Editorial

Applications in Genetics and Animal Biotechnology

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The present Special Issue, "Applications in Genetics and Animal Biotechnology", presents the latest advances in the field of animal genetics. The topics of the Special Issue can be divided into the following eight focus areas:

(1) Whole-genome resequencing (WGS);
(2) The integration of old and new sequencing platform data;
(3) The use of new genomic tools and omics data;
(4) Genomic selection and genome-wide association studies (GWAS);
(5) The identification of new genomic variation data;
(6) New phenotyping methods (Precision Livestock Farming—PLF);
(7) Metagenomic analysis using animal models;
(8) The evaluation of new alternative diets (based on algae, insect, and bacterial fermentation biomasses) in breeding programs.

1. Whole-Genome Resequencing (WGS)

The development of next-generation sequencing (NGS) tools and reduced costs have fostered interest in using WGS as an alternative to SNP chips for genotyping [1]. The main advantage of the resequencing method is to use SNPs that are more specific to the population of interest. WGS also offers additional advantages, such as the characterization of rare variants and other sources of variation (structural and copy number variations—CNVs). Accurate imputation allows for these additional sources of variation. Several WGS projects are currently underway in the livestock sector. Thus, the interest in the use of low-coverage techniques and new imputation methods has increased. Three or more densities of SNP chips and non-genotyped animals can be used in breeding programs. So far, few results have been published for mixed-breed populations.

2. Integration of Old and New Sequencing Platform Data

During the sequencing process, certain factors such as DNA quality, library preparation, and the choice of sequencing platform must be optimized [1]. Third-generation sequencing, with the production of reads of tens or even hundreds of thousands of base pairs, allows for improved genome assembly and the production of a complete, contiguous sequence. However, in some cases the combined use of short reads can further improve the result. The combined use of different technologies is generally expensive. Instead, it is preferable to use subsets of long reads (using Oxford Nanopore or PacBio sequencing platforms) and short reads. The combined use of different sequencing platforms will continue to develop over time.

3. Use of New Genomic Tools and Omics Data

Over the past two decades, new genomic methods have become available for analyzing animal species. These new tools (Genotyping by Sequencing—GBS; RNAseq; scRNA-seq; and Whole Genome Bisulfite Sequencing—WGBS) enable a more accurate and effective selective process. Different SNP chips are also available for cattle, pigs, sheep, chickens, and fish. Multi-omics analysis allows for the combined use of two or more types of data, such as genomics, transcriptomics, epigenetics, proteomics, and metabolomics.

4. Genomic Selection and Genome-Wide Association Studies (GWAS)

The availability of new methods and the reduced cost of sequencing have encouraged the increasing use of WGS methods. Currently, genomic evaluation is based on SNP arrays [2], but the use of WGS data could provide advantages because it is not constrained by linkage disequilibrium (LD) between SNPs markers [3]. Thus, the use of NGS data and nonlinear models can improve the accuracy of genomic evaluations. The GWAS method in combination with the genotyping of high-density SNPs is routinely used in the studies of pathogen resistance and health traits in domestic animals.

5. Identification of New Genomic Variation

Tens of millions of SNPs have been identified for key productive and reproductive traits over the past decades through various projects carried out in the livestock sector. The quality of the results and methods for annotating animal genome sequences continue to steadily improve. Several pipelines are available for the variant analysis of SNPs. In the future, new methods will be needed for the analysis of increasingly large and complex datasets carried out in a single step. Thus, for example, transcriptomics enables the identification of genes expressed by differential analysis and metabolomics in animals with a higher carcass quality.

6. New Phenotyping Methods (Precision Livestock Farming—PLF)

Recently, there has been growing interest in the livestock industry regarding a new data collection system based on the use of sensors, cameras, accelerometers, gas analyzers, microphones, and disease diagnostic and internet-related methods [4]. Sensor technologies can continuously record milk/manure volumes, weather parameters, and nutrient management plans. The main objective of PLF is a continuous real-time monitoring of productive/reproductive, health-related, welfare-related, and environmental animal characteristics. Some methods such as data mining, artificial intelligence, and machine learning are already being used to analyze and manage complex data from livestock systems [5]. The automatic collection of new traits enables improved farm management and the selection of genetically superior animals.

7. Metagenomic Analysis Using Animal Models

In farm animals, gastro-intestinal microorganisms are very important in the feeding stage and in disease development. In this regard, both host—microbe and microbe—microbe interactions are crucial. NGS technologies (metagenomic analysis) facilitate extremely in-depth analyses of the livestock microbiota.

8. Evaluation of New Alternative Diets (Based on Algae, Insect, and Bacterial Fermentation Biomasses) in Breeding Programs

The economic and environmental sustainability of animal husbandry significantly depends on the nature and type of ingredients used in animal feeds [6]. Further studies need to be conducted on the effects of by-products, algae, insect meal, and bacterial fermentation biomasses used as sources of oil and protein in animal feeds. In particular, some questions related to gene expression, the gut microbiota, and disease resistance need to be addressed.

Conflicts of Interest: The authors declare no conflict of interest.

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