



Advancements and possibilities in animal production using genomics

K Tanizaki*

Department of Genetics, Osaka University, Suita, Osaka, Japan

*Corresponding author. E-mail: tanizaki@gmail.com

Received: 05-Aug-2022, Manuscript no: GJABG-22-72986, **Editor assigned:** 08-Aug-2022, PreQC no: GJABG-22-72986 (PQ), **Reviewed:** 22-Aug-2022, QC no: GJABG-22-72986, **Revised:** 29-Aug-2022, Manuscript no: GJABG-22-72986 (R), **Published:** 05-Sep-2022, DOI:10.15651/2408-5502.22.10.006.

DESCRIPTION

The animal sector has played an important role in breeding animals selectively to better suit particular environments, management methods, and various market needs for centuries. This has contributed to the abundance of farm animal genetic resources that we see today across the globe. Significant technical developments over the past century have accelerated the rate of development and shaped what has evolved into a crucial facet of the livestock business. The transmission of high-merit genetics and a higher selection intensity to be used for breeding were initially made possible by advancements in reproductive procedures. The rate of genetic improvement has increased over time thanks to simultaneous advancements in breeding value estimate, computer techniques, and selection accuracy, initially through the use of quantitative genetic approaches and more recently through the addition of genomic technologies.

The efficiency of animal production was greatly increased as a consequence of these innovations. Through a mix of better management and genetic advancement, with the latter playing a significant influence, North American cows' average milk yield also grew by 400% over the same time span. Similar rates of progress have been attained in a number of nations due to the regular use of international genetic evaluations for dairy cattle for more than 25 years. A variety of farmed species have seen considerable decreases in greenhouse gas emissions per unit product as a consequence of the recent progress. The main purpose of using genetic and genomic knowledge has been to speed up natural evolution in order to meet certain requirements or goals. The bulk of interesting animal traits have been found to have naturally occurring genetic variation as measurement technology have advanced. A strong method like this has excellent chances to enhance production processes, but it also carries the risk of decreasing efficiency and endangering animal welfare if it is put to use.

Using Whole-Genome Resequencing

The motivation in employing whole-genome resequencing as a substitute for Single Nucleotide Polymorphism (SNP) chips for genotyping to support Genomics Selection (GS) in breeding programmes has increased with the introduction of next-generation sequencing and the ensuing decreases in costs. Instead of defining variance through a subset of common SNPs normally chosen based on data gathered on other populations, resequencing allows for the collection of a wider range of variation specific to the population of interest. The initial awareness that, compared to genotypes derived from SNP arrays, the quality of genotypes obtained with GBS tended to be worse when just low levels of genome coverage were used curtailed the usage of genotyping by sequencing as a feasible cost-effective option. Costs went up along with quality as coverage depth grew. In order to reduce the effect on genotype quality, complete sequences were generated using imputation. Use of Whole Genome Sequencing (WGS) offers several additional advantages, including characterizing rare variants and other sources of variation, such as structural changes and copy number variations, in addition to characterizing the common variants generally contained on SNP chips (CNVs). The availability of appropriate reference populations is necessary for accurate imputation to the whole-genome level to help capture these additional sources of variation.

Implementing GS can be difficult because Linkage Disequilibrium (LD) between SNPs and QTLs gradually breaks down owing to recombination, necessitating periodic retraining of the evaluation models. When recording is only done sometimes through specific campaigns or programmes, as is frequently the case for many features and populations, it can significantly affect the cost of GS adoption. There has been some focus on the creation of strategies and tactics to lessen this impact. WGS, nonlinear models, and multi breed training populations have all been found to have certain

advantages; however, using all three together provides the greatest level of mitigation in the majority of situations. The implementation of GS in small populations, which is a common difficulty for many breeds, can also be supported by the use of multi breed training populations. When considering such populations, the adoption of nonlinear models can also help to increase forecast accuracy.

Because the research communities for livestock are smaller than those for humans, significant work has been made in creating numerous crucial genetic resources for farmed animals. The production of reference genome sequences for the majority of common livestock species, including poultry, cattle, pigs, goats, and sheep, as well as various aquaculture species, has been covered extensively.