

Measure, predict and act; a paradigm of genetics applied to livestock production now and into the future

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Abstract

Rapid developments in phenotyping and genomic technologies are contributing to lakes of data on animals. Concurrent developments in prediction algorithms are leading to a proliferation of (genomic and phenotypic) predictions on individual animals. Using genetics applied to livestock to reduce the impact of livestock on climate change, while addressing livestock welfare concerns and meeting more sophisticated and diverse nutritional demands of the consumer, are likely to continue to be emerging trends in this and future WCGALP. Being able to measure, predict and act will continue to be the fundamental principles to achieving these objectives. Failure to do so will jeopardise the success of animal breeders into the future, especially if growing numbers of consumers favour entirely plant-based sources of nutrition.

Introduction

Livestock breeding programs can be broadly summarised by the principles of *Measure, Predict and Act*. This paper takes a journey through these three components highlighting the advances made, but also the gaps in knowledge. Being able to collapse the deluge of predictions constantly streaming towards producers into actionable information will be one of the greatest challenges to achieving meaningful change. Animal breeders are well versed in not only collapsing vast quantities of data on a whole gamut of traits into a single index value per animal, but also providing the necessary communications/extension and validation of such tools to build trust among stakeholders.

Measure

The breadth of livestock breeding objectives has generally been limited to those traits with data available, either directly or indirectly; health, fertility and growth traits comprised between 12% (1974) and 30% (2006) of the WCGALP papers to-date (Figure 1a). Focussing on those traits may disadvantage traits that are less well recorded (e.g., feed intake, environment), especially in breeds/strains that are less numerous and subsequently have smaller reference populations, which may be exacerbated in a paradigm of market-driven investment in genetic improvement. The biggest challenge for the current generation of animal breeders is most likely to rapidly address the contribution of livestock to the environment; with livestock being the most significant anthropogenic methane source. Ruminants emit methane as a by-product of rumen fermentation, while poultry are the second largest producer of ammonia, phosphorus, nitrogen, carbon dioxide, and methane, meaning that the challenge spans the main-stream species considered at WCGALP conferences (e.g. de Haas *et al.* 2018, Sell-Kubiak *et al.* 2018). Focusing on the efficient use of feed (especially from sources that cannot be used for human consumption), will likely continue to feature in all animal breeding programs. Feed efficiency

was, in fact, a hot topic across species at the 2014 and 2018 WCGALP and continues to be in 2022, with over 5% of papers presented being on the topic (Figure 1b). This rise is likely due to the increased interest in these traits in cattle breeding, while measuring traits associated with feed efficiency has been common in pigs and poultry for a long time. Figure 1b also shows how papers on methane emissions have been increasing exponentially from the 2014 to 2022 WCGALP. The WCGALP2022 sees an increased focus on selecting for a reduction in all pollutants, with ingenious phenotyping strategies and the use of indirect predictors being used as ways to increase the accuracy of genomic prediction anticipated.

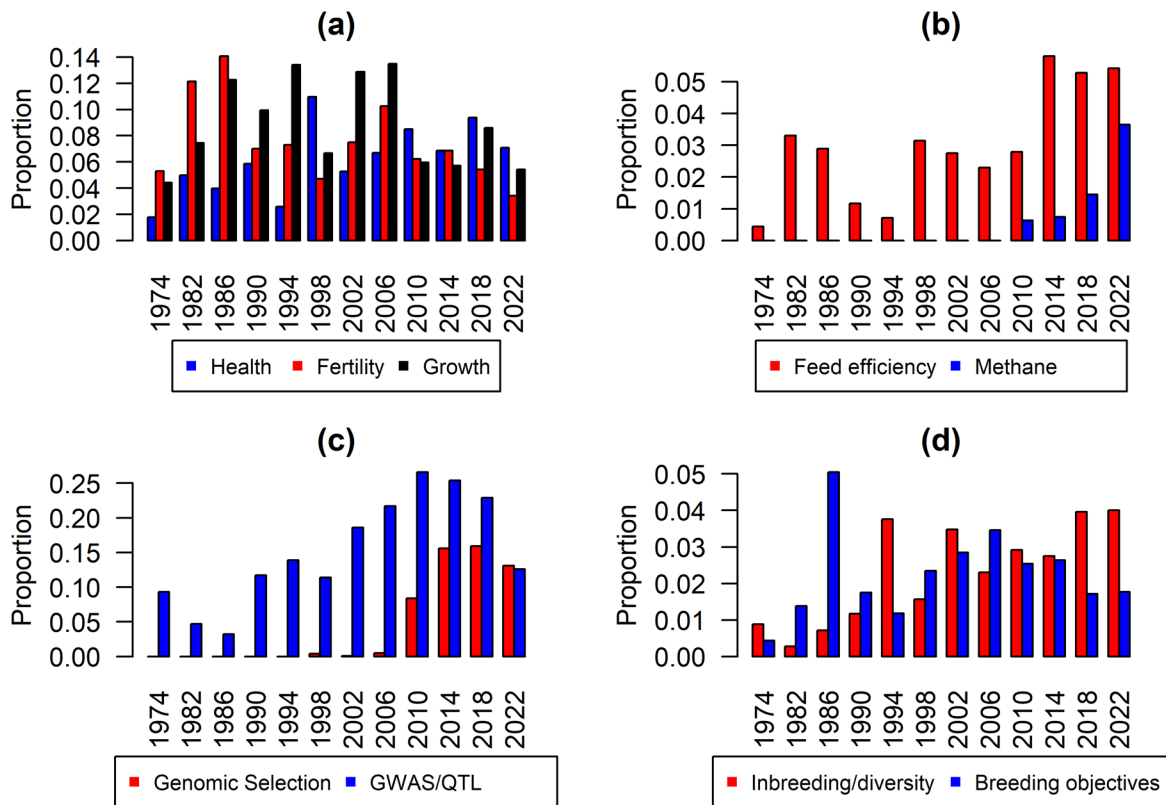


Figure 1. Representation of traits (a & b) and topics (c & d) for each WCGALP year.

Consumers are increasingly demanding high-quality nutritious products. Genetics can be used to select for the best nutritional profile using data from technologies to measure these characteristics. We may see food being tailored to match a person's own requirements. We envisage that animal welfare and sustainability will continue to be important themes. Notable examples are previously observed deterioration in fertility (in dairy cows) and rise of leg weakness (in broiler chickens). Both are, of course, examples of unintended consequences of selection and a warning to animal breeders. To counteract these trends, health and fitness traits have been included in breeding objectives for 20+ years in many cases.

Across many traits discussed, and even ones not thought of yet, it seems very likely that sensors and automated phenotyping will become the primary strategy to collect data for animal breeding purposes and there will be many more high-tech approaches presented at WCGALP2022. For example, CT scanning has been used for non-invasive measurements of (small) carcasses for quite a long time, but such precision phenotyping technologies are coming into their own through its combination with genomic technologies (Byrne and Amer 2018). The challenge

from this will be processing high volumes of data, data quality control steps and combining it in an informative way with other omics data.

Predict

Genomic selection (GS) has undeniably accelerated the wide-spread use of individual genome-wide information in animal breeding programs, facilitated by the availability of affordable 50k genotyping arrays, all within just one decade. This is supported by the rapidly increasing number of GS papers since WCGALP2006, for the first time being more numerous than GWAS papers at WCGALP in 2022, the latter declining after peaking at WCGALP2010 (Figure 1c). Methodological and technological developments have enabled computational requirements to stay within reasonable limits, despite reference populations increasing in size exponentially. We expect several reported applications using >50M genotyped animals at WCGALP2026.

Sequencing strategies in the past decade took either the 1000-bulls' genome approach by genotyping key ancestors in the population at high coverage and imputing to other genotyped animals, or a low-pass sequencing approach, genotyping very many animals at (ultra)low coverage followed by imputation taking advantage of high coverage at the haplotype level (Hickey *et al.* 2014). Large scale individual level actual sequence data, including long reads, will be available soon. Unlocking its full potential include routine detection of chromosome anomalies, optimizing selection and mating considering deleterious alleles, and frequent GWAS for all breeding goal traits. We envisage that GWAS results at base pair resolution will become standard output of genomic predictions, which will develop from being a pure *prediction machine* to also be a *discovery machine*. Combining this phenotype-driven discovery with biological information based on increasingly more accurate functional annotation maps, will enable continuous refinement of SNP sets used in genomic prediction (Goddard *et al.* 2018). Finally, other omics data including microbiome, gene expression, and epigenetic profiles, will help by enabling more accurate phenotyping, refining functional annotation maps, and more accurately dissecting phenotypic variances into its underlying components.

Thirty years ago, the idea of “velo genetics” or germ-line selection was described, with the promise to reduce generations intervals drastically (Georges and Massey 1991). GS indeed has enabled embryo selection in practice. The application of embryo selection based on GS, however, mostly enables to further increase selection intensity, but not to further shorten generation intervals. Genome editing has been a futuristic topic for a long time, but is now part of the available toolbox thanks to CRISPR-CAS. The eventual contribution of gene editing will rely heavily on the ability to identify sufficient numbers of loci that are worthwhile targeting (Simianer *et al.* 2018) coupled with societal acceptance of the technique. With the foreseen *discovery machine* as a “by-product” of GS, and the increasingly more accurate annotation maps, eventually a list of targets worthwhile pursuing is expected to be available.

Act

The breeding goals of the future will need to explicitly consider three consumer-interest areas of environmental responsibility, animal welfare and nutritive characteristics and product quality (Byrne and Amer 2018). While productivity and feeding the world are still of great importance, ignoring consumer-interests is incredibly risky. Approaches to appropriately weight these features in breeding goals will be important, prompting greater research into the optimal construction of breeding objectives and more so than has been presented to-date (Figure 1d). Predictions in themselves are merely outputs and must therefore be acted upon to create impact. Whereas artificial intelligence (AI) is being heralded as a disruptive technology to the prediction processes, the field of eXplainable Artificial Intelligence (XAI) could have a role helping comprehend and trust the predictions. Moreover, prescription (i.e., how to deal with

predicted outcomes) and, more importantly, the ability to diagnose the root of sub-optimal performance will be crucial in the future as decision support tools. Breeders will have to engage more with the developers of decision support systems to a) ensure genetic merit is included as a feature in prediction algorithms, b) ensure that such support systems diagnoses the root of the sub-optimal performance – such support systems must also be able to detect risk into the future given the current trajectory, and c) note any remedial measures undertaken for consideration either in data editing or statistical modelling of the resulting genetic evaluation.

While strategies to control inbreeding were popular in the WCGALPs of the 1990s (e.g. optimal contribution selection (Meuwissen 1997); Figure 1d), there is likely to be a resurgence in the future, especially in ways that are easy to implement and utilise genomic information.

Outlook

Breeding is a well proven technology to deliver genetic change; of course, this genetic change has not always been favourable. Whereas the breeding programs of some species has consolidated considerably (e.g., pigs, poultry, aqua), the breeding programs of other species, most notably ruminants, are still largely underpinned by national genetic evaluations. Of strategic importance is data ownership, which is becoming a contentious issue and as yet, has not been unequivocally addressed in ruminant breeding programs. The time is approaching for mega-corporations to realise the power of genetic gain in delivering food security (i.e., power) while also remaining stewards of the environment. Many of these corporations (e.g., Amazon, Google, Facebook) already have the analytical expertise and potential access to data. More importantly they are now part of everybody's (i.e., consumers) home and have strong influential powers through algorithms like recommender systems. While this will jeopardise the *modus operandi* of current ruminant breeding programs, consolidation may lead to new opportunities and exciting challenges. Nevertheless, issues on data ownership and propriety evaluations could impact what is published at future WCGALP.

The biggest challenge faced by livestock production in the near future, is retaining societal acceptance, at least partly by contributing to healthy tailor-made diets and decreasing its environmental footprint. The world is awash with commentary of silver bullets to grand challenges; breeding programs have proven time and time again to deliver on grand challenges but will need to be more vocal. Now is the time to capitalise on the full potential of highly technological and data intensive breeding programs to deliver on carbon neutrality, in close dialogue with its stakeholders and in particular the consumers.

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