Editorial

Application of Genetics and Genomics in Livestock Production

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1. The Value of Genetics and Genomics in Improving the Productivity and Profitability of Livestock Enterprises

The delivery of genomic sequences for most livestock species over the past 10–15 years has generated the potential to revolutionize livestock production globally, by providing farmers with the ability to match individual animals to the requirements of rapidly changing climates, production systems and markets. The technology which has had the greatest impact to date is genomic selection [1]. Genomic selection uses information from a large number of genetic markers or single nucleotide polymorphisms (SNPs) in conjunction with measurements (phenotypes) of important traits in livestock and plants to estimate breeding values, without requiring precise knowledge of where specific genes are located in the genome. Since the principles of genomic selection were initially proposed in 2001, genomic selection has been widely adopted in animal and plant breeding programs globally because of its ability to improve selection accuracy, reduce phenotyping and generation intervals and increase genetic gains. It has transformed the livestock and plant industries, as well as delivered human health diagnostic applications, adding billions of dollars and strong social and environmental benefits, particularly across the world's higher income countries.

However, genomic selection also requires improvements to the discovery of causal variations and genomic selection methodologies, greater efforts to overcome limitations associated with lack of essential phenotypes for expensive or difficult-to-measure traits, and the ongoing challenges with implementing genomic selection by smallholder livestock farmers in low–middle income countries. This Special Issue examines some of these issues to identify successes and ongoing limitations that must be overcome to achieve practical applications and social, economic and environmental benefits for all livestock producers in the future.

2. Review Process

All articles published in this Special Issue "Application of Genetics and Genomics in Livestock Production" underwent peer review by independent subject matter experts in the fields of livestock genetics and genomics.

3. Application of Genetics and Genomics to Livestock Production: Summary of Articles

3.1. Discovery of Causal Variations for Economically Important Traits

Most of the economically important traits of livestock are complex or quantitative traits under the control of hundreds or thousands of variants in the DNA sequence of individual animals, as well as environmental factors. Identification of these causal variants would be advantageous for genomic prediction and to understand the physiology and evolution of important traits. It would also be advantageous for genome editing. However, because the effect size of such causal variants is small and they are in linkage disequilibrium with other DNA variants, they are also very difficult to identify. Meuwissen et al. [2] therefore

reviewed the literature to evaluate eight types of evidence needed to identify causal variants. They concluded that large and diverse samples of animals, accurate genotypes, multiple phenotypes, annotation of genomic sites, comparisons across species, comparisons across the genome, the physiological role of candidate genes and experimental mutation of the candidate genomic site would all be needed in order to discover the causal variations for the most economically important traits in livestock.

3.2. Improving Genomic Prediction Methodologies

In this Special Issue, a number of papers examined options aimed at improving genomic prediction methodologies. McEwin et al. [3] examined the selection of the best livestock candidates for high-density genotyping, with the aim of improving the accuracy of imputing high-density genotypes from low-density SNP panels. They recommended the use of relationship matrix data already available in routine BLUP and GBLUP analyses as the starting point to obtain accurate sequence information.

Keele et al. [4] examined the use of pooling animals with extreme phenotypes to improve the accuracy of genetic predictions and provide genetic evaluations for novel traits at relatively low cost by exploiting large amounts of low-cost phenotypic data from animals in the commercial sector without pedigree information.

Koivula et al. [5] acknowledged that, while genomic selection is widely used in dairy cattle breeding, single-step models are rarely used in national dairy cattle evaluations. Hence, they compared methods to build genomic and pedigree relationship matrices that satisfied theoretical assumptions and overcome incompatibility issues.

Three additional papers [6–8] utilized a range of new and different 'omics' approaches (e.g., functional genomics, transcriptomics, proteomics, and metabolomics) that target specific genes to better understand gene regulation and function, and potentially, in the future, to improve genomic predictions. Zhang et al. [9] detected positive selection and introgression by runs of homozygosity in cattle.

3.3. Overcoming Limitations to Phenotypes for Expensive or Difficult-to-Measure Traits

Genomic selection is particularly useful for traits that are difficult to measure early in the animal's life. However, it can be difficult to set up a reference population for these traits. This is particularly true for expensive, late-in-life or difficult-to-measure traits such as the reproductive performance of breeding animals or traits reflecting an animal's resistance or tolerance to environmental stresses and diseases.

In this Special Issue, Bennett et al. [10] examined the potential for using genomic information to measure bull prolificacy in multiple-sire breeding herds. They found that the use of easy-to-measure traits such as bull age class and scrotal circumference accounted for less than 5% of the variation, whereas simulated estimation of prolificacy by pooling the DNA of calves was accurate and the addition of pooled cow DNA or actual genotypes both increased the accuracy further.

Facy et al. [11] also examined alternative approaches to measuring cow reproductive performance that might enable measurement to occur in a much shorter timeframe than waiting many years before sufficient records of calving are available for use in genetic improvement programs. They found that genetic correlations between days to calving for first and mature cow joinings was moderate to high, though correlations across lactating and non-lactating cows were close to zero. They recommended that for multi-parous cows, lactating and non-lactating days to calving should be treated as separate traits, with the traits most likely to maximize genetic gain being first joining days to calving, second joining days to calving and lactating mature cow days to calving.

3.4. Implementing Genomic Selection Programs

Following the development of genomic selection in 2001 [1] and the very rapid decrease in costs of genotyping since then, genomic selection has now been implemented across a wide range of livestock and plant species. Hence, Banks [12] undertook a survey

of organizations involved in genetic improvement across species, countries and roles both public and private. While there were differences across organizations in what were considered the most significant outcomes to date, both an increase in accuracy of breeding values underpinning faster genetic gains and a re-balancing of genetic change to include real progress in the difficult-to-measure traits were widely observed. Across organizations, key learnings included the increased importance of investment in phenotyping and opportunities to evolve business models to engage directly with a wider range of stakeholders, leading to significant increases in agricultural productivity, profitability and sustainability.

However, significant challenges still remain with the implementation of genomic selection amongst smallholder livestock farmers in low–middle income countries. One of the challenges is the impact of genotype–environment interactions across vastly different production systems. Hence, Wahinya et al. [13] examined a range of breeding strategies relevant to the progeny testing of dairy bulls across low-, medium- and high-production systems in Kenya, using both phenotypic and genomic information. They found that the optimal breeding strategy was to progeny test bulls within their separate production systems using a combination of both phenotypic and genomic information.

A major consideration of genetic improvement programs in many low–middle income countries is the need to not only achieve genetic gains but also to conserve local indigenous livestock breeds. Widyas et al. [14] reviewed literature relevant to breeding beef cattle grazed in tropical environments, particularly in Indonesia, with the aim of identifying new breeding opportunities for cattle owned by Indonesian smallholder farmers while also conserving unique local breeds. The review indicated that, despite the implementation of extensive crossbreeding programs over several decades in Indonesia, no discernable genetic improvement had been achieved. A single within-breed selection program focused on live weight whilst ignoring all other productive and adaptive traits. The authors found that it was unlikely that smallholder farmers could effectively manage crossbreeding programs due to the management complexities required. However, establishing reference populations of local cattle breeds or composites and using genomic selection to genetically improve herds should be feasible, particularly if international collaborations could be established to allow data-pooling across countries.

Finally, Burrow et al. [15] examined a wide range of ongoing challenges that limit the implementation of genomic selection in low–middle income countries. They included: the difficulties and expenses of effective phenotyping; the complex funding arrangements for a limited number of essential reference populations in only a handful of countries; the questions around the long-term sustainability of those livestock resource populations; the lack of on-farm, laboratory and computing infrastructure; and the lack of researchers, extension officers and others with appropriate expertise to implement these programs. They proposed a range of possible solutions to these challenges and suggested an operational framework to enable new resource populations to be established and genomic selection to be implemented in low–middle income countries.

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