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Phenomics Evaluation in Cattle Breeding

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Abstract: The progress of technology, namely in the realm of computer science, has resulted in the capability to handle extensive sets of information, sometimes referred to as big data, which has substantially influenced the field of genetic science. The discipline of livestock farming has witnessed the emergence of several branches of study, including genomics, proteomics, transcriptomics, and metabolomics. Using phenomics in cattle breeding has gained significant importance in augmenting production and efficiency. Scientists have created livestock phenomics platforms to enhance the welfare and productivity of animals by employing cutting-edge digital technologies and real-time sensors. Incorporating phenomics with genomics has expanded the potential for genetic assessment and breeding initiatives in the livestock sector. Phenomics allows for the assessment of the intricate reactions of animals to environmental stimuli, hence aiding in the advancement of more robust and productive cattle. In summary, of phenomics in cattle breeding has significant potential for the future of livestock production, providing prospects for better breeding objectives, promoting animal well-being, and boosting overall output.

Introduction

Advancements in technology, particularly computer science, have facilitated the emergence of big data, creating opportunities for advancements in genetic science. These advancements have brought to light research fields such as genomics, proteomics, transcriptomics, and metabolomics (1). The progress in genetics and livestock breeding has led to the development of many application areas that use genomic information for selection (2-5). These applications commonly arise from DNA sequencing and genotyping technologies that have a high efficiency level (5).

The emergence of big data has led to the continuing development of the discipline of OMICS sciences. This field provides the opportunity to perform research and analysis on massive quantities of data that explain the structure and function of a whole biological system at some particular level (1, 6-9). The four major omics sciences, namely genomics, transcriptomics, proteomics, and metabolomics sciences, are organized in a hierarchical order. These sciences encompass various subfields such as epigenomics, epitranscriptomics, epiprotenomics, interactomics, immunomics, microbiomics, pangenomics, metagenomics, nutrigenomics, lipidomics, pharmacogenomics, and phenomics (Figure 1) (1, 7-13).

The emergence of various technologies, particularly genomic studies, in the past two decades has greatly facilitated the development of sustainable livestock systems by enabling efficient breeding of animal populations (2, 15-17). To ensure the long-term viability of livestock farming, enhancing the development and utilization of species-specific genetic tools and resources is imperative.

Genomic selection is a type of marker-assisted selection (MAS) that employs genetic markers throughout the entire genome, ensuring that all quantitative trait loci (QTL) are in linkage disequilibrium with at least one marker (18, 19). Animal breeding projects have substantially researched the notion of marker-assisted selection (MAS) using marker information(18, 19). Using QTL markers, one can assess an individual's genetic worth. This genetic value may be more

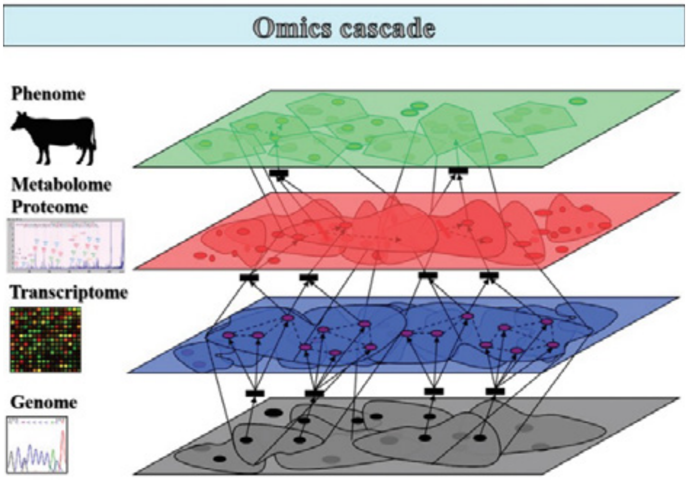


Figure 1: In systemic biology, the omics cascade chain connects multiple levels of biological data related to a specific phenotype (14)

precise than that derived from pedigree and phenotypic data(19).

Nevertheless, despite the current state of technological advancement in genomic science, it is seeing a decline in its initial rate of progress (5). Consortia, like the Functional Description of Animal Genomes (FAANG), aim to develop genomic tools specific to each species. Their goal is to uncover fundamental information about how genomes function and to understand the relationship between genotype and phenotype in livestock animals. They then seek to model this relationship at various levels, including cells, tissues, and the entire animal, to gain insights into the genotype-phenotype connection within animal populations (15, 20-22). The measurement and identification of discernible traits in animals are crucial for the efficacy of animal breeding (5, 15). The absence of accurate and comprehensive phenotypic data is acknowledged as a substantial obstacle in multiple domains of animal genetics and genomics (5, 15). It is important essential to obtain records of appropriate phenotype or phenotypic values (phenotypic data) so that live animal populations can be managed regularly and daily to maximize reproductive strategies, control diseases, ensure animal welfare, and minimize the environmental impacts of animal production (23, 24). Phenotypes are recorded to provide the basis for datasets utilized to monitor to monitor the profitability of growers and develop agricultural policy for the United States of America and other countries (24). The research findings establish that revealing the accuracy of expected genetic characteristics in various genetic models for evaluating animals with phenotypic records impacts the possibility of genetic advancements (25).

Genomic studies have made significant progress in determining animal breeding values. However, the role of epigenetic factors in determining the breeding value has led to the emergence of phenomic studies. Phenomics is rapidly becoming a significant new technology in the field of biology, and its development is accelerating. In this review, omics sciences will be presented briefly, and the notion of phenomics, which is now in its early stages of development, as well as its various fields of research, will be discussed.

What are the omics sciences?

The complete analysis of a vast amount of data, sometimes known as "big data, " that depicts the entire structure and function of a particular biological system at a specific level is what is meant by the phrase "organic molecular information processing" (OMICS). This strategy has had a significant impact on the approaches that are generally used to investigate biological systems. The combination of the "top-down" strategy, which is frequently utilized in the process of developing the omic, with the "bottom-up" techniques results in the creation of a comprehensive instrument that enables the effective investigation of biological systems. The study of complicated illnesses such as cancer has developed from a straightforward differentiation between cancerous and healthy cells to a full investigation of complex systems in a slow and restricted manner. A comprehensive and objective investigation of a large number of alteration layers at the genomic, transcriptomic, proteomic, and metabolic levels is included in this work (7, 26, 27).

Since the introduction of the DNA microarray, the first high-throughput device, researchers have rapidly progressed in developing tools for omics research. Omics technologies have been employed following the central dogma to capture several biological changes. These include static genomic alterations, temporal transcriptome perturbations, alternative splicing, as well as spatiotemporal proteome dynamics, and post-translational modifications (PTM). This is in accordance with the core dogma. Furthermore, omics technologies have broadened their range to explore different omics at the epigenetic level, including the epigenome, epitranscriptome, and epiproteome. These phrases encompass all alterations of the corresponding omics that extend beyond the data they offer in an individual cell. Moreover, omics technologies let us look at molecular interactions at different levels of the interactome, as well as features linked to disease, like the metabolome and immunome. Incorporating various omics data has emerged as a prevailing practice in creating a complete and causal relationship between the molecular characteristics and phenotypic manifestations of a particular disease. A single-cell array offers enhanced sensitivity, enabling studies at the level of individual cells. The field of omics, which is quickly progressing and growing, allows us to systematically and precisely investigate the intricate molecular processes that underlie many abnormal characteristics and their observable traits. Yet, the complicated characteristics of cellular activity and its decision-making mechanisms consistently stimulate the advancement of novel omics and associated methodologies (7).

As our understanding of cellular omics continues to grow, it continuously reshapes our perception of how cells behave, bringing us closer to reality. This poses a challenge in attaining the objective of complete regulation over the reorganization of cellular pathological states. Hence, it is vital to thoroughly assess advancements and continue investigations in omics to forecast future probabilities and expedite the objective (7).

The field of omics sciences, which has had significant growth in recent years, is continuously witnessing the emergence of new topics. Phenomics, the central focus of this review, refers to the quantification of how the phenotype responds to genetic mutations and environmental influences (25, 28-30).

What is phenomics?

The primary objective of biology is to understand phenotypic characteristics, including aspects related to health, diseases, and adaptive fitness (29, 31). In recent years, there has been an explanation for integrated and multivariate biological responses. The primary advantage of this explanation is that new omics techniques decrease the element of chance typically associated with research design and the potential for selecting features (31). Nevertheless, the omics field primarily concentrates on the molecular level. Some molecular changes may not directly impact the observable characteristics of an organism, potentially restricting their ecological significance. Therefore, it is imperative to incorporate additional comprehensive and observable methods (32). Phenomics, a term introduced by Dr. Steven A. Garan in 1996, refers to of quantifying how phenotypes react to genetic alterations and environmental factors. The primary goal of phenomics is to thoroughly and expeditiously characterize the phenotype, encompassing the organism's physical and biological attributes (25, 28-30). These biological features encompass a range of quantitative characteristics, such as individuals' and communities' physical, chemical, and biological attributes. These traits arise from the intricate interplay of genes, epigenetics, microbes, diet, and environmental factors (28). Phenomics is a field of science that covers the methods and tools that enable the application of technologies that allow the collection, analysis, and use of large amounts of phenotypic data related to the characteristics of an organism in various dimensions inexpensively and easily (24-31). Phenomics plays a crucial role in ensuring precise and consistent assessment of traits or phenotyping, effective management of livestock, and enhancement of genetic qualities (33).

In the present day, where climate change is happening rapidly due to increased global temperatures, it is important to measure the many and constantly changing effects of the environment on the physical characteristics of organisms. The significance of phenomic techniques is growing since they allow for the consideration of the many responses of organisms to the environment, therefore aiding in resolving intricate tasks (32). Although phenomics and genomics share similarities in terms of expression, it is important to note that phenomics does not encompass everything related to the field of phenomics. Currently, it is possible to identify practically the entire genome, but the same level of identification cannot be achieved for phenomics. The disparity arises from the fact that the quantity of data present in the phenotype surpasses the number of pieces of data present in the genotype (31). The fact that phenotypes differ from cell to cell and moment to moment makes it impossible to define and explain them exactly. Phenomics requires prioritizing the measurement of certain characteristics and achieving a harmonious equilibrium between research and explanation (31, 32).

An exceptional conceptual framework is crucial for comprehending the intricate phenomenological realities at different organizational levels. Fortunately, this method may utilize established intellectual frameworks for analyzing phenotypic data, including quantitative genetics, evolutionary biology, epidemiology, and physiology. These disciplines offer approaches for systematically studying and assessing the numerous elements that contribute to variation, as well as discerning between causal relationships and simple correlations (31).

The production of phenotypic variation results from intricate interactions between genotype and environment. In order to thoroughly explore these interactions, it is essential to have enough phenotypic data to rebuild the 'genotype-phenotype' map representations accurately (31).

To understand the complex relationship between genetic variety and changes in economically significant features, it is essential to analyze the underlying biological and physiological systems. This can be accomplished by creating a precise delineation of phenotypic data. Phenomics-level data are required to understand which genomic variants affect phenotypes, to understand epistasis and pleiotropy, and to provide the raw data needed to decipher the causes of complex biological phenomena (31).

The vitality of phenomics in breeding

By 2050, the global population is projected to reach 9.1 billion individuals, with the majority residing in developing countries (34, 35). A seventy percent boost in food production is necessary in the agricultural and livestock systems to adequately feed this population. Meat production from primary food sources is projected to rise by roughly 200 million tons annually, reaching an estimated 470 million tons by 2050. This increase in demand is driven by population expansion and shifting demographic patterns, particularly in developing countries with increasing incomes (33, 36). Global climate change will make this already challenging process even more difficult for developing countries (36).

Present genetic breeding in livestock depends on genomic data, such as single nucleotide polymorphism genotyping and sequencing, together with accurate recording of essential traits. Integrating pre-existing phenotypes and genomic data has facilitated the identification of economically significant genes and quantitative trait loci (QTL). Furthermore, it has resulted in developing genome-enhanced predicted breeding values that can be effectively utilized in genomic selection (36).

Genomic selection has been used extensively for breeding values of animals (19), milk yield (19, 37-41), milk fat(X7), meat yield(42), meat quality(41), carcass characteristics(42), feed efficiency(40), fattening performance(43), growth(40, 42), bone development(41), reproductive performance(44), fertility(40), heat stress(45), adaptation ability to heat and humidity(46), hereditary diseases(47), udder and foot health(48), and BRD resistance(49).

In recent years, the area of molecular genetics has made significant progress, leading to a reduction in genotyping costs. The routine genotyping of many young females and almost all young possible bulls is no longer constrained by the genotype's availability. The present obstacle to future assessments of new economically significant characteristics is in phenotypes, and precise phenotyping remains a substantial limitation for animal breeding (36, 50). The absence of continuous phenotyping limits the development of production efficiency in livestock, providing an important barrier to breeding improvement (36, 51).

There is a need for better definitions of certain traits that are important for the economy to understand better the intricate relationships between animals and their biological and physiological systems. Gathering comprehensive phenotypic and environmental data poses a major challenge in livestock breeding research studies. It is essential to recognize and establish consistent new observable traits, ranging from gene expression to the attributes of the animal product, and systematically compile them in formats that computers can process. This requires the development of top-notch data collection methods encompassing various research fields at different biological scales. The integration and interpretation of vast amounts of data created by many sources now require vital bioinformatics approaches and modern technologies for data management, processing, and analysis. These remarkable advancements will enable a more comprehensive comprehension of the phenotype and its role in economically significant traits for cattle production systems (51).

The usefulness of phenomics in livestock depends on its ability to produce and show essential results from the large amounts of phenotypic data shared in recent years. This data can be used as a starting point for enhancing the performance and efficiency of livestock systems by utilizing genetic, genomic, and other 'omics' technologies. Furthermore, it may facilitate more precise livestock management and the optimization of feed supplies (33).

Phenomics is the scientific investigation of multiple variables in grasslands or shelters with a previously unknown degree of accuracy and precision. It aims to identify economically significant new traits, such as monitoring feed consumption and determining feed utilization during animal grazing in pastures or within shelters. Implementing this method in phenotyping might enhance the precision of predicting quantitative traits by optimizing the use of nutritional and other management measures, hence expediting the rate of genetic improvement for both current and novel qualities (33).

Emerging characters in the era of phenomics

The definition of the phenotype of an organism can be broad; it generally refers to a set of morphological and physiological characteristics of an organism and also includes behavioral characteristics (14, 52). Characters refer to distinct traits shown by animals that can be objectively quantified and subjected to statistical analysis. Crucial factors in animal breeding are features that possess a substantial genetic profile and yield direct economic, social, and environmental benefits (14).

Mike Coffey's often-cited statement, “Dairy cows: phenotype is king in the age of genotypes, ” highlights the importance of accurately measuring and documenting relevant phenotypes to successfully implement genomic selection (50). In the era of phenomena, phenotypes have received significant attention in research. The significance of complex interactions between challenging-to-assess phenotypes and both established and new breeding traits has increased. In the future, the three primary character complexes, namely energy efficiency, nutritional and environmental resource use, and health and disease resistance traits, as well as animal welfare, are expected to have even greater significance(53). The importance of these characters emphasizes the need to have accurate and thorough knowledge about them(14).

Advancements in engineering technologies and the declining cost of electronic technologies enable the creation of sensing solutions that assist in monitoring livestock by automatically gathering data on specific traits, including physiological parameters, production measures, and behavioral characteristics. One of the present objectives is to measure the activity patterns of animals using sensor-based methods such as pedometers, transponders, boluses, and camera systems. By analyzing the unique variations derived from the patterns formed by animal-specific data, one can draw inferences about their health, fertility, or overall well-being. Furthermore, aside from the interplay between animals and their social, and behavioral traits (such as aggression or calmness), one can also acquire insights about the social networks inside the herd (14, 52).

Moreover, mid-RI spectroscopy in dairy farming has been acknowledged as a promising method for gathering data on a large scale for phenotypic and genetic analysis, making it a subject of ongoing research. Typically, mid-RI spectroscopy is employed to assess the quality attributes of milk samples. Aside from the conventional properties of milk, such as protein, fat, lactose, and urea content, other milk properties, such as fatty acid composition, protein and mineral composition, milk coagulation, milk acidity, melamine content, and ketone bodies, can also be estimated and utilized to predict factors like body energy status and methane emissions(14).

The complexities of new phenotypes

Dairy farms and breeders encounter numerous unusual characteristics as they endeavor to attain their breeding objectives. As a result, farmers are faced with multiple new obstacles. Most brand-new characters are challenging to quantify. The complete understanding of these novel features' biochemical and genetic bases of these novel features, as well as their correlation to other notable traits, remains incomplete, impeding their effective utilization in breeding programs. Utilizing phenomics science in gathering this novel character data and implementing innovative techniques will facilitate the development of an interdisciplinary and nationwide infrastructure for data collection and study. This will enable the breeding goals to be more effectively aligned with the rapidly evolving and emerging requirements (14).

Animal husbandry has been and continues to be an essential factor in increasing the productivity of animals, such as dairy cattle, around the world. The emergence of cost-effective genotyping techniques, such as single nucleotide polymorphisms (SNPs) and sequential genotyping, has made genomic evaluations essential for contemporary dairy cattle breeding methods and programs (2, 14, 54). These evaluations have yielded more significant advancements than the successful adoption of artificial insemination (14, 54). Nevertheless, the accuracy of a genomic breeding value estimate depends primarily on the number of animals with recorded phenotypes and the heritability of the observed characteristics (54). The efficacy of animal breeding is predominantly dependent on phenotypic animal observations, and significant advancements are largely attributed to accurate feature definitions and comprehensive performance tests (14).

Phenomics approaches

To cope with the increasing global need for animal protein, the dairy sector must maximize the cow's capacity to transform inedible plant material efficiently. This necessitates the optimal utilization of all required agricultural inputs on the farm. To minimize undesirable outputs from livestock, ensure effective management of cows and their surroundings, and provide consumers with confidence in the health and welfare of dairy animals, it is imperative to employ cutting-edge technologies that utilize affordable sensors and advanced data processing tools. Practical cooperation among dairy producers, scientists, and the associated sector is crucial for converting new technologies into feasible solutions (55).

Given the increasing complexity of dairy cattle production systems, measuring all aspects of animal performance throughout an individual's life is critical. The selection concept has evolved from focusing solely on traits related to animal productivity to encompassing traits linked to effective resource utilization, enhanced well-being, resilience, and overall welfare. The primary objective of phenome data is to furnish pertinent information to make informed judgments regarding on-farm management and genetic enhancement (55).

The recent surge in interest in animal phenotypic data can be attributed to the emergence of advanced electronic sensors capable of gathering precise and frequent measurements of animal performance and environmental conditions in real-time or near-real-time. Figure 2 provides an easy-to-understand summary of the data that can be obtained by selecting these devices (55). To reduce labor requirements, automated data collection and management systems incorporate real-time sensor platform technologies, e-management systems, and predictive characteristics (33).

Comprehensive and precise phenotyping is critical for breeding programs as well as the genetic study of complex characteristics. High-intensity genotyping sequences can recognize an organism's genome, but its "phenotype" is a more intricate concept that is not entirely explicable due to its unpredictability over time and susceptibility to

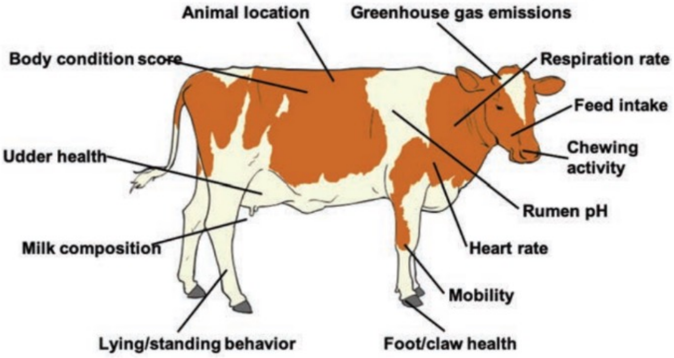


Figure 2: Phenotypes that are gathered on an individual cattle basis with sensor-based devices (55)

environmental influences(16, 31). Despite the decreasing cost of genotyping, there is a need for enhancements to get high-performance phenotypes at a more affordable rate. The number of phenotypes recorded in conventional cattle breeding systems is restricted because of the expensive registration process. For instance, farmers typically calculate yearly milk yield by extrapolating from a small set of lactation data. They can now directly evaluate the real-time milk yield for each cow daily. Automated milking robots revolutionize the dairy industry (16).

Dairy cow breeders are concerned with body composition and milk yield traits. These measures are not only important for aesthetics, but they also play a critical role in determining an animal's breeding value. An individual's body shape significantly influences their milk production capacity and overall lifespan, affecting the total milk output during their lives. There is a direct relationship between milk production and teat size (16). Dairy farmers are primarily economically affected by leg difficulties or lameness caused by injuries. Claw abnormalities leading to lameness are a significant issue in contemporary global dairy cattle farming, resulting in pain, discomfort, reduced weight, lower milk yield, decreased reproductive efficiency, higher chances of being removed from the herd, increased treatment expenses, and mortality. This syndrome arises from various causes and predisposing factors, including environmental variables and specific factors in dairy cattle (16, 56). Acquiring comprehensive body composition-related traits that can impact the offspring's success requires significant time and resources. Farmers frequently rely on qualitative assessments of morphometric data without quantitative methods (16).

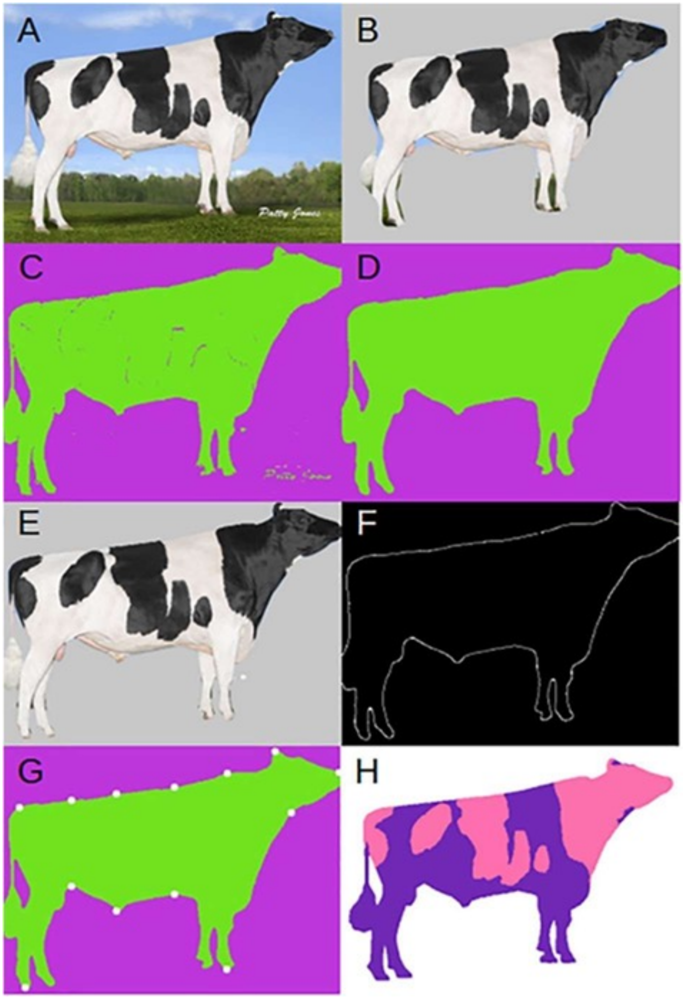
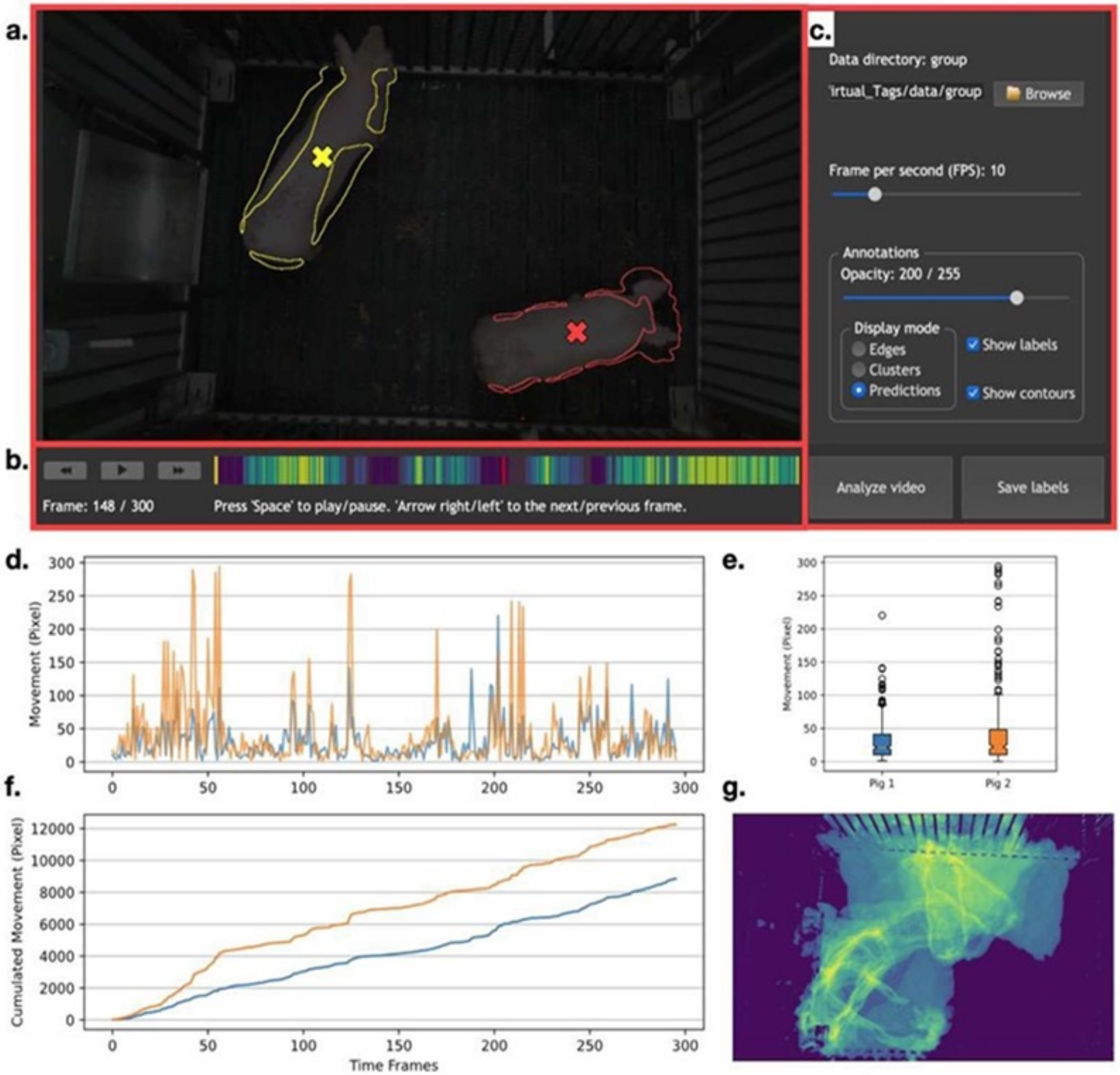


Figure 3: Sample inputs and outputs. (A) Initial input image. (B) Mask R-CNN utilized masks.. (C) Raw output from DeepAPS. (D) DeepAPS final result after applying all filters. (E) The last DeepAPS mask that was used on the input image.(F) Sketch the initial input image. (G) Implied physical point positions.(H) Manual color segmentation. Image: Semex (16)

Sophisticated machine learning algorithms have brought about significant advances that have profoundly impacted many fields relying on computerized image analysis. These advancements can potentially enhance the results of herd management and animal and plant breeding initiatives. These latest advancements have enabled accurate object detection and classification of many components inside intricate images(16).

Web-based catalog databases can be automatically analyzed to derive genetic parameters from morphological measures in dairy cattle, turning them into valuable information. Nye et al.(16) utilized web scraping, deep learning, and statistical methodologies in their study to accomplish their objective. The research suggests combining an unsupervised technique for exact automatic picture segmentation with Mask R-CNN, a supervised deep learning method. After removing the backdrop, phenotypic information such as frost color and body composition characteristics can be readily quantified (Figure 3). This method combines genetic and other phenotypic data from dairy cows to reveal the entire phenotype of the animal. This work exemplifies the use of cost-effective and non-invasive computer vision methods in dairy cattle breeding operations (16).

Precision livestock farming (PLF) is critical to optimizing resource efficiency on production farms by gathering accurate measurements of animal characteristics due to the increasing demand for animal products. The efficiency of computer vision (CV) systems depends on the manual collection of detailed annotated data, including the x-y coordinates of objects in images. Furthermore, the absence of a standardized annotation format for phenomics investigations makes it challenging for scientists to share annotated data for validation and further development (52, 57). Chen et al. aimed to improve video data with explanations and generate attractive training assistance using their software, VTag (Figure 4). These sources are a valuable method for examining behavioral traits as well as conducting complex investigations in animal phenomics (57).



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Annotations

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Display mode

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Figure 2: Effects of subcutaneous irisin perfusion and/or high-fat diet-induced obesity on A) serum insulin levels and B) serum FNDC5 levels in female rats. Data were expressed as mean ± SEM (one-way ANOVA followed by Tukey's *post-hoc* test or Student's t-test, n = 10 in each group)

Conclusion

Changing climatic conditions have presented challenges for livestock enterprises and farmers in maintaining the sustainability of dairy production systems. The difficulties encompass animal husbandry's environmental and climatic effects, the rise in natural resources and feed shortages, biodiversity, animal welfare and health concerns, and antimicrobial resistance (14, 35, 52, 58). Having strong phenotypes for these new problems is crucial during the phenomics age. In this scenario, technological advancements and access to large amounts of data are critical factors (11, 59, 60). Sophisticated and high-capacity measurement methods determine newer phenotypes. Sensors are becoming more crucial for many characteristics, like methane emissions, rumen microbiome analysis, mid-infrared spectra of milk samples, and behavioral features (14, 35, 52, 61-63).

Modern dairy cow breeding programs strive for high production efficiency, considering ideal animal health and welfare requirements as well as low environmental impact. In the phenomics era, research and practical advancements are concentrated on developing novel phenotypes for animal breeding to address emerging difficulties. Significant gaps remain in comprehending these new characteristics' biological basis and genetic structure.

The connection between the genome and phenome is not well known, especially for poorly defined phenotypes that are challenging or costly to measure accurately. Strong interdisciplinary collaboration is essential for developing suitable measuring technologies, study procedures, and assessment methodologies, as well as for analyzing relationships between critical aspects.

Some of the investigated qualities may not be suitable for breeding, but they can still be valuable for management purposes. The growing quantity and complexity of breeding goal qualities have made the development of balanced breeding goals more complex compared to previous times.

Pooling data from different countries with comparable problems and objective directions can accelerate progress by creating a more extensive reference population for overall selection(14, 33, 35).

The development of computer technologies has led to significant progress in biology, genetics, and plant and animal breeding. This review focuses on the science of phenomics, which is thought to greatly contribute to animal breeding. Phenomics has emerged as a newly developing multidisciplinary science in which the data obtained from biology, technology, and climate sciences is searched for ways to cultivate economics.

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Vrednotenje fenomike v govedoreji

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Izvleček: Tehnološki napredek, zlasti na področju računalništva, je omogočil obdelavo obsežnih nizov informacij, ki se včasih imenujejo masovni podatki, kar je bistveno vplivalo na področje genetike. Na področju živinoreje se je pojavilo več raziskovalnih vej, vključno z genomiko, proteomiko, transkriptomiko in metabolomiko. Fenomika je v govedoreji pridobila velik pomen pri povečanju proizvodnje in učinkovitosti. Znanstveniki so ustvarili platforme za fenomiko v živinoreji, da bi z uporabo najsodobnejših digitalnih tehnologij in senzorjev v realnem času izboljšali dobrobit in produktivnost živali. Vključevanje fenomike z genomiko je razširilo možnosti za genetsko ocenjevanje in vzrejne iniciative v živinorejskem sektorju. Fenomika omogoča ocenjevanje zapletenih odzivov živali na okoljske dražljaje, kar pripomore k razvoju močnejšega in produktivnejšega goveda. Če povzamemo, ima fenomika v govedoreji velik potencial za prihodnost živinoreje, saj zagotavlja možnosti za boljše rejske cilje, spodbuja dobrobit živali in povečuje splošno proizvodnjo.

Ključne besede: učinkovitost živali; vedenje; masovni podatki; bioinformatika; govedoreja; genomika; fenomika; PLF; dobrobit živali