based on total milk yield and penalized based on microbiological aspects of the milk. This has started to change in some regions, but still needs more research and investment. The usefulness of mid-infrared (MIR) analysis has been investigated as a phenotyping tool. For instance, Petrini et al. (2016) predicted milk components in Brazilian Holstein based on MIR and validated the results through gas chromatography. Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry

Figure 3. A dairy goats herd composed by Alpine and Saanen animals, which are raised in a semi-intensive production system.
(MALDI-TOF) has been offered as a service by some laboratories and also at the research level as an alternative method for bacteria identification. On-farm culture systems, aiming to fast identify milk pathogens, have been implemented on several herds across South America.

Systems for monitoring individual feeding and drinking behavior have been recently tested in dairy cattle (e.g., Oliveira et al., 2018). The frequency and duration of each visit can be captured (feed and water), as well as feed and water intake. Correlations between the true data (obtained via video observation and manual weights) and predicted parameters were extremely high (0.917 for duration of feed visit, and >0.963 for all others). Computer vision is an expanding area in precision livestock, which enables identification of individual animals and posterior assigning of phenotypic records (e.g., eating time) to each individual (Figure 4).

There are several challenges involving dairy production in South America. First, there is a lack of centralized institutions integrating on-farm data collection, laboratory analysis of milk samples, and technical assistance to producers. Second, similarly to other regions around the world, the low profit margin and unstable milk prices make it difficult for producers to commit to investments in data recording. In most large dairy operations, protein and fat are usually controlled at the bulk tank level and not individually per cow. Somatic cell score, as part of a management protocol, is generally evaluated once a month in most herds. The lack of adequate payment and incentive to producers with regards to milk composition does not incentivize phenotyping and selection for such traits. However, there are some cases of success regarding data collection and genetic evaluations. For instance, the Holstein Association of Paraná (Parana, Brazil; www.apcbrh.com.br) provides a well-organized infrastructure to coordinate data collection, including laboratory milk analysis and genetic evaluations.

**Aquaculture**

The aquaculture species with more advancements in terms of the implementation of genetic improvement approaches are salmonid and tilapia. The main trait included in the breeding goal for all aquaculture species is growth rate (Ponzoni et al., 2011; Lhorente et al., 2019). In addition, some other desirable traits are related with increased survival (resistance against viral, bacterial, and parasitic agents) and carcass-quality traits (fillet yield, fat content, and composition and flesh color; Gjedrem, 2012).

In general, growth-related traits can be directly measured in the selection candidates. However, disease resistance and carcass-quality traits are typically measured using sib-testing strategies (Yáñez et al., 2014). For instance, phenotypes for resistance to specific pathogens are usually recorded in highly controlled conditions using large-scale experimental challenges performed on thousands of full- and half-sibs of the selection candidates. Additionally, carcass-quality phenotypes are recorded in harvested fish at the processing plant using similar family-based designs (i.e., full- and half-sib testing).

The main drawback of phenotyping for disease resistance using experimental challenges is related to the correspondence between the traits measured in controlled versus field conditions, which might not be high enough, thus decreasing the rate of genetic progress achievable. In addition, the high cost associated with these experiments needs to be considered. With regards to the traits measured in processing plants, these are typically obtained using nonautomated measurements, which makes the procedures very labor-intensive, and in some cases biased due to human error. Therefore, the main opportunities for high-throughput phenotyping in aquaculture are related to the automation of phenotyping procedures. For instance, technologies combining automated image recording and computational algorithms that can predict individual body mass, sanitary condition (e.g., quantifying skin lesions and ectoparasite counting) and survival status from field conditions (i.e., sea sites, ponds, and tanks) will allow recording of tens of thousands of phenotypes per day (Føre et al., 2018). This will not only allow capture of longitudinal phenotypic data for growth and disease resistance traits but also recording data in the same environment in which the fishes are actually produced. Similar image-based approaches can be used at the processing plant to avoid manual manipulation and recording, aiming at having highly automated and digital phenotypes for carcass quality traits. Altogether, these approaches will improve accuracy and repeatability of phenotypic measurements, allowing continuous monitoring in the field and larger sample sizes, with a positive impact on fish welfare given a reduced need for fish management and experimental trials.

**Other Species**

The majority of swine and poultry raised in commercial farms in South America are from genetic resources developed in other countries, especially in North America and Europe.
For minor species (e.g., quail in Brazil), there are examples of ongoing breeding program initiatives and national technologies mainly related with automatic feeding intake (to quantify feed efficiency). According to Caetano et al. (2017a), improving feed conversion by identifying animals that require the same amount of feed but have higher body weight gain is key in modern quail breeding. Feeding represents the main production cost in meat quail (Caetano et al., 2017b), especially as protein is the highest cost component in their diets. Therefore, one possible strategy is to select quails based on their genetic performance over different protein levels in the diet. In summary, the investments in producing automatic feeders for quail is a good example of measuring novel traits with high economic value.

Many international genetic companies have applied modern phenotyping tools to obtain information on heat stress and behavior in pigs. This information is used at nucleus herds to obtain complementary traits when calculating selection indexes. The success of this strategy is maximized by using genomic information from both nucleus and commercial animals. In addition to the species mentioned above, meat sheep and goats, and South American camelids (mainly alpacas and llamas) are also of considerable importance to livestock production in South America. This is especially found in Uruguay, Southern Brazil, and Argentina (largest meat sheep producer region in South America), small-holder farmers in the Northeast and Central regions of Brazil (meat sheep and goats), and in the Andes Mountain region in Bolivia and Peru (small camelids). The main breeding goals in meat or dual-purpose (meat and wool) sheep include the following: wool (or fiber) weight and quality (e.g., dirty fleece weight, fiber diameter, clean fleece weight, and length of wick), body weight and growth rate (birth weight, weaning weight, and mature weight), carcass (e.g., loin-eye area, backfat thickness, leg score, primal cuts, and carcass weight), reproductive (e.g., litter size, age at first lambing, and lambing interval), and resilience (e.g., endoparasite resistance, disease resistance, maternal behavior, survival, longevity) traits. Meat sheep production systems in South America usually have low adoption of technologies with reduced to no phenotype recording, with the exception of Uruguay, Argentina, and some isolated regions of Brazil. In Brazil, there is a large number of locally developed sheep (e.g., Santa Ines hair sheep) and meat goats (e.g., Moxoto) breeds. The meat goat breeding goals are similar to those described above for meat sheep, with exception of wool/fiber traits. Phenotypic and pedigree recording in small ruminants is still limited in South America, but there are some breeding program initiatives with recent success.

**Conclusions**

South America is a major livestock and aquaculture producer in the world. However, production efficiency is still lower than what could be achieved. This is partially due to the reduced adoption of phenotyping technologies, advanced breeding schemes and efficient management strategies. Furthermore, there is a great diversity of production systems, which makes it more challenging to collect certain phenotypes and also requires accounting for GxE interactions in genetic evaluation models. More recently, governments and industries are investing more in research and extension activities and there are clearer breeding goals, but the organization of data collection schemes and data sharing still needs to be substantially improved. We expect that phenomics will play an important role in improving livestock and aquaculture production efficiency in South America over the next few decades, considering that the industry continues (or increases) investments in phenotyping, pedigree recording and genotyping.

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