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Invited review: Using data from sensors and other precision farming technologies to enhance the sustainability of dairy cattle breeding programs

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ABSTRACT

The increased uptake of sensor technologies and precision farming tools for the dairy cattle sector is enabling real-time monitoring of animal health, welfare, and productivity. These digital advancements provide high-frequency, objective, and large-scale phenotypic data for breeding purposes. This review explores the potential of sensor-derived data to improve genetic and genomic evaluations in dairy cattle and outlines key challenges, opportunities, and approaches associated with their implementation. While these data streams have great potential for genetic evaluations, their integration into national and international breeding programs remains limited due to fragmentation across sensor brands, lack of standardization, and challenges related to data accessibility, data access and portability rights, business interests, and governance. A crucial aspect of leveraging digital technologies in dairy cattle breeding is data harmonization and integration. We highlight the importance of establishing standardized data collection and data sharing protocols, implementing robust quality control and data cleaning methodologies, as well as defining novel sensor-based traits and estimating their genetic background. In this context, we compiled heritability estimates for novel traits derived from data recorded by sensors and other technologies in dairy cattle populations. The development of phenomics in breeding programs, which involves integrating multisource data—including sensor-based, genomic, and management information—will be key to accelerating genetic progress, especially for traits related to animal welfare, health, resilience, and efficiency. This review presents a roadmap for the effective use of sensor-derived data in genetic evaluations, advocating for centralized data infrastructures, transparent data-sharing agreements, and the role of different stakeholders from academia and industry, including organizations such as the International Committee on Animal Recording (ICAR) in establishing global standards and guidelines. By addressing these challenges, dairy breeding programs can fully harness precision dairy farming technologies to enhance production and environmental efficiency, improve animal health and welfare, and drive sustainable genetic advancements in the dairy cattle sector.
Key words: genomic selection, genetic parameters, heritability, novel traits, precision livestock farming

INTRODUCTION

Sensor systems and other precision dairy farming technologies can partially replace human labor, contribute to improving the quality of life of dairy farmers (Tse et al., 2017; Lovarelli et al., 2020; Hogan et al., 2022), enhance labor output and labor cost over time (Liu et al., 2023), increase reproduction efficiency (Reith and Hoy, 2018), contribute to improving animal health and welfare

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(Dawkins, 2021) and productive efficiency (Simitzis et al., 2021), optimize on-farm management, and increase the long-term sustainability of dairy farms (Gargiulo et al., 2018; Kaur et al., 2023). On-farm sensor systems collect large amounts of data, which are only shared to a limited extent and with the farmer's consent outside the farm (e.g., with milk recording organizations, breeding organizations, milk processors, or other stakeholders along the dairy value chain). Other data frequently collected on farms include documented treatments with related diagnoses and hoof-trimming registrations; results of laboratory tests from biological samples, such as milk and blood; data from breeding and performance recording organizations; and data from feed and dairy processing operations (Steeneveld and Hogeveen, 2015). Although large amounts of sensor data are being collected on-farm, the data generated is so far not being fully used across herds, such as in national genetic evaluations, breeding programs, quality assurance programs by dairy processors, or by other actors along the dairy value chain. The value of the datasets generated can be maximized through data integration. Data integration in precision dairy farming refers to the process of combining and synchronizing data from multiple sources (e.g., sensors, automated systems, and management software) into a unified platform. Therefore, the main goals of this review are to (1) discuss the challenges and opportunities for integrating and leveraging data sets from sensor systems and other technologies for improving dairy genetic and genomic evaluations; (2) present a roadmap for the standardization and integration of data from digital technologies for use in dairy cattle breeding programs; (3) describe the process of novel trait development; and (4) provide examples of potentially useful sensor-derived traits, along with available heritability estimates when available, for inclusion in breeding programs. This work is part of a joint initiative between the International Committee of Animal Recording (**ICAR**; www.icar.org) and the International Dairy Federation (**IDF**; https://fil-idf.org) through the ICAR Functional Traits Working Group (**FTWG**) and the IDF Standing Committee of Animal Health and Welfare in collaboration with international experts from academia and industry organizations (Egger-Danner et al., 2024). The main aim of this initiative is to promote the integrated use of data from sensors and other precision technologies and derived traits along the dairy value chain with the goal of improving the sustainability of dairy cattle production.

SENSORS AND OTHER TECHNOLOGIES USED IN DAIRY FARMS

Recent advancements in sensor systems and other precision technologies (digital technologies) have enabled the development of various tools for precision dairy farming that support farmers and their advisors in monitoring the health and welfare, performance, reproductive status, and environmental efficiency of dairy animals. A wide range of technologies are commercially available and have been implemented in dairy farms around the world to support herd management and animal monitoring (Stygar et al., 2021; Linstädt et al., 2024). In addition to perform tasks such as milking cows (i.e., by automated milking systems [**AMS**], also known as milking robots; Marino et al., 2021), sensor technologies can be used for automatically recording various physiological parameters (Cerri et al., 2021; Tsai et al., 2021), animal behaviors (Halachmi and Guarino, 2016), performance- and efficiency-related characteristics (e.g., milk production and composition, milking speed, feed efficiency), physical attributes (e.g., body condition, BW; Silva et al., 2021), environmental footprint (e.g., methane emission; Tullo et al., 2019), and many others. Some technologies are used for applications at the herd or group level, whereas others monitor individual animals. The sources of data for genetic evaluations are mainly those technologies that record data on individual animals.

A plethora of equipment is available on the market, which is usually supported by algorithms and computing tools to provide summarized and processed information (Rutten et al., 2013). For instance, accelerometers placed on or in different parts of the animal's body (e.g., leg, neck, ear, reticulorumen, vagina, tail) can recognize rumination, eating, lying, standing, and other behaviors, and provide alerts and other information to the dairy farmers and their possible advisors. Various sensor systems developed and used in dairy farms have been widely described in the literature (Schillings et al., 2021; Silva et al., 2021; Stygar et al., 2021; Hut et al., 2022; Singh et al., 2022; Džermeikaitė et al., 2023; Linstädt et al., 2024; Lovarelli et al., 2024).

Sensors and other technologies generate large amounts of heterogeneous data (high recording frequency combined with measurement over extended periods of time and in different formats). In many cases, only summarized or aggregated data based on the needs of the users is made available to the users through proprietary algorithms and web tools. Datasets from different technologies and technology providers tend to be of incompatible formats, which make it difficult for dairy producers (and their advisors or partners) to integrate the data from multiple sources in comprehensive tools and analyses. These circumstances may lead to the creation of data silos on dairy farms, hindering the usefulness of the complementary datasets for timely decision making. Furthermore, these datasets usually need to be processed using statistical methods and often require high performance computers for analyzing them comprehensively. In this context, modern dairy farms require a data-oriented and technology literate labor force to take full advantage of the on-farm sensor technologies and datasets available.

On-farm sensors are used for improving herd management (Gargiulo et al., 2018; Liu et al., 2023), calving or estrus detection (Reith and Hoy, 2018; Szenci, 2022; Umaña Sedó et al., 2024), and identification of cows needing attention or treatment (Džermeikaitė et al., 2023; Lemmens et al., 2023). In addition, the datasets generated can be used for supplementing genetic and genomic evaluations. Sensor systems and other technologies are potentially valuable sources of data for genetic and genomic evaluations because data are collected automatically, more objectively (higher precision and less human errors), and continuously (or in high frequency). Furthermore, as these digital technologies have been used for many years in various farms, data may already be available for a large proportion of the population of cows that is currently included in the genomic evaluations. The automatically recorded data can also be helpful for the definition and large-scale phenotyping of proxies for traits that are costly to record or have low measurement frequencies, such as functional traits (Egger-Danner et al., 2015; Brito et al., 2020). More accurate phenotypes translate into greater genetic progress of the target traits and breeding goals (Goddard et al., 2016; Jones and Wilson, 2022).

ROLE OF PHENOTYPING IN DAIRY CATTLE BREEDING PROGRAMS

Different sources of data have been used in breeding programs over time, including data from sensors and other technologies (e.g., Rojas de Oliveira et al., 2024). The usefulness of variables recorded by sensor systems for breeding purposes depends on several factors. Derived traits must exhibit sufficient phenotypic variation, be heritable and repeatable within the target population, capture the biological mechanisms relevant to the breeding goal of interest or show a genetic correlation with the target or breeding goal trait, be measured reliably and frequently over an extended time period (i.e., longitudinal measurements), and be objectively recorded in a standardized manner. Data collected by several precision technologies meet many of these criteria, but are not well documented in the literature.

In addition to measuring the traits of interest (or auxiliary traits), there is a need for recording environmental (systematic) effects influencing the phenotypic records to allow appropriate statistical modeling. When performing genetic and genomic evaluations, fitting as many as possible significant systematic effects (commonly known as “fixed effects”) in the models removes nongenetic influence on the traits resulting in more accurate breeding values. Examples of systematic effects include cow parity, age at measurement, contemporary group (e.g., concatenation of herd, year, and season of calving), measurement time, sensor type, climatic variables, and others. Digital technologies can also be useful for recording variables allowing to derive some of these systematic effects.

Another important point to emphasize is the value of having many animals from the same herds with measurements for multiple variables (i.e., various sensor types on the same animal or close relatives as well as direct and indirect traits related to the breeding goal). Having the same animals with phenotypic records for all (or most) traits facilitate the estimation of phenotypic and genetic covariances between traits. This is important for accurate estimation of the genetic correlations among all measured traits which is needed for the proper design or refinement of selection indexes.

The effectiveness of dairy cattle breeding programs depends on large-scale and diverse datasets for multiple traits measured ideally throughout the life of a dairy animal or across prolonged periods. This includes routinely recorded datasets (e.g., records from dairy farmers through DHIA, veterinarians, claw trimmers; farm management systems; pedigree and conformation variables from breed associations), data from sensors and other precision technologies, multi-omic intermediate data such as genomics, metabolomics (from biological samples, such as milk, saliva, and blood), microbiome, transcriptomics (gene expression), epigenomics, proteomics, lipidomics, and many others. Full integration of these data into a common platform has a huge potential for optimization of dairy cattle genetic evaluation and management purposes. The individual reliability of breeding values relies, among other factors, on the amount of phenotypic information available for the animals themselves and on genetically related individuals. As digital technologies enable the collection of more objective data in higher frequency as compared with traditional data collection schemes (e.g., test-day records), (genomic- or pedigree-based) EBV for traits derived from precision technologies have the potential to be more reliable, and consequently, greater genetic progress can be obtained for such traits (Poppe et al., 2019; Pedrosa et al., 2023; Schodl et al., 2024b).

CHALLENGES IN COLLECTING AND USING DATA FROM SENSORS AND OTHER TECHNOLOGIES FOR BREEDING PURPOSES

Despite the great and clear potential of sensor data for genetic and genomic analyses, several challenges must be overcome. The main challenges described here in more details is not an exhaustive list. First, the global market of digital technologies for the dairy sector is very fragmented. Already in 2020, there were 67 different providers of various sensor technologies, including 37 suppliers of accelerometer-based technologies and 13 producers of milking robots (Stygar et al., 2021). The increasing number of start-ups with focus on precision livestock farming imply that the overall figures today might be even higher. Uniform standards exist for some of these technologies, but only for limited devices and technology-derived variables. For instance, ICAR has developed standards and recommendations for testing, approval, and periodic checking of milk recording devices including milk yield and composition (ICAR, 2020). However, there are no guidelines for using records from accelerometer-based technologies, making it more difficult to use sensor data from more than one brand in genetic evaluations.

For better use for genetic evaluations, sensors and other technologies should be tested in more diverse farming environments (i.e., not only in experimental farm conditions), across different management systems (e.g., intensive dairy production, pasture-based systems, freestall and tiestall housing) and geographical locations with diverse climatic conditions, in different breeds, and in animals of different ages and in varied physiological stages (e.g., lactation stage, reproductive stage). As this testing is time consuming and costly, collaboration among academia and manufacturers is essential for improving the quality assessment of sensor technologies and for increasing the accessibility of independent validations of commercially available sensors.

In most cases, comprehensive information on the sensor systems is lacking, which complicates their evaluation and application for breeding purposes. This challenge is exacerbated by the wide variety of approaches employed to address similar problems or collect similar types of data, leading to inconsistencies in methodologies and outcomes. For instance, many sensors are available for measuring activity and rumination time, but they may use different algorithms, perform different data editing and quality control, or may capture different information, and consequently, the phenotypic records obtained may be quite different even when multiple sensors are used in the same animals (Mayo et al., 2019). In many cases, "gold standard" variables or procedures to validate the sensors are lacking (or the gold standard approach may be time or cost prohibitive), contributing to unsatisfactory agreement among sensors recording the same type of information. Some variables are easier to validate (e.g., milk yield, milk composition, SCC), whereas others are more complex such as animal activity across sensors and alerts based on multiple and different parameters depending on the sensor brand.

Many data providers exist (e.g., manufacturers of sensor systems, data integration organizations), and often producers are unsure of which sensor to use, as validation and comparison among the sensor systems are currently lacking. This is an important challenge for genetic evaluations, especially national genetic evaluations that combine data from multiple farms, as the data from different types of sensor technologies or sensor technologies targeting the same condition but provided by different brands may represent different traits. Therefore, several analyses (e.g., estimation of genetic correlations between traits recorded by different sensor types) must be performed before merging datasets on a routine basis. As a first step, it is important to enhance the transparency of the testing conditions (e.g., farm type, breed, life stage of the animals) and, subsequently, to clarify the potential and limitations of each commercial technology for genetic evaluations that are made available in the market. In the case of wearable sensors, the animal's body location where the sensors are attached may influence the data recorded and must accordingly be indicated. Additional validation of existing sensor systems is an important research task to be completed.

In general, sensor systems consist of measuring devices, algorithms, and computer applications or interfaces, which are often proprietary information. Sensor outputs can be measurements of certain individual conditions, or outputs based on multiple parameters, given as indexes or alerts (e.g., for estrus or health issues). As sensor systems were developed to support farmers in managing their herds, they have been optimized to provide actionable information. However, the use of sensor data across herds and along the dairy value chain (e.g., for genetic evaluations) will require more information or additional variables and definitions. There is significant lack of background information on the data generation procedures and detailed metadata with information on the type of data recorded, units, and resolution or frequency of the records (Rutten et al., 2013). In many cases, manufacturers may only provide information on a few variables of greater interest to the dairy farmers (e.g., estrous alert), but the data used for generating these alerts could be of great value for deriving traits for inclusion in genetic evaluations. Many providers of sensor technology do not have (or provide) any information about the variables that are being collected by the sensors (e.g., variable definition, units, plausible ranges, calculation approach). This results in data being underused or misused as communication between academia or data analysts working with the farmers and manufacturers may not always be straightforward. The publication of data user guides associated with each digital technology would be of great value for geneticists and other data analysts. It is worth noting that manufacturers of sensor systems may be willing to share additional data for research purposes but may be more restrictive when sharing data publicly or for other commercial purposes. To promote data sharing (e.g., for genetic evaluations), clear communication between stakeholders and development of interinstitutional guidelines and agreements are of great importance. Organizations such as ICAR can develop standards and guidelines to technically facilitate data exchange, thus creating an environment that facilitates negotiations and agreements for commercial use between different parties.

Sensors and algorithms are believed to have been improved over time, which is positive because the data generated is expected to become more accurate. However, there tends to be a lack of recording (or sharing) of important information such as algorithm or sensor updates that may affect the accuracy of the data being recorded on individual animals. If not recorded and accounted for in the statistical models, this could result in artificial differences in the phenotypic measurements collected over time (i.e., biased phenotypic trends). When these changes are homogeneous across all animals in the same contemporary group (animals with similar conditions; e.g., concatenation of farm, calving season, and calving year), the lack of updates' information may be less of an issue. However, when farmers combine animals with older and recent versions of the equipment in the same contemporary group, the lack of information on these versions (or updates) could result in less accurate breeding values. Even if this information is shared, geneticists or other data analysts need to carefully adjust their pipelines for the genetic analyses to include the changes made by the data providers.

As dairy farms are using many sensors and technologies, there are consequently different data sources with multiple data retrieval protocols (e.g., through application programming interface, data provider's website, farm back-ups). Some additional challenges for retrieving and merging the datasets include (1) datasets are generated in heterogeneous data formats; (2) sensors may record data with different frequencies (e.g., every 2 h vs. daily summaries); (3) data sources may use different animal identification systems; (4) datasets generated are in many cases proprietary implying limitations of the access to the raw datasets (defined here as unprocessed data as originally recorded by the sensors); (5) the scripts and pipelines developed may be nontransferable across data sources; (6) lack or poor internet connectivity in rural areas, which makes it more difficult to transfer data from the farms to data processing stations; (7) on-farm hardware and software may be outdated, making the herd management and sensor systems unstable and data extraction more difficult; (8) datasets can be very large (e.g., video data) and require a lot of computing power for storage and analyses, which can become expensive in the long term; and (9) data provider platforms may only store the data at a lower resolution (e.g., daily sum or averages instead of per-visit measurements). All these challenges contribute to increasing data silos within and between farms and to an underutilization of the information contained in these datasets that could be used for herd management and breeding.

Within different research projects, data integration platforms have been set up including, for example, the Purdue Animal Science Data Ecosystem (Boerman et al., 2025), DairyBrain (Cabrera et al., 2020), and Gigacow (Klingström et al., 2022). Within other projects such as D4Dairy (www.d4dairy.com; Egger-Danner et al. 2022a,b), routine data exchange pipelines have been elaborated and implemented in the central cattle database and manufacturers. In collaboration between DHIA, breeding organizations, and manufactures routine data exchange pipelines have been or are being established and integrated data are being made available. Examples are the Nordic Cattle Database (www.nordicebv.info) and the Central Cattle Database Cooperation between Germany and Austria (www.rdv-gmbh.net). The International Dairy Data Exchange Network (www.idden.org) is also working on simplifying data flow with one seamless interface connecting dairy stakeholders. Furthermore, many companies are working on this area, including Iyotah Solutions (www.iyotah.com/), Vyla (www.vyla.com/), Dairy Data Warehouse (dairydatawarehouse.com), Join-Data (www.join-data.nl), Dairy Performance Network (www.dairyperformancenetwork.com/), AgriGates (https://agrigates.io/), Connecterra (www.connecterra.ai/), and others.

Once data collected by sensor technologies have been received, extensive preprocessing and cleaning of the data are often needed to ensure its usability and reliability (van der Voort et al., 2021; Schodl et al., 2024b). Limited data editing and cleaning protocols are available in the scientific literature. Data scientists may also have access to different types of data requiring different handling. Raw data, defined here as unprocessed or minimally processed data directly collected by sensors and monitoring devices before any form of cleaning, filtering, analysis, or interpretation within the sensor systems will likely vary much more than summarized or processed data. The absence of standardized protocols for editing sensor data undermines the comparability and reliability of the results generated. Therefore, we encourage the development of automated pipelines for data collection, processing, editing, analytics, and data visualization.

Last, but certainly not least, a need exists for continuous dialog between stakeholders along the dairy value chain from sensor manufacturers to farmers and researchers from different organizations to create a common understanding on the potential and value of sensor data for genetic evaluation. Such dialog will facilitate the definition of suitable data sharing models, which ideally, will increase the benefits for all stakeholders along the dairy value chain, while strengthening academic and industrial research and innovation. Addressing all these challenging topics is essential to enhance the consistency, quality, and utility of sensor-based systems for genetic and genomic evaluations as well as for many other purposes.

DATA CLEANING, EDITING, AND QUALITY ASSURANCE

Considering the growing amount of sensor devices, applications, data, and computational methods, the need for comprehensive data cleaning procedures has grown to ensure data quality, accuracy, and utility. Despite established data cleaning protocols in bioinformatics (e.g., Chicco et al., 2022) and health informatics (e.g., Van den Broeck et al., 2005) or for the use in routine genetic evaluation and tools provided by DHI and breeding organizations (see ICAR, 2022), comparable guidelines specific to high-resolution dairy sensor data remain limited. Based on experiences within the D4Dairy project (https://d4dairy.com; Egger-Danner et al., 2022a,b) and review of relevant literature, Schodl et al. (2024b) proposed a 5-step framework for cleaning sensor data, including

1. Validating the data merging process. Accurate alignment between animal identifiers and sensor data is critical. Errors such as nonunique device by animal combination, broken sensors, and time zone mismatches must be identified and corrected, if possible. It is recommended to consult with digital technology companies for information on proper alignment, as well as algorithm learning periods.
2. Understanding the data. This step involves identifying the type of data (e.g., raw sensor data or processed data retrieved from interfaces), its nature including units and whether it is a single point measurement or an aggregated value, and sampling rates. Proper data visualization is recommended to facilitate detection of patterns, distributions, or anomalies.
3. Checking data completeness. Missing data causing gaps in time series is a common issue and often caused by sensor malfunctions, low battery, or poor connectivity. Depending on the subsequent analyses, missing data may require interpolation, imputation, or exclusion. Conversely, duplicate or inconsistent timestamps should be resolved to maintain data integrity.
4. Evaluating data plausibility and detecting outliers. This step may be the most critical one requiring well-considered decisions by the data user. Outlier detection may be based on biologically meaningful ranges, cross-checks using additional information, if available, statistical thresholds (e.g., ± 3 SD from the mean), or advanced modeling techniques such as Dynamic Linear Models incorporating Kalman filters (e.g., Stygar et al., 2017) or utilizing the co-dependency of data quality and model robustness (e.g., Papst et al., 2021). Regarding the management of outliers, attention should be paid to avoid removal of genuine outliers that may provide critical insights.
5. Addressing technology-related noise. Inconsistencies in the data may be caused by sensor drift, calibration issues, and hardware or software updates. Information on updates and handling of drift and calibration issues by the sensor company may be helpful but not necessarily easily available. Indications to look for in the data are for example the introduction of new variables, different temporal resolutions, and sudden or persistent changes in scale.

In addition to these steps summarized by Schodl et al. (2024b), broader aspects such as the purpose and context of data analyses, as well as their thorough documentation. Data for applications in herd management may have different requirements than those for breeding. As an example, if different versions of a software were used in a certain farm, but all animals from the same contemporary group had the same sensor version, the data would be useful for genetic purposes as geneticists are interested in differences among animals from the same group rather than the absolute values. Conversely, alerts generated by sensors are important for management purposes, but for genetic evaluations, the continuous variable used for generating the alerts (e.g., activity level to predict estrus events) might be preferred because of its independence from the quality of would already be useful even if the system's algorithm used for generating the alerts was not highly accurate.

Data cleaning process is both costly and time consuming (Wang and Wang, 2020). However, some savings can be achieved by broad implementation of automated procedures. Regarding dairy cows, automatic sensor data cleaning pipelines have been successfully applied to improve the accuracy of positioning algorithms (Pastell et al., 2018), to detect leg problems using load sensors (Pastell et al., 2008), or even to track mastitis control options (Rustas et al., 2024). Furthermore, automatic repair methods exist for non-sensor data, but the authors are not aware of their application in dairy science (for instance, filling in missing information on breed or herd number). Therefore, in the future, more standardized approaches should be considered and (open source) data cleaning solutions should be made available.

Table 1. Heritability estimates for automatically recorded indicators of health in dairy cattle populations[1]

Trait	Sensor type	N	Breed	h^2	Reference
EC	AMS integrated sensor	1,714	Holstein	0.22 ± 0.04	Dechow et al. (2020)
Daily average EC	AMS integrated sensor	8,455	Holstein	0.48 ± 0.10	Lu et al. (2024)
EC at milking session 1	AMS integrated sensor	8,455	Holstein	0.46 ± 0.10	Lu et al. (2024)
EC at milking session 2	AMS integrated sensor	8,455	Holstein	0.47 ± 0.10	Lu et al. (2024)
EC at milking session 3	AMS integrated sensor	8,455	Holstein	0.47 ± 0.10	Lu et al. (2024)
EC	AMS integrated sensor	4,280	Holstein	0.46 ± 0.02	Medeiros et al. (2024)
EC	AMS integrated sensor	4,507	Holstein	0.38 to 0.49	Pedrosa et al. (2023)
EC	AMS integrated sensor	1,899	Holstein	0.38 ± 0.01	Piwczyński et al. (2021)
EC, front left	AMS integrated sensor	922	Holstein	0.46 ± 0.09	Santos et al. (2018)
EC, front right	AMS integrated sensor	922	Holstein	0.44 ± 0.09	Santos et al. (2018)
EC, rear left	AMS integrated sensor	922	Holstein	0.37 ± 0.08	Santos et al. (2018)
EC, rear right	AMS integrated sensor	922	Holstein	0.38 ± 0.09	Santos et al. (2018)
Overall EC	AMS integrated sensor	922	Holstein	0.53 ± 0.09	Santos et al. (2018)
EC	AMS integrated sensor	1,486	Holstein	0.36 ± 0.04	Sitkowska et al. (2024)
EC, mean	AMS integrated sensor	4,714	Norwegian Red	0.35 ± 0.03	Wethal et al. (2020a)
EC, maximum	AMS integrated sensor	4,714	Norwegian Red	0.23 ± 0.02	Wethal et al. (2020a)
Blood in milk	AMS integrated sensor	1,714	Holstein	0.09 ± 0.03	Dechow et al. (2020)
Smoothed milk BHB values (parity 1)	Herd Navigator (BHB)	794	Nordic Red	0.09 ± 0.07	Häggman et al. (2019)
Smoothed milk BHB values (parity 2)	Herd Navigator (BHB)	794	Nordic Red	0.07 ± 0.07	Häggman et al. (2019)
Milk temperature	AMS integrated sensor	1,899	Holstein	0.41 ± 0.01	Piwczyński et al. (2021)
SCS	AMS integrated sensor	1,899	Holstein	0.36 ± 0.01	Piwczyński et al. (2021)
Mastitis susceptibility	AMS integrated sensor	1,791	Holstein	0.07 ± 0.03	Welderufael et al. (2017)
Mastitis recovery	AMS integrated sensor	1,791	Holstein	0.08 ± 0.03	Welderufael et al. (2017)
Log-transformed online cell count	AMS integrated sensor	1,490	Norwegian Red	0.09 ± 0.03	Wethal et al. (2020a)

[1] AMS = automated milking system; EC = electrical conductivity. Values for h^2 are reported as ± SE or range.

DERIVING NOVEL TRAITS FROM SENSORS AND OTHER TECHNOLOGIES

Sensors and other technologies provide an opportunity for recording such traits in a more frequent and accurate manner and could, consequently, fasten the rate of genetic progress for these key breeding goals. Ideally, the derived traits should have sufficient phenotypic variation, be heritable and repeatable, capture the biological mechanisms of interest (or be genetically correlated with the breeding goal trait), be clearly defined and evaluated in a standard way across the population being jointly genetically evaluated, and be recorded routinely and in large-scale at a low cost per data point. First, it is essential to obtain detailed documentation on the recording methods and units of the variables of interest. This information, which needs to be provided by the manufacturers of sensors or technologies, includes how data are recorded and the handling of missing values (e.g., zeros, blanks, or other symbols). Accurate documentation ensures consistency and reliability in subsequent analyses. When working with the same variables recorded by sensors from different brands, it is important to assess the variance of the variables and not merely correct for the mean effect by including the brand or company as a fixed effect. This evaluation ensures comparability across different sources and informs whether data from different sensors can be combined effectively. In some cases, similar types of data may represent different (but correlated) traits. Once the data are harmonized, traits of interest should be derived. It is also critical to define the gold standard measures of the breeding goal of interest to facilitate comparisons with derived traits.

After the breeding goals and the potential data sources (with the selection criteria variables) have been clearly identified (e.g., improved fertility based on variability in activity level recorded by activity monitors; Heringstad and Wethal, 2023), statistical models must then be developed to test systematic effects that influence the trait(s) of interest. These effects should be incorporated into genetic models to ensure accurate predictions of breeding values. Understanding the influence of each systematic effect (e.g., parity, lactation stage, herd, season, diet, reproductive stage, housing time) on traits can also inform future management decisions; for instance, assessing the effect of ambient temperature and humidity on rumination patterns could guide feeding strategies. Modeling systematic effects that significantly influence the target trait is enabled by integrating sensor data into the established data infrastructure for dairy cattle. This highlights the need for data integration as systematic effects are usually recorded in herd management software and not directly by the sensors. Finally, variance components and genetic parameters, including heritability and genetic correlations among all derived and existing traits, should be estimated for all derived traits. The accuracy of (G)EBV and the potential re-ranking of selection candidates should also be assessed to ensure robust decision mak-

Table 2. Heritability (h^2) estimates for cow behavioral traits derived from automated milking systems (milking robots)

Trait	N	Breed	h^2 ± SE	Reference
Choice consistency score (5–50 DIM, primiparous)	730	Holstein	0.04 ± 0.06	Løvendahl et al. (2016b)
Choice consistency score (5–50 DIM, multiparous)	1,231	Holstein	0.05 ± 0.04	Løvendahl et al. (2016b)
Choice consistency score (51–110 DIM, primiparous)	730	Holstein	0.11 ± 0.08	Løvendahl et al. (2016b)
Choice consistency score (51–110 DIM, multiparous)	1,231	Holstein	0.07 ± 0.05	Løvendahl et al. (2016b)
Choice consistency score (111–215 DIM, primiparous)	730	Holstein	0.14 ± 0.08	Løvendahl et al. (2016b)
Choice consistency score (111–215 DIM, multiparous)	1,231	Holstein	0.07 ± 0.04	Løvendahl et al. (2016b)
Choice consistency score (216–305 DIM, primiparous)	730	Holstein	0.08 ± 0.07	Løvendahl et al. (2016b)
Choice consistency score (216–305 DIM, multiparous)	1,231	Holstein	0.02 ± 0.03	Løvendahl et al. (2016b)
Knock off (binary)	922	Holstein	0.03 ± 0.03	Santos et al. (2018)
Log-transformed handling time	4,883	Norwegian Red	0.07 ± 0.02	Wethal and Heringstad (2019)
Number of kick-offs	4,883	Norwegian Red	0.06 ± 0.01	Wethal and Heringstad (2019)
Number of kick-offs	1,714	Holstein	0.08 ± 0.02	Dechow et al. (2020)
Proportion of milkings with kick-offs	4,883	Norwegian Red	0.13 ± 0.03	Wethal and Heringstad (2019)
Preference consistency score	4,249	Holstein	0.09 ± 0.01	Bérat et al. (2025)
Preference consistency score	2,258	Holstein	0.07 ± 0.02	Løvendahl and Buitenhuis (2022)
Preference consistency score	2,407	Jersey	0.13 ± 0.03	Løvendahl and Buitenhuis (2022)
Temperament	72,683	Norwegian Red	0.05 ± 0.01	Wethal et al. (2020b)
Time profile (profile of the diurnal milking time)	2,258	Holstein	0.11 ± 0.02	Løvendahl and Buitenhuis (2022)
Time profile (profile of the diurnal milking time)	2,407	Jersey	0.04 ± 0.02	Løvendahl and Buitenhuis (2022)

ing in breeding programs. When the same variable (e.g., rumination time) is recorded by different sensors, before merging all the data for genetically evaluating the animals for a single trait, one should assess the genetic correlation between the traits derived from different sensors and the phenotypic records recorded by different sensors should only be merged and considered as the same (or similar) trait when very high (e.g., >0.90) genetic correlations are observed between them. Otherwise, the records from different sensors should be evaluated as different and correlated traits in the genetic evaluations. Additional genomic analyses could be performed to better understand the underlying mechanisms influencing the derived traits such as GWAS and post-GWAS analyses to identify candidate genes and metabolic pathways associated with the target traits.

In the past few years, various sensor-based traits have been derived and some of them have already been included in corporate or national selection indexes. In the subsequent sections and in Tables 1, 2, 3, 4, 5, 6, 7, 8, and 9, we describe examples of novel traits that have been derived based on data from sensors and other technologies along with their heritability estimates (when available) and respective references. In general, higher heritability estimates, and accordingly higher accuracies of (G)EBV, can be expected for sensor-based traits than for traditionally recorded traits, which relates to the different levels of phenotyping accuracy and frequency.

Health and Welfare

Several animal welfare and health parameters are currently collected routinely through technologies for the primary purpose of on-farm monitoring of animal status.

Body Temperature. Wearable sensors such as rumen boluses, ear tags, or skin-mounted devices are commonly used for continuously monitoring body temperature (Woodward et al., 2024). Body temperature data are stored on different resolutions (e.g., every 5 or 10 min) and analyzed to detect deviations from normal temperature ranges, indicating potential health issues such as infections or heat stress (Woodward et al., 2024). Body temperature data enable early detection of diseases, allowing for prompt interventions. In addition, body temperature data are used for monitoring heat stress to adjust management practices accordingly and also for breeding for improved heat tolerance, as discussed below. Body temperature in dairy cattle is heritable (Luo et al., 2021a) and influenced by key genes (Luo et al., 2021b), suggesting potential for selection. A challenge with body temperature is that it varies depending on the sensor location on the animal's body (Bewley et al., 2008a). Further research investigating the genetic background of sensor-based body temperature variability in dairy cattle is still needed.

Heart and Respiration Rate. Wearable biometric sensors, such as heart rate monitors and respiratory sensors, collect data continuously (Vakulya et al., 2024). Fluctuations in heart and respiration rates can indicate stress, pain, or disease (von Borell et al., 2007). Therefore, such variables can be used for assessing animal welfare and stress levels and early detection of respiratory or cardiovascular issues. Limited studies are available on the heritability of heart and respiration rate in dairy cattle populations. Thus far, sensors for measuring heart and respiration rates are cumbersome, invasive, and not suitable for long-term data collection. Cameras may provide an avenue for automatically recording res-

Table 3. Heritability (h^2) estimates for sensor-based activity traits measured in Holstein dairy cows

Trait	Sensor type or brand	N	$h^2 \pm$ SE	Reference
Activity time (min/24 h)	SenseHub (Allflex Livestock Intelligence) collar	453	0.14 ± 0.06	Lemal et al. (2024)
Activity (daily)	Pedometer	635	0.19 ± 0.06	Nascimento et al. (2024)
Activity (weekly)	Pedometer	635	0.23 ± 0.07	Nascimento et al. (2024)
Activity	Electronic activity neck tags (SCR Heatime HR system)	1,171	0.09 ± 0.05	Schöpke and Weigel (2014)
Duration of high activity episode	Electronic activity tags (neckbands)	11,522	0.03 ± 0.01	Ismael et al. (2016)
Eating rate (kg/h)	Automated feeders	842	0.46 ± 0.09	Lin et al. (2013)
Eating time (first parity)	SenseHub dairy sensors (Allflex)	142	0.42 ± 0.09	Atashi et al. (2024)
Eating time (second parity)	SenseHub dairy sensors (Allflex)	243	0.45 ± 0.04	Atashi et al. (2024)
Eating time (first parity)	SenseHub dairy sensor (Allflex)	142	0.42 ± 0.09	Atashi et al. (2024)
Eating time (second parity)	SenseHub dairy sensor (Allflex)	243	0.45 ± 0.04	Atashi et al. (2024)
Eating time (min/24 h)	SenseHub (Allflex) collar	453	0.12 ± 0.05	Lemal et al. (2024)
Interval from calving to first high activity	Electronic activity tags fitted on neckbands	11,522	0.11 ± 0.02	Ismael et al. (2016)
Lying time (daily)	SMARTBOW ear-tag accelerometer	728	0.37 ± 0.07	Nascimento et al. (2024)
Lying time (weekly)	SMARTBOW ear-tag accelerometer	728	0.48 ± 0.09	Nascimento et al. (2024)
Strength of high activity episode	Electronic activity tags (neckbands)	11,522	0.03	Ismael et al. (2016)
Daily sum activity (DIM 7 and 14)	Lely	1,084	0.13 ± 0.09	Schodl et al. (2024a)
Daily SD activity (DIM 7 and 14)	Lely	1,084	0.33 ± 0.14	Schodl et al. (2024a)
Mean daily activity sum over 5–7 and 12–14 DIM	Lely	1,084	0.24 ± 0.07	Schodl et al. (2024a)
Mean daily activity SD over 5–7 and 12–14 DIM	Lely	1,084	0.35 ± 0.09	Schodl et al. (2024a)
Regression slope of activity daily sum over 5–7 and 12–14 DIM	Lely	1,084	0.12 ± 0.03	Schodl et al. (2024a)
Regression slope of daily SD over 5–7 and 12–14 DIM	Lely	1,084	0.18 ± 0.04	Schodl et al. (2024a)
Mean daily activity sum over 150 DIM	Lely	1,084	0.15 ± 0.06	Schodl et al. (2024a)
Mean daily activity SD over 150 DIM	Lely	1,084	0.19 ± 0.07	Schodl et al. (2024a)
Regression slope of daily activity sum over 150 DIM	Lely	1,084	0.22 ± 0.13	Schodl et al. (2024a)
Regression slope of daily activity SD over 150 DIM	Lely	1,084	0.11 ± 0.14	Schodl et al. (2024a)
Mean daily activity sum over 305 DIM	Lely	1,084	0.18 ± 0.05	Schodl et al. (2024a)
Mean daily activity SD over 305 DIM	Lely	1,084	0.18 ± 0.06	Schodl et al. (2024a)
Regression slope of daily activity sum over 305 DIM	Lely	1,084	0.18 ± 0.13	Schodl et al. (2024a)
Regression slope of daily activity SD over 305 DIM	Lely	1,084	0.26 ± 0.17	Schodl et al. (2024a)
Daily activity sum on 7 and 14 DIM	Smaxtec	409	0.18 ± 0.11	Schodl et al. (2024a)
Daily activity SD on 7 and 14 DIM	Smaxtec	409	0.55 ± 0.21	Schodl et al. (2024a)
Mean daily activity sum over 5–7 DIM and 12–14 DIM	Smaxtec	409	0.34 ± 0.11	Schodl et al. (2024a)
Mean daily activity SD over 5–7 DIM and 12–14 DIM	Smaxtec	409	0.47 ± 0.11	Schodl et al. (2024a)
Regression slope of daily activity sum over 5–7 DIM and 12–14 DIM	Smaxtec	409	0.00 ± 0.00	Schodl et al. (2024a)
Regression slope of daily activity SD over 5–7 DIM and 12–14 DIM	Smaxtec	409	0.07 ± 0.03	Schodl et al. (2024a)
Mean daily activity sum over 150 DIM	Smaxtec	409	0.00 ± 0.00	Schodl et al. (2024a)
Mean daily activity SD over 150 DIM	Smaxtec	409	0.00 ± 0.00	Schodl et al. (2024a)
Regression slope of daily activity sum over 150 DIM	Smaxtec	409	0.00 ± 0.00	Schodl et al. (2024a)
Regression slope of daily activity SD over 150 DIM	Smaxtec	409	0.00 ± 0.00	Schodl et al. (2024a)
Mean daily activity sum over 305 DIM	Smaxtec	409	0.00 ± 0.00	Schodl et al. (2024a)
Mean daily activity SD over 305 DIM	Smaxtec	409	0.00 ± 0.00	Schodl et al. (2024a)
Regression slope of daily activity sum over 305 DIM	Smaxtec	409	0.00 ± 0.00	Schodl et al. (2024a)
Regression slope of daily activity SD over 305 DIM	Smaxtec	409	0.00 ± 0.00	Schodl et al. (2024a)
Activity: mean, SD, and median on the day of milk recording (test day)	Lely	1,289	0.09–0.16 (±0.01–0.04)	Schodl et al. (2023)
Activity: deviation between mean and SD at test day and 5 and 10 d before	Lely	1,289	0.12–0.19 (±0.01–0.05)	Schodl et al. (2023)
Activity: mean, SD, mean SD, and median over 3–305 DIM	Lely	1,289	0.17–0.20 (±0.03)	Schodl et al. (2023)
Eating time: mean, SD, and median on the day of milk recording (test day)	Lely	1,289	0.11–0.33 (±0.01–0.06)	Schodl et al. (2023)
Eating time: deviation between mean and SD at test day and 5 and 10 d before	Lely	1,289	0.20–0.37 (±0.03–0.07)	Schodl et al. (2023)
Eating time: mean, SD, mean SD, and median over 3–305 DIM	Lely	1,289	0.34–0.39 (±0.06–0.07)	Schodl et al. (2023)

piration rate data but, to our knowledge, it has not yet been tested in large scale.

Rumen Activity and Reticuloruminal pH. Boluses equipped with sensors measure parameters such as pH and temperature in the rumen and reticulum (Denwood et al., 2018; Mensching et al., 2020). Continuous monitoring helps in assessing digestive health and detecting disorders such as acidosis (Simoni et al., 2023, 2024). This type of data can be used for managing feeding strategies to prevent metabolic disorders, for optimizing rumen health for better feed efficiency, and for breeding purposes. However, heritability estimates for rumen activity and reticuloruminal pH stability are scarce.

Lameness and Hoof Disorders. Accelerometers, pressure-sensitive walkways, and advanced video analyses (2- and 3-dimensional [**3D**]) are employed for assessing the presence and severity of lameness (Nejati et al., 2023). For instance, computer vision techniques analyze gait and posture to identify lameness. Recent advancements use deep learning models to enhance detection accuracy (Karoui et al., 2021; Dervić et al., 2024). Such tools have the potential to enable early identification of lameness, allowing for timely treatment, improving animal welfare and reducing economic losses. Lemmens et al. (2023) showed differences in sensor-based behavior (e.g., eating time, activity) between cows with different lameness scores. Lameness has been found to have a heritable component, with heritability estimates ranging from low to moderate (Heringstad et al., 2018; Köck et al., 2019) and are of highly polygenic nature (Sousa Junior et al., 2024). This indicates potential for genetic selection to reduce lameness incidence through genomic selection.

Udder Health. Table 1 presents heritability estimates for various sensor-derived udder health traits, with heritability estimates ranging from 0.07 to 0.53. Somatic cell count is a widely used indicator of udder health, with genetic studies showing moderate heritability (0.15–0.32), suggesting potential for selection to improve mastitis resistance (Martin et al., 2018; Piwczyński et al., 2021). Changes in milk electrical conductivity (**EC**) have also been proposed as an early indicator of subclinical mastitis, as bacterial infections alter the ionic composition of milk. Studies on Chinese Holstein cows indicate moderate-to-high heritability of EC (0.46–0.49), but its genetic correlation with SCC remains limited, suggesting that EC alone is not a fully reliable predictor (Lu et al., 2024). Other studies have reported heritability estimates for EC traits ranging from 0.22 to 0.53 (Table 1). Behavioral changes, such as reduced milking speed and increased milking time, have also been linked to mastitis, with milking speed exhibiting a genetic correlation of 0.31 with SCC (Piwczyński et al., 2021).

Different studies show that mastitis in dairy cows results in a change in behavior. The changes in activity are more unregularly in cows with mastitis (Veissier et al., 2017) and time of standing is increased (Fogsgaard et al., 2012). Cows with mastitis have been shown to have reduced feed intake (Siivonen et al., 2011) and reduced daily rumination time (Fogsgaard et al., 2015; Anatanaitis et al., 2022). Studies on genetic correlations between sensor based behavioral traits and udder health traits are rare, but Moretti et al. (2018) reported low genetic correlations. In addition to SCC records and clinical mastitis diagnoses, results of bacteriological milk analyses provide valuable information regarding udder health (Suntinger et al., 2022). Although first heritability analyses showed low heritability, the genetic correlation with the routinely recorded udder health traits is high.

The use of AMS allows for continuous monitoring of udder health indicators, including online cell count (**OCC**), EC variations, and elevated mastitis risk, providing valuable data for genetic evaluation and herd management (Wethal et al., 2020a; Table 1). Wethal et al. (2020a) assessed the values of maximum and mean EC as indicators of udder health and suggested OCC to be more valuable. Given the economic and welfare impacts of mastitis, incorporating multiple phenotypic and genetic indicators, including SCC, EC, milking speed, and AMS-based health markers, could enhance early detection and genetic selection strategies for improved udder health.

Metabolic Disorders. Wearable biometric sensors, such as automated health-monitoring systems, continuously collect data on rumination time and physical activity (Stangaferro et al., 2016). Alterations in patterns of these parameters can indicate metabolic and digestive disorders, including displaced abomasum, ketosis, and indigestion (Rial et al., 2023). Therefore, such variables can be used for assessing animal health status, early disease detection, and improving dairy cow management (Paudyal et al., 2018), even more so when combined with other available health data (Sturm et al., 2020). Genetic parameters for sensor-based metabolic disease traits need to be explored to assess their potential for genetic selection. Mid-infrared spectroscopy (**MIR**)-based predictors for ketosis show potential for screening and preventing ketosis in dairy herds (Köck et al., 2024). Köck et al. (2022) estimated heritabilities between 0.16 and 0.30 for MIR-based predictors (Aceton-MIR, BHB-MIR and KetoMIR) and genetic correlations between 0.60 and 0.73 with BHB measures using a handheld device. Fuerst-Waltl et al. (2022) analyzed different direct and indirect traits for ketosis. The genetic correlation between KetoMIR and the veterinarian diagnoses ketosis was >0.90.

Heat Stress. Heat stress in dairy cattle is a major concern as it can result in reduced milk production, impaired fertility, and increased susceptibility to diseases, leading to significant economic losses (Polsky and von Keyserlingk, 2017). Effective management strategies and genet-

Table 4. Heritability estimates for sensor-based rumination time traits in dairy cattle populations

Trait	Sensor type or brand	N	$h^2 \pm SE$	Reference
Rumination time (first parity)	SenseHub dairy sensor (Allflex)	142	0.45 ± 0.06	Atashi et al. (2024)
Rumination time (second parity)	SenseHub dairy sensors (Allflex)	243	0.43 ± 0.02	Atashi et al. (2024)
Rumination time (first lactation)	SenseHub dairy sensors (Allflex)	142	0.45 ± 0.06	Atashi et al. (2024)
Rumination time (second parity)	SenseHub dairy sensor (Allflex)	243	0.43 ± 0.02	Atashi et al. (2024)
Rumination time (early)—research herds	Microphone-based rumination monitoring sensor	159	0.14 ± 0.27	Byskov et al. (2017)
Rumination time (late)—research herds	Microphone-based rumination monitoring sensor	159	0.23 ± 0.26	Byskov et al. (2017)
Rumination time (peak)—research herds	Microphone-based rumination monitoring sensor	159	0.44 ± 0.34	Byskov et al. (2017)
Rumination time (total)—research herds	Microphone-based rumination monitoring sensor	159	0.33 ± 0.16	Byskov et al. (2017)
Rumination time (early)—commercial herds	Microphone-based rumination monitoring sensor	10,475	0.29 ± 0.03	Byskov et al. (2017)
Rumination time (peak)—commercial herds	Microphone-based rumination monitoring sensor	10,475	0.28 ± 0.03	Byskov et al. (2017)
Rumination time (mid)—commercial herds	Microphone-based rumination monitoring sensor	10,475	0.32 ± 0.04	Byskov et al. (2017)
Rumination time (late)—commercial herds	Microphone-based rumination monitoring sensor	10,475	0.31 ± 0.04	Byskov et al. (2017)
Rumination time (total)—commercial herds	Microphone-based rumination monitoring sensor	10,475	0.30 ± 0.03	Byskov et al. (2017)
Rumination time	Accelerometer-based neck tag (Lely Qwes HR-LDn)	1,486	0.14 ± 0.04	Sitkowska et al. (2024)
Rumination time	SenseHub collar (Allflex)	453	0.19 ± 0.05	Lemal et al. (2024)
Rumination time	Electronic collar with acoustic sensors (Allflex SCR, Hi Tag)	656	0.45 ± 0.14	Lopes et al. (2024)
Rumination time	Collar with tag (Lely Qwes)	775	0.17 ± 0.06	López-Paredes et al. (2020)
Rumination time (early)	Neck collar with a tag (microphone + 3-axis accelerometer)	710	0.32	Moretti et al. (2018)
Rumination time (mid)	Neck collar with a tag (microphone + 3-axis accelerometer)	710	0.34	Moretti et al. (2018)
Rumination time (late)	Neck collar with a tag (microphone + 3-axis accelerometer)	710	0.35	Moretti et al. (2018)
Rumination Time (weekly)	SMARTBOW ear-tag accelerometer	728	0.25 ± 0.08	Nascimento et al. (2024)
Rumination time (daily)	SMARTBOW ear-tag accelerometer	728	0.19 ± 0.06	Nascimento et al. (2024)
Mean, SD and median on the day of milk recording (test day)	Lely	1,289	0.03–0.30 ± 0.01–0.04	Schodl et al. (2023)
Deviation between mean and SD at test day and 5 and 10 d before	Lely	1,289	0.10–0.37 ± 0.01–0.05	Schodl et al. (2023)
Mean, SD, mean SD, and median over 3–305 DIM	Lely	1,289	0.39–0.50 ± 0.06	Schodl et al. (2023)
Mean and SD on day of milk recording (test day)	Lely	834	0.06–0.18 ± 0.03–0.04	Schodl et al. (2022)
Deviation between mean and SD at test day and 5 d before	Lely	834	<0.01–0.04 ± 0.01–0.02	Schodl et al. (2022)
Regression slope of daily mean and SD over 5days before to test day	Lely	834	<0.01–0.04 ± 0.01–0.02	Schodl et al. (2022)
Rumination time	SCR recording system (accelerometer)	77,697	0.32 ± 0.01 to 0.45 ± 0.02	Weller and Ezra (2024)

Table 5. Heritability (h^2) estimates for indicators of fertility derived based on automatically recorded data in dairy cattle populations

Trait	Sensor type	N	Breed	$h^2 \pm$ SE	Reference
Calving to first heat	Herd Navigator (P4)	676	Nordic Red	0.19 ± 0.11	Häggman et al. (2019)
Calving to first heat	Herd Navigator in-line milk progesterone system	2,645	Swedish Red and Holstein	0.18 ± 0.05	Tarekegn et al. (2019)
Commencement of luteal activity	Herd Navigator (P4)	766	Nordic Red	0.24 ± 0.12	Häggman et al. (2019)
Commencement of luteal activity	Herd Navigator in-line milk progesterone system	2,645	Swedish Red and Holstein	0.24 ± 0.04	Tarekegn et al. (2019)
Days from calving to first high activity episode	Electronic activity tag	517	Holstein, Red Dane, Jersey	0.18 ± 0.07	Løvendahl and Chagunda (2009)
Duration of estrus episode	Electronic activity tag	517	Holstein, Red Dane, Jersey	0.05 ± 0.02	Løvendahl and Chagunda (2009)
Estrus period activity variation	SCR Heatime HR system (accelerometer neck tag)	1,070	Holstein	0.11 ± 0.06	Schöpke and Weigel (2014)
Estrus period average activity	SCR Heatime HR system (accelerometer neck tag)	1,070	Holstein	0.12 ± 0.05	Schöpke and Weigel (2014)
First luteal phase length	Herd Navigator in-line milk progesterone system	2,645	Swedish Red and Holstein	0.08 ± 0.04	Tarekegn et al. (2019)
Interval from calving to first high activity	Automatic milking system (Lely)	8,139	Norwegian Red	0.05 ± 0.01	Heringstad and Wethal (2023)
Interval from commencement of luteal activity to first service	Herd Navigator in-line milk progesterone system	2,645	Swedish Red and Holstein	0.03 ± 0.04	Tarekegn et al. (2019)
Interval from commencement of luteal activity to first service	Herd Navigator in-line milk progesterone system	1,561	Holstein	0.11 ± 0.06	Tenghe et al. (2015)
Length of first interovulatory interval	Herd Navigator in-line milk progesterone system	2,645	Swedish Red and Holstein	0.03 ± 0.04	Tarekegn et al. (2019)
Luteal activity between 25 and 60 DIM	Herd Navigator in-line milk progesterone system	1,561	Holstein	0.06 ± 0.04	Tenghe et al. (2015)
Luteal activity during first 60 DIM	Herd Navigator in-line milk progesterone system	2,645	Swedish Red and Holstein	0.15 ± 0.04	Tarekegn et al. (2019)
MIR-predicted fertility	MIR spectroscopy	4,124	Holstein	0.16 ± 0.03	van den Berg et al. (2021)
Natural log of commencement of luteal activity	Herd Navigator in-line milk progesterone system	1,561	Holstein	0.12 ± 0.05	Tenghe et al. (2015)
Postestrus activity variation	SCR Heatime HR system (accelerometer neck tag)	1,070	Holstein	0.14 ± 0.05	Schöpke and Weigel (2014)
Postestrus average activity	SCR Heatime HR system (accelerometer neck tag)	1,070	Holstein	0.03 ± 0.03	Schöpke and Weigel (2014)
Pre-estrus activity variation	SCR Heatime HR system (accelerometer neck tag)	1,070	Holstein	0.15 ± 0.05	Schöpke and Weigel (2014)
Pre-estrus average activity	SCR Heatime HR system (accelerometer neck tag)	1,070	Holstein	0.05 ± 0.04	Schöpke and Weigel (2014)
Proportion of samples in luteal activity between 25 and 60 DIM	Herd Navigator in-line milk progesterone system	1,561	Holstein	0.12 ± 0.05	Tenghe et al. (2015)
Proportion of samples with luteal activity	Herd Navigator in-line milk progesterone system	2,645	Swedish Red and Holstein	0.13 ± 0.03	Tarekegn et al. (2019)
Regularity of estrus episodes	Electronic activity tag	483	Holstein, Red Dane, Jersey	0.00 ± 0.02	Løvendahl and Chagunda (2009)
Strength of estrus	Electronic activity tag	517	Holstein, Red Dane, Jersey	0.06 ± 0.02	Løvendahl and Chagunda (2009)

Table 6. Estimates of heritability (h^2) for traits related to feed intake, feeding behavior, and feed efficiency in dairy cattle populations[1]

Trait	Sensor type or brand	N	Breed	Life stage	$h^2 \pm$ SE	Reference
DMI	Feed bins from Biocontrol (weights for roughage intake)	557	Norwegian Red	Lactating cows	0.29	Bakke and Heringstad (2024)
DMI	Electronic feeder (Gallagher)	1,598 to 1,958	Holstein	Lactating cows	0.19 ± 0.04 to 0.36 ± 0.04	Bolormaa et al. (2023)
DMI	Feed bins, feed gates controlled by neck collars		Holstein	Lactating cows	0.32 ± 0.07 to 0.49 ± 0.08	Byskov et al. (2017)
DMI	Automated feed intake system (recorded in AMS)	3,075	Holstein	Lactating cows (P1)	0.32 ± 0.03	Hardie et al. (2017)
DMI	Automated feed intake system (recorded in AMS)	2,667	Holstein	Lactating cows (multiparous)	0.23 ± 0.03	Hardie et al. (2017)
DMI	Electronic feeder	842	Holstein	Dairy heifers (~6 mo)	0.50 ± 0.09	Lin et al. (2013)
DMI	Cattle Feed Intake System (3D cameras)	2,688	Holstein	Lactating cows	0.25 ± 0.02	Manzanilla-Pech et al. (2023)
DMI	Cattle Feed Intake System (3D cameras)	1,378	Jersey	Lactating cows	0.17 ± 0.03	Manzanilla-Pech et al. (2023)
DMI	Cattle Feed Intake System (3D cameras)	1,951	Nordic Red	Lactating cows	0.18 ± 0.02	Manzanilla-Pech et al. (2023)
DMI	Electronic feed recording system	379	Australian dairy cows	Lactating cows	0.33 ± 0.13	Richardson et al. (2021)
DMI	Electronic feeding system (RIC system, Insentec)	7,379	Holstein	Lactating cows	0.20–0.37	Stephansen et al. (2023)
RFI	Feed bins, feed gates controlled by neck collars		Holstein	Lactating cows	0.23 ± 0.07 to 0.36 ± 0.08	Byskov et al. (2017)
RFI	Derived from automated feed intake, milk yield, and BW records	2,667 and 3,075	Holstein	Lactating cows	0.13 ± 0.03 and 0.14 ± 0.03	Hardie et al. (2017)
RFI	Electronic feeder (Gallagher)	842	Holstein	Heifers (~6 mo)	0.48 ± 0.09	Lin et al. (2013)
Genetic RFI	Derived from DMI, ECM, and BW data	7,379	Holstein	Lactating cows	0.22–0.34	Stephansen et al. (2023)
Residual energy intake	Derived from AMS records, electronic scale, and n-alkane–based DMI estimates	1,274	Holstein	Lactating cows	0.08 ± 0.03	Hurley et al. (2017)
Residual energy production	Derived from AMS records, electronic scale, and n-alkane–based DMI estimates	1,274	Holstein	Lactating cows	0.24 ± 0.05	Hurley et al. (2017)
Net energy intake	Derived from AMS records, electronic scale, and n-alkane–based DMI estimates	1,274	Holstein	Lactating cows	0.17 ± 0.05	Hurley et al. (2017)
Energy balance	Derived from AMS records, electronic scale, and n-alkane–based DMI estimates	1,274	Holstein	Lactating cows	0.12 ± 0.04	Hurley et al. (2017)
Duration of each feeder visit	Automated intake recording system	1,328	Holstein	Mid-lactation	0.16 ± 0.03	Cavani et al. (2022)
Duration of each meal	Automated intake recording system	1,328	Holstein	Mid-lactation	0.14 ± 0.02	Cavani et al. (2022)
Energy conversion efficiency	Derived from AMS records, electronic scale, and n-alkane–based DMI estimates	1,274	Holstein	Lactating cows	0.17 ± 0.05	Hurley et al. (2017)
Feeding duration	Electronic feeder (Gallagher)	842	Holstein	Heifers (~6 mo)	0.45 ± 0.08	Lin et al. (2013)
Feeding interval	AMF	4,572	Holstein	Calves	0.008 ± 0.01	Graham et al. (2024a)
Feeding rate per meal	Automated intake recording system (RIC)	1,328	Holstein	Mid-lactation	0.23 ± 0.03	Cavani et al. (2022)
Feeding rate per visit	Automated intake recording system (RIC)	1,328	Holstein	Mid-lactation	0.11 ± 0.02	Cavani et al. (2022)
Intake per meal	Automated intake recording system (RIC)	1,328	Holstein	Mid-lactation	0.13 ± 0.02	Cavani et al. (2022)
Intake per visit	Automated intake recording system (RIC)	1,328	Holstein	Mid-lactation	0.16 ± 0.03	Cavani et al. (2022)
Number of feeder visits per day	Automated intake recording system (RIC; Hokofarm Group)	1,328	Holstein	Mid-lactation	0.16 ± 0.03	Cavani et al. (2022)
Number of meals per day	Automated intake recording system (RIC)	1,328	Holstein	Mid-lactation	0.09 ± 0.02	Cavani et al. (2022)
Number of meals	Electronic feeder (Gallagher)	842	Holstein	Heifers (~6 mo)	0.40 ± 0.09	Lin et al. (2013)
Per-visit milk consumption	AMF	4,572	Holstein	Calves	0.025 ± 0.01	Graham et al. (2024a)
Average meal size	Electronic feeder (Gallagher)	842	Holstein	Heifers (~6 mo)	0.46 ± 0.09	Lin et al. (2013)
Daily milk consumption	AMF	10,076	Holstein	Calves	0.07 ± 0.01	Graham et al. (2024a)
Daily number of rewarded visits	AMF	10,076	Holstein	Calves	0.03 ± 0.01	Graham et al. (2024a)
Daily sum of drinking duration	AMF	10,076	Holstein	Calves	0.07 ± 0.01	Graham et al. (2024a)
Drinking duration per visit	AMF	4,572	Holstein	Calves	0.02 ± 0.01	Graham et al. (2024a)
Drinking speed	AMF	10,076	Holstein	Calves	0.08 ± 0.01	Graham et al. (2024a)
Total consumption variance	AMF	4,572	Holstein	Calves	0.21 ± 0.02	Graham et al. (2024a)
Total drinking duration variance	AMF	4,572	Holstein	Calves	0.23 ± 0.02	Graham et al. (2024a)
Total duration of feeder visits per day	Automated intake recording system (RIC)	1,328	Holstein	Mid-lactation	0.16 ± 0.03	Cavani et al. (2022)
Total number of visits	AMF	10,076	Holstein	Calves	0.05 ± 0.01	Graham et al. (2024a)

[1] 3D = 3-dimensional; AMS = automated milking system; AMF = automated milk feeding machine; N = number of cattle; P1 = first parity; RFI = residual feed intake.

ic selection for heat tolerance are essential to maintaining productivity and animal welfare. Several variables can be measured to assess heat tolerance in dairy cattle, aiding in genetic selection for improved thermotolerance (Luo et al., 2021a,b; Hu et al., 2023). Physiological indicators such as rectal or vaginal temperature, respiration rate, and sweating rate provide direct measures of an animal's ability to dissipate heat. Coat characteristics, including hair length, coat color, and hair density, influence heat absorption and retention. Most studies evaluating the genetic background of heat tolerance in dairy cattle have focused on variability of performance data (e.g., milk yield, fertility) across environmental gradients usually defined based on data from public weather stations (Silva Neto et al., 2024; Misztal et al., 2025; Shi et al., 2025). To our knowledge no estimates of heritability exist for sensor-derived indicators of heat stress in dairy cattle. Recent studies have investigated variability in automatically recorded vaginal temperature in lactating sows based on random regression models (Wen et al., 2023) and also derived resilience indicators with moderate heritability estimates (Wen et al., 2024). The same sensors could be used in dairy cattle studies.

Dairy Cow Behavior

Behavior encompasses a complex set of activities exhibited by animals in response to various stimuli, including environmental, social, internal factors, and human handling. Understanding and quantifying phenotypic variability in behavioral traits within dairy cattle populations is crucial for identifying new traits that can be incorporated into breeding programs (Pacheco et al., 2025). As reviewed by Pacheco et al. (2025) and Chang et al. (2020), dairy cattle exhibit a wide range of behaviors throughout their lives, which can be categorized into several groups. These include, but are not limited to, calf behavior, feeding and drinking behavior, rumination patterns, estrus expression, reproductive behaviors in both males and females, responses to milking, interactions with on-farm technologies, reactions to stressors (such as heat stress, infectious diseases, nutritional challenges, and novel objects), maternal behavior, and social interactions. Tables 2, 3, and 4 present heritability estimates for sensor-based behavioral traits, including activity (Table 3) and rumination traits (Table 4). Heritability estimates for sensor-based traits tend to be higher than for manually recorded variables. For instance, using manual observations of cow behavior across 24 h, Løvendahl and Munksgaard (2016a) found very low heritabilities for activity traits (e.g., daily lying time: 0.00 ± 0.10, number of lying bouts/day: 0.01 ± 0.09; lying bout duration 0.07 ± 0.08). However, studies using pedometers or neck collars found higher values (e.g., 0.09 ± 0.05: Schöpke and Weigel, 2014; 0.23 ± 0.07: Lemal et al., 2024; 0.19 ± 0.06: Nascimento et al., 2024 and see Table 3). This is likely because the use of sensors allows for continuous recording for larger numbers of animals across longer time periods. Interestingly, heritability was higher when lying was considered over periods longer than a day. This supports the idea that lying time is elastic and related to eating time (Løvendahl and Munksgaard, 2016a); to support high yields, cows must adjust their lying time within a day to ensure that they have sufficient time to feed. However, that lying time is an important "need" that must be fulfilled over the longer term.

Activity. As discussed above, one of the first applications of sensor technology to dairy farming was the development of an activity monitor that detected the rise in activity associated with estrus (e.g., Dolecheck et al., 2015). Wearable collars, ear-tags, or similar accelerometer-based tools generate data permanently and at relatively low costs which can be related to welfare and health. The discovery that activity changes in response to disease and pain led to the development of systems that predict time of calving, lameness, and milk fever (Beer et al., 2016; Borchers et al., 2017; Barraclough et al., 2020).

Feeding and Rumination. Changes in eating, grazing, and rumination time have also been used to detect poor health (Simoni et al., 2024). Changes in eating time can also be used as a measure of heat tolerance (Lemal et al., 2024). Løvendahl and Munksgaard (2016a) found low to moderate heritabilities for feeding behavior using manual observations (daily feeding time: 0.20 ± 0.13, number of feeding bouts/day: 0.12 ± 0.09; duration of feeding bouts: 0.06 ± 0.09). Estimates of heritability for eating time using sensors are generally higher (e.g., 0.42 ± 0.09: Atashi et al., 2024). Estimates for rumination vary somewhat with the sensor used (between 0.14 to 0.45; see Table 4). Again, heritability values are typically higher when calculated over a longer time period and not just daily. This also suggests that the amount of eating and ruminating within a day may be somewhat flexible, but it is critical that certain levels are maintained in the longer term.

Personality and Other Behavior Patterns. Underlying traits that affect the expression of behavior, such as response to milking (milking temperament), have been shown to have low to moderate heritabilities (e.g., 0.07 ± 0.001 Pryce et al., 2000; 0.13 ± 0.01: Sewalem et al., 2011; see Haskell et al., 2014; Chang et al., 2020; and Pacheco et al., 2025, for literature reviews). The trait of "number of kick-offs" is a similar trait measured in AMS. It also has a low heritability (0.06 ± 0.01; Wethal and Heringstad, 2019). Many other behavior patterns contribute to welfare in dairy, such as positive and negative social interactions in adult cattle and play in calves. Sensor technology has been used to measure play in calves (e.g., Gladden et al., 2020; Vázquez-Diosdado et al., 2024),

Table 7. Heritability estimates for traits related to enteric greenhouse gas emissions by dairy cattle populations

Trait[1]	Technology type or brand	N	Breed	$h^2 \pm$ SE	Reference
CH_4 concentration	Nondispersive infrared methane detector installed in the AMS feed bin	1,501	Holstein	0.11 ± 0.03	López-Paredes et al. (2020)
CH_4 concentration, first lactation	Nondispersive infrared CH_4 sensor	489	Holstein	0.10–0.28 (±0.05–0.06)	Manzanilla-Pech et al. (2022)
CH_4 concentration, second lactation	Nondispersive infrared CH_4 sensor	368	Holstein	0.13–0.29 (±0.05–0.06)	Manzanilla-Pech et al. (2022)
CH_4 concentration	Guardian NG infrared gas monitor installed in the feed bin of the AMS	416	Holstein	0.12 ± 0.01	Saborío-Montero et al. (2020)
CH_4 concentration ($\log_{10}(CH_4)$)	Nondispersive infrared sensor in AMS	1,508	Holstein	0.11 ± 0.02	van Engelen et al. (2018)
CH_4 concentration (ppm, weekly)	Sniffer	1,800	Holstein	0.32 ± 0.02	van Breukelen et al. (2023)
CH_4 concentration (weekly)	Sniffer	4,664	Holstein	0.17 ± 0.04	van Breukelen et al. (2024)
CH_4 concentration (ppm, daily)	Sniffer	1,800	Holstein	0.18 ± 0.01	van Breukelen et al. (2023)
CO_2 concentration	Nondispersive infrared sensor (SenseAir LPL CH_4/CO_2, Rise Acreo) in AMS	1,508	Holstein	0.12 ± 0.02	van Engelen et al. (2018)
CO_2 concentration (ppm, daily)	Sniffer	1,800	Holstein	0.20 ± 0.01	van Breukelen et al. (2023)
CO_2 concentration (ppm, weekly)	Sniffer	1,800	Holstein	0.32 ± 0.02	van Breukelen et al. (2023)
CH_4 conversion factor	Sniffer method integrated in AMS	182	Holstein	0.13 ± 0.13	Uemoto et al. (2024)
CH_4 intensity	GreenFeed	265	Holstein	0.21 ± 0.14	Kamalanathan et al. (2023)
CH_4 intensity	Noninvasive FTIR analyzer	1,745	Holstein	0.21 ± 0.06	Lassen and Løvendahl (2016)
CH_4 intensity	SF6 tracer and daily milk records (MIR)	379	Australian dairy cows	0.33 ± 0.12	Richardson et al. (2021)
CH_4 production (g/d)	GreenFeed	1,370	Norwegian Red	0.39 ±	Bakke and Heringstad (2024)
CH_4 production	Infrared CH_4 analyzer in milking robot	184	Holstein	0.12–0.45	Breider et al. (2019)
CH_4 production (g/d)	GreenFeed	212	Norwegian Red	0.56 ± 0.20	Heringstad and Bakke (2023)
CH_4 production	GreenFeed	330	Holstein	0.16 ± 0.10	Kamalanathan et al. (2023)
CH_4 production	Milking robot (FTIR sensor)	339	Holstein	0.24 ± 0.15	Lassen et al. (2016)
CH_4 production	GreenFeed	451	Holstein	0.36 ± 0.12	Lopes et al. (2024)
CH_4 production	Nondispersive infrared method	1,501	Holstein	0.12 ± 0.04	López-Paredes et al. (2020)
CH_4 production, first lactation	Derived from sensor data (Guardian NG; calculated using ECM and BW)	425	Holstein	0.11–0.49 (±0.07–0.13)	Manzanilla-Pech et al. (2022)
CH_4 production, second lactation	Derived from sensor data (Guardian NG; calculated using ECM and BW)	318	Holstein	0.14–0.36 (±0.07–0.13)	Manzanilla-Pech et al. (2022)
CH_4 production	SF6 tracer method	379	Australian dairy cows	0.16 ± 0.11	Richardson et al. (2021)
CH_4 production	GreenFeed	822	Holstein	0.19 ± 0.02 to 0.33 ± 0.04	van Breukelen et al. (2023)
CO_2 production (g/d)	GreenFeed	822	Holstein	0.24 ± 0.03	van Breukelen et al. (2023)
CH_4 production	FTIR gas analyzer (“sniffer” in AMS)	1,397	Holstein	0.25 ± 0.07	Zetouni et al. (2018)
CH_4 production and intensity predicted from MIR	Milk mid-infrared spectroscopy (MIR)	231,400 to 336,126	Holstein	0.17 ± 0.01 to 0.25 ± 0.01	Kandel et al. (2017)
CH_4 production predicted from MIR	Milk mid-infrared spectroscopy (MIR)	541,565	Holstein	0.23 ± 0.01	Rojas de Oliveira et al. (2024)
CH_4 yield	GreenFeed system	287	Holstein	0.27 ± 0.12	Kamalanathan et al. (2023)
CH_4 yield	SF6 tracer and electronic feed recording system	379	Australian dairy cows	0.23 ± 0.12	Richardson et al. (2021)
CH4_MILK	Milking robot (FTIR sensor)	339	Holstein	0.26 ± 0.14	Lassen et al. (2016)
CH4_RATIO	Milking robot (FTIR sensor)	339	Holstein	0.09 ± 0.11	Lassen et al. (2016)
CH_4/CO_2 ratio	Sniffer method integrated in AMS	182	Holstein	0.12 ± 0.14	Uemoto et al. (2024)
CH_4/CO_2 ratio	Nondispersive infrared sensor (SenseAir LPL CH_4/CO_2, Rise Acreo) in AMS	1,508	Holstein	0.03 ± 0.01	Van Engelen et al. (2018)
CH_4/CO_2 ratio per visit	Sniffer in AMS feed bin	1,746	Holstein	0.01 ± 0.01	van Breukelen et al. (2022)
CH_4/CO_2 ratio per week	Sniffer in AMS feed bin	1,579	Holstein	0.02 ± 0.01	van Breukelen et al. (2022)
Daily CH_4 production	Noninvasive FTIR analyzer	1,745	Holstein	0.21 ± 0.06	Lassen and Løvendahl (2016)
Log-transformed CH_4 emissions per visit	Sniffer in AMS feed bin	1,746	Holstein	0.09 ± 0.01	van Breukelen et al. (2022)
Log-transformed CH_4 emissions per week	Sniffer in AMS feed bin	1,579	Holstein	0.23 ± 0.03	van Breukelen et al. (2022)
Mean CH_4 emissions (ppm) per visit	Sniffer in AMS feed bin	1,746	Holstein	0.13 ± 0.01	van Breukelen et al. (2022)
Mean CH_4 emissions (ppm) per week	Sniffer in AMS feed bin	1,579	Holstein	0.32 ± 0.03	van Breukelen et al. (2022)
Median CH_4 emissions (ppm) per visit	Sniffer in AMS feed bin	1,746	Holstein	0.13 ± 0.01	van Breukelen et al. (2022)
Median CH_4 emissions (ppm) per week	Sniffer in AMS feed bin	1,579	Holstein	0.32 ± 0.03	van Breukelen et al. (2022)
Ratio between CH_4 and CO_2	Noninvasive FTIR analyzer	3,121	Holstein	0.16 ± 0.04	Lassen and Løvendahl (2016)

[1] CH4_RATIO = the ratio between CH_4 and CO_2 in the breath of the cows; CH4_MILK = grams of CH_4 per liter of milk produced.

but heritability has not been estimated. Learning and behavioral plasticity in cattle has been genetically evaluated using longitudinal docility records (Alvarenga et al., 2023), but sensors and cameras could be great tools for deriving cognition and behavioral plasticity traits. The use of technology to classify and count social interactions has been considered, but further research is needed. Although the individual behavior patterns appear to have low heritability, traits do exist that assess overall patterns of behavior and that are important for animal welfare and production, which could be monitored via sensor systems and included in breeding programs.

Animal Resilience

Resilience can be defined based on the ability of animals to be minimally affected by environmental disturbances or quickly return to the unperturbed state (Colditz and Hine, 2016). Dairy cattle are exposed to multiple stressors throughout their lives, including thermal stress, injuries and diseases, social stress, and nutritional stress (Jurkovich et al., 2024). In general, these stressors negatively affect animal performance and other traits longitudinally recorded by digital technologies (e.g., milk yield, feed intake, activity, rumination time). Therefore, over the past few years, there has been a great interest in deriving resilience traits based on longitudinal records in various species. For instance, several authors have derived resilience based on variability in milk yield recorded by AMS and parlor systems (Poppe et al., 2020, 2021; Chen et al., 2023). These traits are heritable in Holstein cattle populations with heritability estimates ranging from 0.01 to 0.25 (Poppe et al., 2020, 2021; Chen et al., 2023; Maskal et al., 2024). Milk losses and variability during environmental perturbations across lactations stages have also been proposed as resilience indicators and shown to be genetically correlated with health traits in Holstein cattle (Wang et al., 2022, 2024). Poppe et al. (2022) also derived resilience indicators based on daily step count measured by Nedap Smarttag leg accelerometers (Nedap, Groenlo, the Netherlands). Heritability estimates were highest for resilience indicators describing mean step count, from 0.22 for the 2-wk period prepartum to 0.45 for the whole lactation. In dairy calves, Graham et al. (2024b) derived various resilience indicators based on variability in milk consumption recorded by automated milk feeders. The derived resilience indicators quantified the degree and duration of perturbations, including amplitude, perturbation time, recovery time, and deviation velocities. Although low, all the derived calf resilience traits were found to be heritable and some of them were moderately genetically correlated with the number of treatments for bovine respiratory

Table 8. Heritability (h^2) estimates for BW and udder conformation traits derived from automatically recorded data[1]

Trait	Sensor type or brand	N	Breed	$h^2 \pm$ SE	Reference
BW	Electronic scale (in AMS)	184	Holstein	0.40–0.67	Breider et al. (2019)
Metabolic BW	Electronic scale (in AMS)	3,075	Holstein	0.51 ± 0.03	Hardie et al. (2017)
Metabolic BW	Electronic scale (in AMS)	2,667	Holstein	0.46 ± 0.03	Hardie et al. (2017)
BW	Cattle Feed Intake System (3D cameras)	2,688	Holstein	0.51 ± 0.04	Manzanilla-Pech et al. (2023)
BW	Cattle Feed Intake System (3D cameras)	1,378	Jersey	0.45 ± 0.04	Manzanilla-Pech et al. (2023)
BW	Cattle Feed Intake System (3D cameras)	1,951	Nordic Red	0.58 ± 0.04	Manzanilla-Pech et al. (2023)
BW	Automated weighing system	7,379	Holstein	0.39–0.52	Stephansen et al. (2023)
Change in BW	Derived from automated weighing system data	7,379	Holstein	<0.02	Stephansen et al. (2023)
Weekly average BW, lactation 1	Electronic scale (in AMS)	3,253	Holstein	0.31–0.53	Tribout et al. (2023)
Weekly average BW, lactation 2	Electronic scale (in AMS)	2,553	Holstein	0.43–0.56	Tribout et al. (2023)
BW loss from wk 1 to wk 5, lactation 1	Derived from sensor-recorded body weight	3,253	Holstein	0.04	Tribout et al. (2023)
BW loss from wk 1 to wk 5, lactation 2	Derived from sensor-recorded body weight	2,553	Holstein	0.02	Tribout et al. (2023)
Udder balance	AMS	4,280	Holstein	0.41 ± 0.02	Medeiros et al. (2024)
Distance front–rear	AMS	4,280	Holstein	0.65 ± 0.02	Medeiros et al. (2024)
Front teat distance	AMS	4,279	Holstein	0.53 ± 0.02	Medeiros et al. (2024)
Rear teat distance	AMS	4,278	Holstein	0.40 ± 0.02	Medeiros et al. (2024)
Udder depth	AMS	4,280	Holstein	0.79 ± 0.01	Medeiros et al. (2024)
Rear teat distance	AMS	12,663	Holstein	0.47 ± 0.02	Poppe et al. (2019)
Front teat distance	AMS	12,663	Holstein	0.60 ± 0.02	Poppe et al. (2019)
Udder depth	AMS	12,663	Holstein	0.69 ± 0.02	Poppe et al. (2019)
Distance front–rear	AMS	12,663	Holstein	0.61 ± 0.02	Poppe et al. (2019)
Udder balance	AMS	12,663	Holstein	0.40 ± 0.02	Poppe et al. (2019)

[1] AMS = automated milking system.

diseases (Graham et al., 2024b). This is an active area of research and sensors are a great source of data for deriving such traits.

Fertility and Reproduction Traits

Fertility and reproduction traits are usually lowly heritable and highly polygenic (Fleming et al., 2019; Chen et al., 2022), implying reasonable interest in identifying novel traits that may be more heritable (Fleming et al., 2019). Cow activity measurements are widely used in herd management tools for estrus detection. Therefore, data from activity sensors can be used to derive novel traits useful for genetic evaluation of cow fertility, which reflect the cow's ability to return to estrus cyclicity and to show estrus after calving. One example of a trait derived from measures of increased level of activity is the interval from calving to first high activity (**CFHA**). Estimated heritability of CFHA range between 0.05 and 0.18 (Løvendahl and Chagunda, 2009; Heringstad and Wethal, 2023; Table 5). Other possibilities could be to define heat strength from measures of the height and duration of the increased activity peak. Cow activity data could also be used to derive traits such as conception rate.

Progesterone in milk is an indicator of cow fertility and can be used to derive a variety of traits, measuring different aspects of cow fertility. On-farm technology such as Herd Navigator (DeLaval Int., Tumba, Sweden), with in-line systems for automatic sampling and analyses of milk, provides measures of the cow's estrus and pregnancy status. Research from Häggman et al. (2019), Tarekegn et al. (2019), and Tenghe et al. (2015) demonstrated that information from in-line milk progesterone measures can be used to define novel fertility traits for genetic evaluation such as commencement of luteal activity, defined as the number of days from calving to the commencement of luteal activity. Automatic, continuous recording of cow activity or progesterone in milk may provide objective and frequent measures of traits related to different aspects of cow fertility. Traits derived from such measures would be less affected by herd management decisions than traditional fertility traits based on insemination dates, and these new traits can supplement or replace current cow fertility traits.

Feed Intake, Feeding Behavior, and Feed Efficiency

Feeding represents one of the largest costs of dairy cattle production. Therefore, improving feed efficiency through genomic selection has been a key goal of the dairy cattle sector over the past few decades. In addition to feed efficiency traits, feed intake variability and feeding behavior can be related to health status and other stressors. For instance, fluctuations in rumination time and regurgitation frequency can indicate changes in digestion, stress, or disease (Simoni et al., 2023; Hoffmann et al., 2024). Therefore, such variables can be used for assessing animal health status, early disease detection, and improving dairy cow management. Various equipment has been employed for recording feeding related traits, including 3D cameras and various types of electronic feeders. Table 6 presents heritability estimates for various indicators of feed efficiency, feeding behavior, and feeding intake. Traits such as DMI and residual feed intake (**RFI**) are moderately heritable with estimates ranging from 0.13 to 0.49 (Table 6). It is worth noting that a cost-effective system based on 3D cameras has been proposed in Denmark (Cattle Feed Intake System) with heritability estimates for DMI of 0.25 ± 0.02 in Holstein and 0.17 ± 0.03 in Jersey cattle (Manzanilla-Pech et al., 2023). Various other feed-related traits have been derived over time (Table 6), but most dairy breeding programs have only included feed efficiency traits in their selection indexes.

Methane Emissions

Breeding is an efficient tool that can be used to reduce the environmental footprint of dairy production. Various methods and sensors for individual measures of enteric GHG emissions in cattle have been developed, where "sniffers" installed in AMS feed bins and GreenFeed systems are most common in genetic studies (Table 7). A common proxy for methane production predicted from MIR, which has the advantage that it can be used to generate large amounts of data (Table 7). Heritability estimates of methane emissions in dairy cows range from 0.10 to 0.39 (Table 7). The substantial genetic variation for methane emissions illustrates a potential for reducing methane emissions from dairy cows through breeding.

Body Condition, BW, and Conformation

Body condition and conformation are critical aspects of dairy cattle management and play a significant role in many breeding programs. These traits interact with health, productivity, fertility, and overall welfare of dairy cows being the reason for issues, but also visible consequences. The integration of sensor technologies offers new opportunities for the accurate and continuous monitoring of these traits, thereby enhancing genetic evaluations and breeding decisions. Basic technologies are mostly relying on 3D Imaging Systems capturing detailed images of the bodies of cows, allowing for precise measurements of body condition and conformation traits leading to the prediction of BW. Three-dimensional imaging can be used to assess body shape, udder depth, teat placement, and other conformation characteristics. Related technologies

Table 9. Heritability (h^2) estimates for milking efficiency and milk-related traits derived from automated milking systems (AMS; milking robots) in dairy cattle populations

Trait	N	Breed	$h^2 \pm$ SE	Reference
Attachment time	1,899	Holstein	0.25 ± 0.007	Piwczyński et al. (2021)
Average flow rate	1,645	Swedish Holstein	0.37 ± 0.06	Carlström et al. (2013)
Average flow rate	1,512	Swedish Holstein	0.40 ± 0.08	Carlström et al. (2013)
Average flow rate	1,447	Swedish Red	0.37 ± 0.07	Carlström et al. (2013)
Average flow rate	1,544	Swedish Red	0.48 ± 0.08	Carlström et al. (2013)
Milk flow rate	1,714	Holstein	0.55 ± 0.14	Dechow et al. (2020)
Milk harvest rate	1,714	Holstein	0.30 ± 0.10	Dechow et al. (2020)
Average milk flow rate	401	Holstein	0.49 ± 0.06	Gäde et al. (2006)
Maximum milk flow rate	401	Holstein	0.55 ± 0.05	Gäde et al. (2006)
Average milk flow rate	4,507	Holstein	0.43 to 0.52	Pedrosa et al. (2023)
Maximum milk flow rate	4,507	Holstein	0.47 to 0.58	Pedrosa et al. (2023)
Flow rate	4,883	Norwegian Red	0.48 ± 0.04	Wethal and Heringstad (2019)
Box time	1,645	Swedish Holstein	0.21 ± 0.05	Carlström et al. (2013)
Box time	1,512	Swedish Holstein	0.24 ± 0.07	Carlström et al. (2013)
Box time	1,447	Swedish Red	0.38 ± 0.06	Carlström et al. (2013)
Box time	1,544	Swedish Red	0.44 ± 0.07	Carlström et al. (2013)
Box time	1,053	Swedish Holstein	0.24	Carlström et al. (2014)
Box time	1,749	Swedish Red	0.45	Carlström et al. (2014)
Box time	2,258	Holstein	0.25 ± 0.05	Løvendahl and Buitenhuis (2022)
Box time	2,407	Jersey	0.27 ± 0.05	Løvendahl and Buitenhuis (2022)
Box time	1,486	Holstein	0.21 ± 0.03	Sitkowska et al. (2024)
Box time	4,883	Norwegian Red	0.27 ± 0.03	Wethal and Heringstad (2019)
Connection time	27,726	Danish Holstein (including Danish Red Holstein)	0.36 ± 0.02	Stephansen et al. (2018)
Handling time	4,883	Norwegian Red	0.05 ± 0.01	Wethal and Heringstad (2019)
Incomplete milkings	1,714	Holstein	0.03 ± 0.01	Dechow et al. (2020)
Incomplete milkings	4,883	Norwegian Red	0.01 ± 0.005	Wethal and Heringstad (2019)
Leakage	66,743	Norwegian Red	0.04 ± 0.01	Wethal et al. (2020a)
Milk yield	1,713	Holstein	0.25 ± 0.05	Aerts et al. (2021)
305-d mature-equivalent milk yield	1,714	Holstein	0.30 ± 0.02	Dechow et al. (2020)
Milk yield (5 to 70 d postpartum)	670	Nordic Red	0.29 ± 0.13	Häggman et al. (2019)
Milk yield	401	Holstein	0.20 ± 0.03	Gäde et al. (2006)
Daily milk yield	953	Holstein	0.14–0.20	Nixon et al. (2009)
Daily milk yield	4,507	Holstein	0.07 to 0.28	Pedrosa et al. (2023)
Daily milking frequency	953	Holstein	0.02–0.08	Nixon et al. (2009)
Milking efficiency	4,506	Holstein	0.45 to 0.56	Pedrosa et al. (2023)
Milking frequency	1,713	Holstein	0.23 ± 0.04	Aerts et al. (2021)
Milking failures	4,511	Holstein	0.02 ± 0.01	Pedrosa et al. (2023)
Milking efficiency	1,486	Holstein	0.35 ± 0.01	Sitkowska et al. (2024)
Milking efficiency	4,883	Norwegian Red	0.22 ± 0.03	Wethal and Heringstad (2019)
Milking frequency	2,258	Holstein	0.22 ± 0.04	Løvendahl and Buitenhuis (2022)
Milking frequency	2,407	Jersey	0.17 ± 0.04	Løvendahl and Buitenhuis (2022)
Milking frequency	1,899	Holstein	0.51 ± 0.01	Piwczyński et al. (2021)
Milking frequency	4,883	Norwegian Red	0.05 ± 0.01	Wethal and Heringstad (2019)
Milking frequency (DIM 0–99 d)	1,216	Not reported (dairy cattle)	0.16 ± 0.04	König et al. (2006)
Milking frequency (DIM 100–199 d)	1,112	Not reported (dairy cattle)	0.19 ± 0.05	König et al. (2006)
Milking frequency (DIM 200–299 d)	1,004	Not reported (dairy cattle)	0.22 ± 0.05	König et al. (2006)
Test-day milking frequency	543	Holstein	0.14 ± 0.01	Nixon et al. (2009)
Milking interval	1,645	Swedish Holstein	0.26 ± 0.05	Carlström et al. (2013)
Milking interval	1,512	Swedish Holstein	0.17 ± 0.05	Carlström et al. (2013)
Milking interval	1,447	Swedish Red	0.09 ± 0.03	Carlström et al. (2013)
Milking interval	1,544	Swedish Red	0.23 ± 0.05	Carlström et al. (2013)
Milking interval	4,883	Norwegian Red	0.02 ± 0.01	Wethal and Heringstad (2019)
Milking refusals	4,511	Holstein	0.09 ± 0.01	Pedrosa et al. (2023)
Milking speed	1,713	Holstein	0.42 ± 0.07	Aerts et al. (2021)
Milking speed	1,899	Holstein	0.43 ± 0.01	Piwczyński et al. (2021)
Milking speed	1,486	Holstein	0.36 ± 0.05	Sitkowska et al. (2024)
Milking speed	72,487	Norwegian Red	0.22 ± 0.01	Wethal et al. (2020)
Milking time	1,714	Holstein	0.26 ± 0.04	Dechow et al. (2020)
Milking time	401	Holstein	0.38 ± 0.03	Gäde et al. (2006)
Milking time	4,507	Holstein	0.22 to 0.28	Pedrosa et al. (2023)
Milking time	1,899	Holstein	0.31 ± 0.01	Piwczyński et al. (2021)

Continued

Table 9 (Continued). Heritability (h^2) estimates for milking efficiency and milk-related traits derived from automated milking systems (AMS; milking robots) in dairy cattle populations

Trait	N	Breed	$h^2 \pm$ SE	Reference
Natural logarithm of number of attachments per teat	27,726	Danish Holstein (including Danish Red Holstein)	0.26 ± 0.02	Stephansen et al. (2018)
Number of milkings	1,447 to 1,645	Swedish Holstein and Swedish Red	0.02 ± 0.01 to 0.07 ± 0.01	Carlström et al. (2013)
Number of milkings	1,714	Holstein	0.07 ± 0.02	Dechow et al. (2020)
Incomplete milkings	4,883	Norwegian Red	0.14 ± 0.03	Wethal and Heringstad (2019)
Milkings with teat not found	4,883	Norwegian Red	0.12 ± 0.03	Wethal and Heringstad (2019)
Rejected milkings	4,883	Norwegian Red	0.05 ± 0.02	Wethal and Heringstad (2019)
Teat not found	4,883	Norwegian Red	0.002 ± 0.004	Wethal and Heringstad (2019)

generation spatial coordinated allow, automatically during AMS milking, to acquire udder conformation traits, which were already considered for use in genetic evaluations in several countries (Poppe et al., 2019; Medeiros et al., 2024) because of its low costs (i.e., no need to send an appraiser) and good integration in the development of AMS systems. Advanced technologies are also automated BCS systems using cameras and image analysis software to automatically score body condition with numerous contributions in the last 20 yr (e.g., Bewley et al., 2008b; Hernandez-Gotelli et al., 2023). They provide consistent and objective assessments, reducing the variability associated with manual scoring. Moreover, efforts are ongoing to estimate BW, BCS, and type traits in dairy cows using 3D cameras but also integrating them with manual body measurements (e.g., Martins et al., 2020). Finally, indirectly through devices such as accelerometers and pedometers, one can monitor cow activity and movement patterns, providing indirect indicators of body condition and conformation defects as leg health. Changes in activity levels and movement patterns can signal issues such as lameness (Nejati et al., 2023) or discomfort then leading to lower BCS. As shown in Table 8, BW and body conformation traits have moderate to high heritability estimates, ranging from 0.31 to 0.79 (Table 8).

Milk Production and Milking Efficiency

Automated milking systems facilitate the continuous monitoring of various traits related to lactation performance and animal behavior, providing valuable data for both management and genetic selection. With the wide adoption of AMS in dairy farms, such datasets are being generated in large scale. In addition to milk yield, other traits related to milking efficiency are of great interest, including milking speed or flow rate, box time, number of incomplete milkings, milking interval, milking failures, and milking refusals. As shown in Table 9, most traits related to milk yield and milking efficiency have moderate heritability estimates, indicating that genetic selection for improved performance in robotic dairy farms is feasible.

DATA ACCESS, OWNERSHIP, STORAGE, AND INFRASTRUCTURE

Effective genetic evaluations and breeding programs incorporating data from sensors and other technologies are based on large-scale datasets. The storage and management of data for dairy cattle genetic evaluations require a robust and scalable infrastructure capable of handling large and multidimensional datasets (Wangen et al., 2021). As large amounts of data are generated, an important step is the definition of the variables and data that should be stored for long-term usage to ensure consistency, relevance, and efficiency in genetic evaluations. The primary challenges include ensuring data integrity, security, and accessibility while maintaining computational efficiency for real-time or near-real-time analyses. High-throughput storage solutions, such as distributed databases and cloud-based platforms, are essential to accommodate the continuous influx of genomic and phenotypic data from diverse sources. Additionally, standardized data formats and interoperability frameworks are necessary to facilitate seamless integration and analyses across research institutions, breeding organizations, and industry stakeholders. Efficient indexing, redundancy mechanisms, and scalable computing resources are critical to optimizing data retrieval and processing for accurate and timely genetic evaluations. However, many factors must be considered before a structured data flow system can be incorporated into genetic evaluations. This includes regulatory considerations such as data access and portability rights, data access modalities (automatic and secure data transfer pipelines on site or off site), data storage (format, resolution), data governance, robust data security, and ethical considerations. Therefore, a need exists for clear data sharing agreements, which include the above-mentioned points for parties involved in data generation. Stakeholders (with support from regulatory agencies) should foster trust and develop business models that are of mutual benefit. Examples of stakeholders include dairy farmers, DHIA organizations, technology providers, ICAR, universities, and other research organizations, breeding companies, national genetic evaluation centers, and others.

In general, dairy producers own and control the use of data generated in their herds, including genomic information, and access to their data is regulated by agreements signed with DHIA service providers, research organizations, or other institutions. However, getting access to data sets from on-farm technologies in the first place usually require agreements between relevant stakeholders for the specific purpose, good data governance practices, and efficient computing infrastructure.

The use of sensor-derived data for genetic improvement introduces critical questions about legal data allocation (commonly called “data ownership”) and the allocation of the results of data sharing, intellectual property rights, and privacy. Although farmers generate and manage these data streams through on-farm technologies, access and portability rights become ambiguous when the farmer generates data, which it does not control factually because they are “possessed” by the manufacturer. The lack of explicit data governance frameworks poses risks of data misuse, restricted farmer access, and inequitable value distribution. Therefore, ensuring that farmers retain appropriate control over their sensor data while enabling its use for genetic advancements is essential to fostering trust and maximizing industry benefits (Barton et al., 2025).

As the role of sensor data in genetic evaluations expands, the need for standardized policies on data access, sharing, and monetization becomes increasingly important. Regulatory frameworks in Europe, such as the General Data Protection Regulation for personal data and the upcoming Data Act as a horizontal regulation for user access to all Internet of Things data and the Data Governance Act as data governance regulation, will facilitate data sharing in the future while preserving privacy of personal data and trade secrets, and creating trust in data sharing. Without clear policies, farmers risk losing control over their sensor-derived data, potentially leading to restricted access to genetic insights derived from their own contributions. Transparent policies and contracts should define access and portability rights, provide mechanisms for opt-in or opt-out participation, and ensure equitable value distribution among all stakeholders (Majcen, 2022; Barton et al., 2025). To efficiently integrate new traits into large-scale breeding programs, several technical and legal problems need to be resolved, especially when it comes to interoperability and data governance.

ROADMAP FOR USING SENSOR DATA FOR GENETIC EVALUATIONS

For the efficient implementation of routine genetic and genomic evaluations, collaboration among various stakeholders and organizations is essential. At the core of this process is the commitment of dairy farmers, whose active participation ensures the availability of sensor data for downstream analyses, which also allows reliability checking of the automated data collection. As sensor technologies become more widespread, dairy farmers may also seek to monetize their data, potentially making agreements with research organizations, national genetic evaluation centers, or even selling their data to private dairy breeding companies that are developing reference populations for novel traits. However, the benefit from reliable genetic and genomic evaluations has sustained the routine centralized data processing, and it is not yet clear whether the availability of new data sources such as sensor technology will, in the long term, lead to split of data flow and limited data sharing with the established national evaluation centers.

As datasets are generated, pipelines must be developed for routine gathering and integration of the sensor data, with frequent data delivery or real-time data flow to a central platform. The DHIA organizations play a crucial role in the routine collection, aggregation, and analyses of recorded variables. As trusted data handlers with long-term experience in data management, they are well positioned to facilitate the integration of sensor data into genetic evaluations. The network of DHIA organizations and related computation centers provide the required infrastructure for data governance, enabling benchmarking and sectoral analyses while maintaining neutrality across different sensor brands and models. Their strong connections with governmental and breeding organizations further enhance their capacity to standardize and validate sensor-derived information. To maximize the benefits of sensor data integration, well-documented metadata, and clear guidelines for data editing, control, and analyses under routine conditions must be established. Implementing data governance principles based on fairness and transparency is essential for building long-term trust among farmers, dairy sector stakeholders (e.g., DHIA, breeding organizations, companies, breed associations, national genetic evaluation centers), and research institutions. In this context, acknowledged international bodies, such as ICAR, must provide the framework for ensuring interoperability and consistency across data sources, including guidelines and reference standards to promote the effective use of sensor data in genetic and genomic evaluations. Standards for data recording and use are developed and agreed upon by experts and include consensus on how to better integrate, edit, and use the different types of automatically recorded data. However, the development of such standards and guidelines implies reasonable efforts and requires collaboration and agreement between different stakeholders. Therefore, working groups such as the ICAR-IDF Sensor Initiative (Egger-Danner et al.,

2024) are valuable to meet these goals. Standards facilitate cooperation between stakeholders and result in more efficient data exchange and use, improved interpretation and more consistent results (Baldin et al., 2025).

All the integrated data needs to be securely stored in central databases for performing genetic and genomic analyses and routine genetic evaluations. For instance, producers-owned central databases could be essential for advancing the dairy sector, making neutral benchmarks available, ensuring autonomy from international providers, and enabling collective research as well as genetic progress through reliable comprehensive evaluation systems. The datasets available can be used for deriving novel traits for refining selection indexes. Data editing, processing, and integration should be highly automatized. After the traits of interest are derived, variance components should be (re)estimated on a regular basis. Genomic evaluations are then performed, followed by aggregation of the (G)EBVs in selection indexes, which are reported to breeding organizations and dairy farmers as basis for selection and culling decisions at the farm and population levels.

Finally, the optimal use of sensor data in dairy genetics requires continuous advancements in education and professional training. The next generation of professionals, including breeders, farm managers, and veterinarians, must be equipped with the knowledge how to make best use of the wealth of information becoming regularly available. Having animal science expertise and strong data science skills is helpful and may become a prerequisite for successful dairy farm management in the future. Strengthening these capacities will ensure that sensor data are effectively leveraged for improving genetic evaluations and overall efficiency of the dairy sector.

CONCLUSIONS

The integration of sensor technologies into dairy cattle breeding offers a major opportunity to enhance genetic evaluations and accelerate progress in traits linked to health, welfare, and sustainability. High-frequency, objective data from automated systems enable more precise selection criteria and improved evaluation reliability. Realizing this potential requires overcoming challenges in data harmonization, standardization, access, and governance. Transparent sharing frameworks, stakeholder collaboration, and robust quality control are essential. Global bodies like ICAR and IDF are key to developing guidelines that ensure interoperability. Success will also depend on policies that balance data ownership, privacy, and fair value, along with scalable infrastructure, artificial intelligence–driven analytics, and professional training. By addressing these needs and fostering innovation, the dairy sector can leverage precision livestock farming to boost productivity, improve welfare, and advance sustainable breeding, transforming dairy herd improvement into a more efficient, data-driven process worldwide.

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Nonstandard abbreviations used: CH4_RATIO = the ratio between CH_4 and CO_2 in the breath of the cows; CH4_MILK = grams of CH_4 per liter of milk produced; 3D = 3-dimensional; AMF = automated feeding machine; AMS = automated milking systems; CFHA = calving to first high activity; EC = electrical conductivity; FTIR = Fourier-transform infrared spectroscopy; FTWG = Functional Traits Working Group; ICAR = International Committee on Animal Recording; IDF = International Dairy Federation; MIR = mid-infrared spectroscopy; OCC = online cell count; RFI = residual feed intake.

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