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Poultry Breeding: From Domestication to Genomic Tools-A Review

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Abstract

The current review article aims to briefly highlight the most important genomics technologies that may be used to create breeds that are productive and well-adapted in a given circumstance. It also emphasizes the role that bioinformatics plays in modern chicken breeding. Advances in genomics information technologies are valuable opportunities for achieving the required improvement, but their implementation implies access to technical and financial resources with suitable adjustment in the local situation. The majority of domesticated livestock species are chickens. The foundation for genomics has been established by the dramatic advancement of molecular genetics. The applications of the newest generations of molecular markers are incredible tools for farm animals' genetic advancement. These markers offer more precise genomic data and an improved understanding of the animal genetic resources. Genomics tools are essential for the accurate, fast, and efficient breeding of animals. Compared to other domesticated animals, chicken is widely accepted and has little to no taboos in terms of cultures, religions, and society. With regard to resolving the issues of food security in a world affected by climatic change and human population expansion, it offers a unique genetic resource due to its resilience to a variety of environmental circumstances and demonstrated potential for breeding improvement. The historical evolutionary history of the chicken has been reconstructed thanks to recent investigations that have revealed new information about its DNA. Breeders of chickens must move more quickly towards creating and choosing enhanced breeds that can withstand environmental stress without compromising production and productivity.

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Introduction

The diversity of domestic animals is crucial to global biodiversity. Animal domestication was the beginning of a lengthy and difficult history that led to the current pattern of animal genetic resource diversity. In recent decades, poultry production has experienced the greatest rate of growth among all animal industries (FAO, 2013), particularly in middle- and low-income nations (Taha, 2003). In the 1950s, the introduction of crossbreeding led to a breakthrough in the chicken industry. Over the past

100 years, commercial breeds of chicken, such as layers and broilers, have been developed by the selective mating of several native breeds (Elferink *et al.*, 2012). Animal scientists are challenged to focus on how to increase efficiency and yield for the long-term sustainability of livestock production due to the distinct growth drivers like an increase in population growth and urbanization putting enormous pressure on natural resources (Telugu *et al.*, 2017). One benefit of the chicken industry is its short production cycle, which enables to adapt fast to consumer demand while also

allowing for speedy genetic advancements, improvements in animal health, and the development of feeding techniques. Therefore, rather than merely depending on the traditional method of the chicken breeding sector, improved strategies for efficient approaches should be adopted to raise the rate of production. Genomic selection is regarded as one of the trustworthy methods for meeting these increasing needs in the shortest generations possible (Fulton, 2012). Animal genetics and effective breeding have greatly benefited from the traditional breeding strategy. Using cutting-edge breeding approaches based on poultry genomics is essential to achieving our breeding goal as quickly as possible because they make it easier to spot phenotypic and genotypic alterations than with traditional procedures.

Massive amounts of data must be processed in the genomic era. Advanced techniques and potent tools are required to be able to organize enormous amounts of data (Shafi *et al.*, 2019). These tools, which scientists and breeders use to get closer to the genomic data, are made available to us by bioinformatics. Thanks to recent developments and technology in genomics, bioinformatics, proteomics, and other omics employed in this period, animal breeders now have access to improved procedures and technologies to produce superior breeds that can endure the severe climate and disease. Therefore, this review paper provides an overview of the most important genomics tools used to acquire productive and well-adapted poultry breeds and also emphasizes the contribution of bioinformatics to advanced poultry breeding in the present era.

Evolution of Poultry: From Domestication to Precise Breeding

A significant turning point in the development of human civilization was the domestication of wild animals (Diamond, 2020). A total of 40 species of livestock have been domesticated throughout human history, and the majority of these domesticated animals are still used in agriculture and food production today (FAO, 2007). Internationally recognized native chicken breeds number close to 1,600 (FAO, 2020). One of the most widely used domesticated animals is the chicken, which is developed for both its meat and eggs (Miao, 2013; Liu, 2006). It is believed that the red jungle fowl (*Gallus gallus*), which is endemic to several areas from Southeast Asia to Southwest China, was the original domesticated animal. Until recently, it was thought that the domestication of chicken took place in the Indus Valley around the year

2000 BC (Zeuner, 1963). However, based on archaeological evidence from China, Southeast Asia, and Europe as well as paleoclimatic evidence in China, (West and Zhou, 1988) hypothesized an earlier origin in Southeast Asia, before 6000 BC. According to archaeological discoveries and literature from early 20th century Chickens arrived in Europe via two main trade routes: a northern route via China and Russia and a southern route via Persia and Greece, (Rubin, 2010). According to a different theory, the two routes diverged from Iran and headed in opposite directions, one via the Mediterranean Sea and the other via the Black Sea. The most ancestor type of domestic chickens in Europe is thought to be the Mediterranean type.

Domestic chicken traveled by land through Egypt and by sea along the Red Sea coast and the Horn of Africa from its domestication centers to Africa (Woldekiros and D'Andrea, 2017). The earliest iconographic evidence of domestic chicken was found in Egypt (Mwacharo *et al.*, 2013), however, the oldest chicken bones in Africa were discovered in Ethiopia at the Mezber site Tigray region and date to 820–595 BC (Woldekiros and D 'Andrea, 2016). Chickens may have been rather widespread, as evidenced by their connection to domestic food waste in the early rural community at Mezber and their appearance in later Aksumite urban environments. By the sixth century AD, chickens were a key part of the iron age economy in West Africa. By 800 AD, chickens had become a well-established species in East Africa (Mwacharo *et al.*, 2013). The first uses of chickens were for ceremonies, such as the use of a crowing cock to announce the hour of dawn. Later, different cockfighting and pet varieties were developed and raised all over the world.

Mammals and birds share a common ancestor that lived 300 million years ago. Quail and chicken's most recent common ancestor lived 40 million years ago. Because of its morphology, *Gallus gallus* is the most similar to domestic chickens and produces fertile offspring when it crosses with domestic chickens, in contrast to the three other wild species, which produce domestic chickens with relatively poor hatchability and chick survival rates.

A history of about 8000 years has been spent domesticating chickens through the breeding of local chickens. As a result, native chickens have accumulated a variety of genetic traits over time that have aided in adaptation to a variety of difficult environmental factors in various places, including heat stress, humidity, and diseases (Tirawattanawanich *et al.*, 2011; Walugembe *et*

al., 2019). Recently, the crossbreeding of indigenous chickens with common commercial chickens has been actively performed to develop breeds that exhibit the aforementioned desirable traits.

Animal breeder aims to improve animal genomes over time through selective breeding, but the rate of progress is inversely correlated with the generational intervals. Following new knowledge and demands, the poultry breeding and selection program has evolved. The individual chicken stocks were evaluated in the 1940s, and the surplus culled birds were sold as a terminal product after the selected birds were kept. The idea of two, three, or four-way crossings in poultry was taken from the maize improvement program in the 1980s, which revolutionized poultry breeding for the development of the high-yielding current layer and broiler breeds. Commercial hybrids such as terminal crosses and the specialized egg and meat types have also replaced purebreds. The requirement for developing specialized male and female lines in both layer and broiler stocks resulted from the negative correlations between production and reproduction traits. These specialized lines were created for meat- and egg-type stocks (Fairfull and Gowe, 1990; Chambers, 1990). The genetic foundations of these specific male and female lines are typically derived from quite diverse genetic origins (O'Sullivan *et al.*, 2010). The method of phenotypic selection was mostly used for increasing body weights, while the index selection (Osborne index) was used in parent line selection for egg production, depending on genetic characteristics like heritability estimates and correlations. The present programs rely on breeding value estimation with animal model best linear unbiased predictor (BLUP) since a growing number of features are now incorporated in selection programs. However, low inheritability traits, such as disease resistance, sex-limited traits, egg production, and quality, or traits that are only available later in the stage of life, like carcass traits, have shown reduced efficiency in the conventional approach and are frequently economically significant traits (Khare and Khare, 2017).

Chicken genetic population resources and diversity

Tilili, Horro, Chefe, Jarso, Tepi, Gelila, Debre-Elias, Melo-Hamusit, Gassay/Farta, Guangua, Mecha, Konso, Mandura, and Sheka are a few indigenous chicken ecotypes from Ethiopia that were listed by DAD-IS and DAGR-IS (Addis *et al.*, 2015). Only seven ecotypes were listed as Ethiopian chicken ecotypes in the DADIS (EBI, 2016).

For understanding the value of livestock species as well as for conservation and enhancement in a variety of production situations, studies on their genetic diversity are essential (Malomane *et al.*, 2019). The significant genetic diversity and strong capacity for local adaptation of Ethiopia's native chickens serve as the foundation for tactics for selective breeding and genetic improvement (Desta, 2015; Lawal *et al.*, 2018; Aberra *et al.*, 2021). Although the genotype and phenotype of Ethiopia's native chicken populations are typically generic (Tadelle *et al.*, 2003; Hassen *et al.*, 2009), certain ecotypes have been discovered based on morphological variation in their natural habitats. According to Nigussie *et al.*, (2010) and Negassa *et al.*, (2014), these native chickens exhibit significant diversity in their body size, conformation, plumage colour, comb type, feather cover, and other morphologic and production traits. Similar authors claimed that the adaptability of these differences in various production environments allowed for their recognition. Additionally, differences in body quantitative measurements can be used to narrow down the possible phenotypes (Bekele *et al.*, 2015; Aberra *et al.*, 2021). The gene pleiotropic effect, which proposes a selection requirement for genetic improvement (Rachma *et al.*, 2013), may be the cause of the greater association between body weight and quantitative measurements for the majority of traits.

The main goal of genetic diversity studies on native chickens is to use multiple phenotypic and molecular markers to evaluate allelic variability, genetic diversity, genetic linkages, and differentiations across diverse locations (Mureda *et al.*, 2015; Lawal and Hanotte, 2021). High genetic variety is anticipated since native chickens are not chosen for performance qualities as a result (Zemelak *et al.*, 2011). For instance, heterozygosity (Ho) values ranged from 50% to 55% in ecotypes, according to a study using 10 microsatellite markers for four native chicken ecotypes. Additionally, these five ecotypes showed genetic heterogeneity amongst them, with an average of 3 to 11 alleles per locus (Emebet, 2015). Similarly, Zemelak *et al.*, (2011) used 26 microsatellite markers to examine the genetic diversity and population structure of Arbaminch-Zuria, Dodota, Gonder-Zuria, Harmaya, and North-Mekele and found that ecotype diversity was medium to high, with an average of 6.1 alleles per locus. A genome-wide association analysis was used to map the genetic variance between five populations of Ethiopian (Horro, Konso, Gumuz, Sheka, and Gondar, Guduro) and African breeds of chicken for phenotypic features (skin and egg colour). Additionally, Hassen *et al.*, (2009) used

microsatellite markers to analyses indigenous chicken populations from seven distinct regions of northwest Ethiopia, three South African genotypes, and RIR genotypes to estimate genetic diversity. The observed heterozygosity (H_o) value for all populations was 0.77 as a consequence, and the RIR breed had a greater genetic distance from the Ethiopian chicken populations than South African breeds. The majority of the microsatellite loci displayed high levels of polymorphism, indicating that they might be utilized in future efforts to assess the genetic diversity of indigenous chickens.

Indigenous chicken populations are anticipated to serve as repositories for adaptive genes that foreign breeds do not have (Aberra *et al.*, 2011; Egahi *et al.*, 2010). The significant diversity at the microsatellite LEI0258 locus (found on chromosome 16 for the MHC region), on 24 different indigenous chicken populations in Ethiopia, is linked to the disease difficulties faced by indigenous chickens across varied agro-ecologies (Adebabay, 2018) Likewise, a study by Gheyas *et al.*, (2021) using whole genome sequences of native chickens from Ethiopia with 25 geographically diverse populations revealed the existence of genomic regions with positive selection information connected to altitude-induced stresses, water scarcity, and difficulty of scavenging behaviors.

Bioinformatics: The Fundamental Tool Underlying Modern Methods of Breeding

Bioinformatics is a science that combines computer programming, statistics, mathematics, and engineering to analyze and handle information on the physiological functions of living things. New high-throughput data consists of complex and noisy information that necessitates the modification of standard statistics or the development of new methods for adapting to its conditions. DNA putting in the correct order and matching-up, genomic expression measuring methods, and more complex modeling studies such as protein folding patterns generate data sets that can extend to trillions of bytes, making analysis and understanding impossible without modern computer-based and machine learning abilities. In the field of animal production area, increasing demand for food, and the need for improvement in production wastes very little while working or producing something. Now, it is known that related to coming from parental genes is represented in the form of DNA molecules with sequences of four nucleotides (A, T, G, and C) that are transmitted to the next generation. The complete sequence information of cellular data is the whole genetics system, which is the

written plan for building something for all cellular structures and activities. It tries to find the truth about molecular information to understand natural different versions and sicknesses. Knowing genetics data sequencing ideas are necessary to choose the right analysis method, understand its limits, make guesses based on what you've been told about the results, and recognize its biological effects while dealing with high-throughput data (Morris, 2012).

Bioinformatics can speed up the isolation of new breeds by enabling genetic and genomic selection to identify the best genotype combination that will result in the desired phenotype. Genome sequencing of livestock, including cattle, buffalo, pigs, sheep, goats, camels, and poultry, is an excellent example of how bioinformatics is used in veterinary and animal sciences. Genome sequencing helps in improving the health and production of eggs, milk, and meat of animals, which in turn adds to human nutrition. In the 20th century, the discovery of the quantitative genetics theory was effectively used to create both experimental lines and commercial lines. Population genetics is used to define population structure and subdivision by identifying genetic diversity among various groups of animals as well as gene frequency across time between geographical regions. In contrast to quantitative genetics, molecular genetics is focused on characterizing specific genes, whether that is their structure, expression, or evolutionary history. If a trait is controlled by a single gene, understanding the underlying genetic mechanism may lead to the development of a genetic test to eliminate an undesired trait. Genomic selection is a type of marker-assisted selection in which genetic markers covering the entire genome are employed to ensure that all QTLs are in linkage disequilibrium with at least one marker. Because of the high number of single nucleotide polymorphisms (SNP) revealed by genome sequencing and new methods for rapidly genotyping a large number of SNP, this strategy has become practical. Computational science and bioinformatics methods are significantly used in modern selection technology (Goddard and Hayes, 2007). Bioinformatics is also used in genetic engineering, to locate and alter genes to produce animals with specific traits. This can result in the development of animals with improved performance or disease resistance. Finally, bioinformatics may be used to investigate gene interactions and their consequences on traits, bringing critical new insights into how animals' genetic makeup affects their health and performance. This has the potential to increase both animal welfare and the efficiency of animal production.

Marker-Assisted Selection

Among livestock species, the poultry genome was the first to be mapped in 1992, followed by cattle, pigs, and sheep (Dekkers, 2004). The chicken genomic toolbox is the most comprehensive for detecting quantitative traits loci and marker-assisted selection. Before exploring the role of the relationship between the markers and the genes of interest for the success of marker-assisted selection, an idea regarding linkage equilibrium and disequilibrium is considered. Linkage equilibrium (LE) exists when the genotype present at one locus is in agreement with the genotype present at another locus, and linkage disequilibrium (LD) exists when the genotypes at the two loci are not in agreement with one another (Slatkin, 2008).

Marker-assisted selection can be divided into three based on their categories and the utility of data as direct Markers, linkage disequilibrium markers (LD), and Linkage Equilibrium Markers (Dekkers, 2005). Molecular marker-assisted selection has also been categorized based on their ability to appraise polymorphism in DNA (Teneva, 2009) as hybridization-based DNA markers, PCR-based DNA Markers, and DNA Chip and Sequencing-based DNA Markers.

In order to select animals with greater genetic merit for traits that are typically either expensive or too challenging to quantify practically, marker-assisted selection uses DNA markers. Using numerous markers and least square approaches, quantitative characteristics loci controlling quality and production traits in layers are being mapped (Tuiskula *et al.*, 2002). Feed efficiency and meat quality are the traits of consideration by the breeders for improvement in broilers with the help of markers, as these are not easy to measure in an accustomed manner. Conventional breeding techniques, influenced by quantitative genetics, treat the animal as a black box with an unlimited number of genes influencing the expression of all features of the animal.

The first development that had an impact on poultry breeding was the discovery of genetic markers. Genetic markers that form the most widely used category were small anonymous repeat sequences of DNA (microsatellites) that are dispersed throughout the entire genome and can be used as landmarks to generate a map of the genome. Marker-assisted selection is a method of directly selecting regions of the genome influencing economic important traits (Fulton, 2012). In other words, animals can be selected for the phenotype of interest

using markers that have a statistical association with a phenotypic trait. The first phase detects one or more markers associated with quantitative traits loci. The second stage determines the underlying gene or direct marker which are genetic loci that have a known function ascribed to them. The third phase increases the frequency of the favorable allele, either using selection or introgression methods. In other words, if the regions were once identified, genetic markers could be used to differentiate those individuals with higher performance, and selection could be practiced at an early age (Fulton, 2012).

Compared to conventional selection methods, Marker-assisted selection has been successfully implemented to improve traits with a simple genetic determinism (Boichard *et al.*, 2016). However, most of the selected traits are determined by a large number of genes, each with minor effects on phenotype (Meuwissen *et al.*, 2016). The Marker-assisted selection technique thus enhances breeding efficiency to a certain extent, but the disadvantage is that it only targets those traits governed by a limited gene (VanRaden *et al.*, 2009) or relies on the identification of a small number of causal variants (Hayes *et al.*, 2013), leading to limited genetic gain while most economically significant traits or complex traits are affected by several regions of the genome, each with a small contribution to the variability.

Genomic revolution

The poultry industry is abounding day by day as it engrosses less cost of investment per bird as compared to large animals. The revolution of genomic selection is already described as an efficient technology in the livestock and poultry improvement program, justified by its increased rate of genetic gain. The 21st century was marked as a genomics advancement era driven by the success of the human genome project (Venter *et al.*, 2001), coupled with the development of many technologies and methods that introduced the genesis of genomics in domestic animals. With continuous effort made by genetic advancement, the evolution of genomics and the discovery of molecular tools is already striking a huge impact in the field of genetic improvement and breeding, offering promising advantages concerning conventional breeding. Meuwissen *et al.*, (2001) first proposed genomic selection in animal breeding, simultaneously, DNA-based tools and technologies were also developed. Thereby, determining the whole genome sequence of chicken in 2004 as the first farm animal to be determined.

Genomics is a specialized branch of science wherein the research into the entire genomes, including their mapping and sequencing, as well as the identification and functional analyses of genes is carried out. Genomic selection has obtained superiority over traditional methods and Marker-assisted selection in various ways such as, candidates can be assessed without progeny as well as their phenotypic information and the method is not limited to a few genes. Selection is also possible as early as the stage of embryos. The accuracy of selection is justified by numerous studies undertaken leading to overall increased productivity by simplifying the selection process and decreasing its cost due to a significant reduction in generation interval, thereby doubling the yearly genetic progress.

Initially, the genomic selection was applied to commercial layers in 2013 by the company, Hy-Line Int., after 3 years of experimental genomic selection (Wolc *et al.*, 2015). The experiment was performed on 16 traits as its index for the selected program and resulted that the genomic-based selected birds outperformed those selected as per the classical method. As we know, most of the layer traits of interest can be measured only in the female and after maturity being sex-limited. Although both the males and females have the gene variants, it is only expressed phenotypically and measured directly by mature females. However, such traits including egg production traits, egg quality traits including shell strength and colour, and egg solids traits, etc. can be measured even in males by direct selection with highly reliable genomic selection (Druet *et al.*, 2020). The first genomic selection implementation in the broiler was done by Aviagen in 2012 (Aviagen, 2012). Although in the case of broilers, the advantages of genomic selection are different than in layers, because in the broiler, with its already short interval of generation, most traits can be recorded at an early age regardless of sex, but the genomic selection still plays a significant role in the traits of reproduction, carcass, growth, and disease resistance that cannot be measured directly during selection (Liu *et al.*, 2014).

The development of high-throughput genotyping of SNPs enabled the development of approaches to predict an animal's genetic merit based on its DNA (Meuwissen *et al.*, 2001). Potential benefits of GS include enhance genetic progress through a more precise prediction of GEBV, does not require information from the pedigree population, the selected candidates not necessarily trait recorded, identifying the relationship between parents and offspring, minimizing the number of individuals

selected for breeding, decreasing the generation interval, overcoming age and sex limitations for traits, and a direct link between the genetic evaluation and the genome (Fulton, 2012). Compared to dairy cattle breeding, where genomic selection using high-density SNP panels was first implemented (Wolc *et al.*, 2016), rapid genetic progress can be achieved in poultry breeding because of the short generation interval and relatively large flock size (Wolc, 2014). Genomic selection is only possible with the development of high-density SNP chips, which enable rapid, massive, and relatively inexpensive genotyping (Wolc *et al.*, 2016).
Genome Sequencing

In addition to being a significant source of protein, the chicken has long served as a key model organism for developmental biology. Each year, billions of chickens are utilized worldwide for the production of meat and eggs. The haploid DNA content of the chicken genome is 1.2×10^9 base pairs (bp), which is around 40% less than that of either the mouse or the human. The first agricultural animal to have its genome sequenced was a chicken in March 2004. In order to build the sequence contigs and scaffolds and align them to the known chicken chromosomes and linkage groups, a comprehensive BAC contig-based physical map was used together with whole genome shotgun Sanger sequencing. That first build has been improved upon by subsequent sequencing and mapping efforts, and work is still being done to find missing and/or unassembled sequences, notably on the smaller microchromosomes and the sex chromosomes. The chicken genome offers fresh perspectives on the composition and structure of mammalian genes as well as new information about the composition of avian genes and the evolution of ncRNA genes.

Among domesticated animals, poultry is the species with the most complete genomic toolkit (Kerje, 2003). The wide variation in chromosomal sizes in bird genomes makes them have unique characteristics. Chickens have 38 pairs of autosomes in total including five macro, five intermediate, and 28 micro chromosomes in addition to a pair of sex chromosomes. The use of comparative genomics is extremely useful in the candidate gene approach, but the added value of the genome assembly of the chicken that resulted from the efforts of the International Chicken Genome Sequencing Consortium (2004a) cannot be overstated. Since March 2004 we have the first draft of the chicken genome assembly and its quality is constantly being upgraded. The latest version is available and predicts some 24,000 genes in the chicken

genome. One way of using the genome information on the chicken is to study candidate genes in the way described above. Another way could be to use an intermediate ("gray box") approach by exploiting the information on huge numbers of genetic markers that were indirectly derived from the sequencing effort.

Genome Editing in Poultry

The most recent method of changing specific genes to enhance the expression of desired traits is called genome editing. A significant step towards the complete understanding of all chicken gene structures has been made with the assembly of the chicken genome.

However, the full picture of how the phenotypic performance of the chicken is controlled won't become clear until we follow the full pathway from gene structure through gene function, gene expression, protein interactions, biochemical and signaling pathways, cellular function, and cell-cell communication.

Researchers can identify genetic variations that contribute to enhanced economic traits using genome sequencing technology, and they can use this DNA knowledge for selective breeding. Genome editing can accurately edit target areas that have been discovered by genome sequencing data and introduce novel alleles associated with economically important traits without retaining transgenes in combination with selective breeding. Intending to increase productivity, several studies have used genome-editing technologies to impose desired traits on livestock, such as disease resistance and heat tolerance (Ricroch, 2019). In the future, this type of study will be substantially expedited.

For the production of animals, including poultry, three common genome-editing approaches are used. The zinc finger nuclease is the first, and it is employed to bind particular DNA domains that complement the target DNA sequences. Secondly, the gene and genome editing method that uses the nuclease domain to create double-strand breaks is transcription activator-Like effector nucleases.

Recent advances in genome-editing technologies, such as the CRISPR/Cas9 system, have allowed for the development of a wide range of genome-edited animals (Ricroch, 2019). The CRISPR/Cas9 technique makes use of a particular RNA sequence known as guide RNA, which binds to a different target DNA sequence before Cas9 cleaves the region where the binding has taken

place. It increases the frequency of precise genome modifications when producing genetically modified animals, the CRISPR/Cas9 system stands out as the most effective gene editing technology (Chu *et al.*, 2015).

Genome editing has been used on chickens to boost disease resistance, feed conversion efficiency, and muscle productivity. In some animal species, MSTN deletion greatly improves muscle mass because of that MSTN encodes a negative regulator of muscle development (Aiello *et al.*, 2018). Therefore, MSTN is a key area of focus for increasing animal productivity (Wang *et al.*, 2018; Crispo *et al.*, 2015). MSTN and GOS2 knockout has been effectively accomplished in poultry. In MSTN knockout chicken and quail, muscle mass was increased, while in GOS2-knockout chicken, the fat composition was decreased (Park *et al.*, 2019; Kim *et al.*, 2020). These days, chicken breeding is using genome sequencing technologies to quickly create and identify genetic markers that affect production. These genetic markers can be edited simultaneously using the CRISPR/Cas9 system. This technology is transforming the animal breeding sector, letting breeders generate animals with improved characteristics, such as enhanced growth rates, improved disease resistance, and meat quality. Genome editing in conjunction with genomics will hasten the breeding of chickens.

Genomic selection could provide a fast genetic improvement through enhanced accuracy in the selection and genetically detecting superior individuals at an early stage, reducing generation interval and subsequent improvement of the individuals in the succeeding next generation. Genomic selection dominates the conventional breeding method by an overall rapid rate of genetic gain in poultry improvement programs. Although, it is still a developing area in poultry, being an industry it is, exclusively involved in generating a profitable and sustainable income source while responding to the global demand for protein-rich meat and eggs through the production traits. Several biotechnologies tools are utilized in poultry genetic improvement, and their effect on the rate of genetic advancement is maximized when combined with integration in a well-planned breeding program with an achievable objective. Genome sequencing initiatives for livestock, the creation of genetic markers, and the use of computer-based techniques contributed to quick advancements in the understanding of farm animal genomes should lead to a better ability to respond to the demands of the market and society's needs. Genomics and bioinformatics are crucial tools to improve the

production efficiency and well-being of farm animals and the quality of their useful products for the wide range of human needs by using genomic, and molecular tools. The new knowledge gained about the molecular basis of poultry phenotypes that are produced along the way will be used to engineer and reshape the poultry genome with cutting-edge technologies, and genetically engineered poultry breeds.

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