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Review Article

Concepts of Genomic Selection in Poultry and its Applications

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Abstract

The conventional breeding method has rendered immense service in animal genetics and breeding successfully. However, there are limitations of this method in the case of traits that are sex-limited, traits with low heritability, traits measured in later stage of life, etc. leading to overall slow genetic progress. On the contrary, the global demand for increased sustainable livestock production is continuously challenged. The poultry industry being one of the major sources is subjected to adopt improved and advanced technologies to meet the demand by increasing its productivity in long run. The revolution of genomic selection is already described as an efficient technology in the livestock and poultry improvement programme, justified by its increased rate of genetic gain. It would therefore be promising to integrate molecular knowledge, rather than relying solely on the conventional approach, by giving due importance in tackling the various limitations and other challenges such as environmental factors and poultry welfare.

Keywords: Genomic Selection, GEBV, Poultry

Introduction

The traditional breeding method for genetic improvement which is entirely based on information about morphological appearance and pedigree record has been successful. However, the conventional approach has shown reduced efficiency on low inheritability traits (such as disease resistance) or limited to either of the sex (Egg production or it's quality) or those only available at later stage like carcass trait or those which cannot be quickly, correctly and inexpensively measured in huge populations which are often economically important traits (Khare & Khare, 2017). The introduction of crossbreeding created a breakthrough in the poultry industry during the 1950s. However, it prompted the extinction of small, pure line and private farm-based programmes among the breeding organisations. Thus, resulting to a very few existing pure line breeding programmes. Additionally, various undesirable correlated traits such as; metabolic disorders, reduced fertility, etc. accompanied spectacular success made by selective breeding in poultry industry with three-fold and four-fold increase in egg production and growth rate respectively, indicative of reaching biological limit in the gains in a short period (Burt, 2002). It is highly important to concentrate on improvement of feed efficiency, enhancing meat quality, egg shell strength and genetic resistance to pathogens, which are traits that are costly and difficult to measure.

Marker Assisted Selection (MAS) is the use of genomic information in addition to phenotypic information to increase reliability in the selection process for the genetic improvement programme. The concept of marker-assisted selection originated in the early 1990's to remove or select genes based on the information of the marker (Eggen, 2012). MAS involved the identification of associated genetic marker with their linked quantitative traits loci (QTL) (Meuwissen & Goddard, 1996) and further the distance between markers and the trait of interest will determine the association (Ron & Weller, 2007). It goes without saying that the combination of both traditional breeding method and MAS is far more advantageous to the selection response. By the MAS, it is possible to recognize traits with low phenotypic expression like disease resistance, sex limited, recessive genes and mutants at a much early stage. In addition, through MAS we can transfer desirable genotypes into the productive breeds. The MAS technique therefore improves the breeding efficiency to some extent, but the drawback is that it only addresses those traits governed by a limited gene (VanRaden *et al.*, 2009) or relies on identification of a limited number of causal variants (Hayes *et al.*, 2013) leading to limited genetic gain while, most economically important traits or complex traits, are affected by several regions of the genome, each with a small contribution to the variability in traits (Cole *et al.*, 2009; Wolc, 2014).

The 21st century, marked as a genomics advancement era driven by the success of human genome project (Venter *et al.*, 2001), coupled with the development of many technologies and methods and introduced the genesis of genomics in domestic animal. With continuous effort made by genetic advancement, the evolution of genomics and discovery of molecular tools is already striking a huge impact in the field of genetic improvement and breeding, offering promising advantages with respect to conventional breeding. Meuwissen *et al.* (2001) first proposed the genomic selection in animal breeding, simultaneously, DNA based tools and technologies were also developed. Thereby, determining whole genome sequence of chicken in 2004 as the first farm animal to be determined, (Hillier *et al.*, 2004) with a refined version made available in 2006 (Warren *et al.*, 2017), and then cattle in 2009, pig in 2009 (Stock & Reents, 2013), and so on to other species as well resulting to the availability of dozens of species with sequenced genome database today. Subsequently, several SNP maps were developed, and genomic selection is applied in the breeding programs and showed significant results (Hayes *et al*., 2009; VanRaden *et al.*, 2009). Additionally, offering a potential resource for the commercial arena and research focus.

Genomic Selection

Initially, Meuwissen *et al.* (2001) proposed the method and it involves the scanning of entire genome-wide genetic markers to generate the breeding value of the selection candidates. This method is based on certain assumption such that there is linkage disequilibrium between the markers and the polymorphisms that causes variation in important traits (Hayes *et al*., 2013). And the principle behind this genomic selection lies on the fact that the information generated from a huge number of markers could be used to predict the genomic estimated breeding values (GEBVs) without actually understanding the gene's specific location on the genome length (Eggen, 2012). This method has shown higher efficiency and reliability in selection for traits of economic importance which are relatively governed by large number of genes (Khare & Khare, 2017), sex-limited traits (such as egg production and egg quality) and traits with low heritability (such as disease resistance) in comparison to the traditional method.

Methodology

The method can be summed briefly as follows-

Construction of reference population with the collation of marker genotypic (genotyped for SNPs of entire genome) and phenotypic information (Boichard *et al.*, 2016). Based on the collected phenotypic and genotypic data, the prediction equation will be obtained, which will then be used to obtain the ultimate GEBV (Fernandes *et al.,* 2016). Various methods for the generation of the genomic breeding value has been developed and applied today, such as-GBLUP, Bayesian variable selection methods (BayesB, BayesC, etc.), Bayesian LASSO and machine learning techniques (Panigrahi and Parida, 2012; Liu *et al*., 2014; Weng *et al.*, 2016; Chang *et al.*, 2018; Druet *et al.*, 2020).After validation of the estimated breeding values in the reference population, the prediction equation is then applied to candidates for selection with marker genotypic information (Ibtisham *et al.*, 2017).

Genomic selection has obtained superiority over traditional methods and MAS in various ways such as, candidates can be assessed without progeny as well as their phenotypic information and the method is not limited to 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 significant reduction in generation interval, thereby doubling the yearly genetic progress. Nevertheless, we should not forget that, no single breeding program, for example, genomic selection will not be a one-size-fits-all situation, a cost-benefit analysis will always accompany the implementation of any strategy in the breeding program (Mrode *et al*., 2018). Over the last decade genomic selection has been widely adopted in various livestock species and poultry, cattle preceding the rest (Hayes *et al*., 2009; VanRaden *et al*., 2009) with the numerous justified advantages gaining accuracy between 0.05 and 0.27.

Genomic Selection in Poultry

The possibility of whole genome sequencing has greatly influenced in the generation of genomic data. Genomic selection being considered as the most appropriate standard breeding method in livestock especially in the dairy cattle today, despite the differences in respect to the poultry breed, poultry breeders have taken huge interest in the application and execution of the same promising programme after numerous successful validation studies carried out (Wang *et al*., 2013; Wolc, 2014) with the main aim to yield a rapid genetic progress in the selection programme like any other livestock. The determination of the chicken genome sequenced has introduced the poultry breeding industry into the field of genomics, enabling the application of new opportunities in the poultry sector. Ever since, studies are being carried out in the upbringing of the poultry breeding programmes utilizing the genomic information investigated so as to enhance its selection efficiencies. Furthermore, studies were carried out with the available genome to boost information on other uncharacterized small yet gene-rich microchromosomes viz; GGA25 (Douaud *et al.*, 2008), GGA30,31,33 (Warren *et al.*, 2017), etc. A diagrammatic representation of genomic selection in poultry is shown in Fig.1.

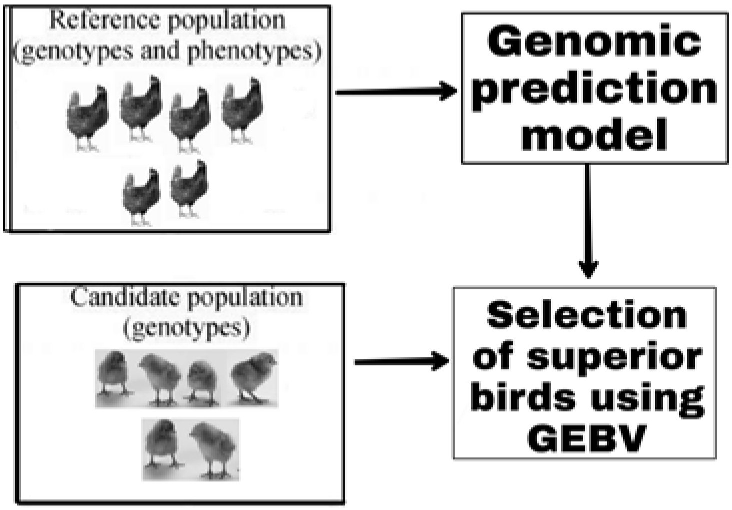

Figure 1: Genomic selection in poultry

The distinct growth drivers such as increase in the population growth, greater purchasing power and urbanisation have brought natural resources under immense pressure, thereby, animal scientists are challenged to emphasise on how to increase efficiency and yield long-term sustainability of livestock production (Telugu *et al* ., 2017). Meat production globally is projected to an increase of 16% in 2025 (i.e. 20% increase from previous statistics). The growth in poultry meat production sector is indicated as the primary driver in correspond to the global demand (Chatterjee *et al.,* 2019; ROECD-FAO agricultural outlook 2016-2025). Poultry continues to occupy its dominant position in meat sector, responsible for nearly half of all the additional meats focused to be produced in the next decade. One of the advantages of poultry industry is having short production cycle which enables the companies to quickly respond to the market demand, simultaneously, allowing rapid genetic improvements, improvement in animal health and development of feeding practices. Therefore, enhanced strategies for efficient techniques should be introduced to increase the rate of production, rather than simply relying on the conventional approach of the poultry breeding industry. And genomic selection is considered as one of the reliable solution in achieving such growing demands (Fulton, 2012) in shortest possible generation interval. After Schaeffer (2006) published his study on the efficient use of potential genomic data in dairy cattle, genomic selection (GS) has been routinely applied in the dairy sector. The key advantage in chicken lies in the prolificacy as compared to cattle or pigs when using traditional methods (Dekkers, 2007) characterised by high population with rich genetic diversity (Siegel, 2006). Another relevant application in the case of poultry which has gained propulsion is the fact that effective genomic selection or genetic progress relies largely on relatively huge reference populations and short generation intervals.

Genomic Selection Tools

The discovery of Single Nucleotide Polymorphic (SNP) marker and its gradual development of commercial SNP arrays opened opportunities for the application of genomic selection and the wide use of its genomic estimated breeding values across the world. Gradually, three SNP panels of sizes 6, 12 & 42K were identified (Groenen *et al.*, 2011) and the development of first high-density 600K chip in public domain was made available, with the help from the Roslin Institute and the BBSRC has taken place (Kranis *et al*., 2013). As we know, efficient genomic selection requires high-density SNP chips, in order to provide means for rapid, massive and relatively inexpensive genotyping. However, it has also been reported (Wolc *et al.*, 2016) that chips that are routinely used for genomic selection in poultry breeding are shifted back to medium density, containing thousands of SNP subsets from the 600 K chip, designed for specific lines. The relative reduced cost of medium-density chips as compared with that of low-density panels and the higher accuracy of genomic prediction and much easier prediction workflow has achieved a broader acceptance to the researchers, breeders and consumers for genomic selection application in poultry breeding. Whilst, by developing high-throughput sequencing technology, genotyping by sequencing (GBS) (Wang *et al*., 2019), it can also overcome the systematic deviation due to the inherent properties of SNP arrays usually and proved greater potential. Additionally, the development of low-cost and high-throughput sequencing and various marker genotyping platforms is an alternative to the high cost routinely used SNP chip genotyping (Liu *et al*., 2020). Crain *et al*. (2018) provided insights on utilizing both high-throughput phenotyping taking into account of plant temperature and light reflection along with genomic information so as to increase yield prediction and its selection accuracy in wheat breeding, resulting increased accuracy of yield predictions by up to 7% over standard genomic selection models. Likewise, poultry scientists can increase the accuracy of their breeding programs and rapidly execute the same to the farmers. In addition, different analysis software has been developed such as Axiom Analysis, for the genomic prediction and selection which plays efficient role equally for the genotype quality control. Traditional and genomic EBV can be computed by using BLUPF90 (Misztal *et al.*, 2014). And various other analysis programme such as PLINK can be used in controlling the quality of the genotyped data, inspection of unexpected changes in allele frequencies over generations and calculating the genotypes variance (Purcell *et al.*, 2007; Zhang *et al.*, 2020). Likewise, other methods for large-scale programs including GenSel (Garrick and Fernando, 2013) are used in generating genomic estimated breeding value (GEBV).

The availability and implementation of improved genomic tools including appropriate statistical models for genomic predictions and analysis software can perform a sound genomic selection.

Accuracy of Genomic Predictions

Accuracy in genomic prediction is the main tool that defines the successful application of genomic selection programme. Increased accuracy in the genomic prediction is the main advantage that can be exploited from the implementation of genomic selection programme by the poultry industry. One of the important factors on which the accuracy depends is the number of the reference populations which should preferably be large (Meuwissen *et al*., 2001). However, it should ensure the close relationship between the reference population and the candidate population and well-represent the candidate's haplotype (Elsen *et al.,* 2016; Rabier *et al.,* 2016). On the contrary, Liu *et al.* (2014) achieved high accuracy in comparison to conventional methods by applying genomic selection in relatively poor number of reference population (381-385) which must be attributable to small effective population size and the newly established F2 generation structured reference population. In addition, the number of training generations *i.e.* the number of the ancestral generations included in the training set also determines the accuracy based on the heritability of traits and Weng *et al.* (2016) found in his study that the optimum number of training generations in 16 layer traits studied was 4 or more in the case of highly heritable traits, whereas the lower number of generations for low heritable traits. Continual retraining of the training population is however required in response to factors linkage disequilibrium patterns, genotype X environment interactions, variation of SNP effects, erosion of accuracy over generation, subjecting to more accurate breeding value. Optimized grouping based on genotyping information, such that closer the group members are in the sense of genomic relationship, higher is the accuracy (Chu *et al.,* 2019). The GEBVs were predicted by applying different methods or models in various traits such as, single-step GBLUP methods (Chu *et al.,* 2019; Druet *et al.,* 2020; Zhang *et al.*, 2020), Bayesian variable selection methods (Weng *et al.,* 2016; Chang *et al.,* 2018), Bayesian LASSO (Liu *et al.,* 2014; Baes *et al.,* 2019), random regression model (Begli *et al.,* 2017) non-parametric methods (González-Recio *et al.,* 2008) and approaches that utilize annotation information (Morota *et al.,* 2014) etc., in both the layers and broilers. Nonetheless, GEBV always outperformed the prediction accuracy over the traditional method. So far, none of these methods or models showed exceedingly superiority over others but obtained more or less similar predictive abilities.

Implementation

With the implementation of DNA based technologies in the poultry breeding, the genomic selection provides possibilities of utilizing more reliable estimated breeding values in contrast to the traditional method. Evaluation of accuracies based on GEBVs in both the layers and broilers for various traits such as; production, reproduction, quality of the products and welfare were reported using several methods and have resulted in much higher accuracy (Wolc *et al*., 2016). One of the obstacle while maintaining the close relationship between the reference and the candidate population, it may give rise to inbreeding but, following a cross-classified mating system along with parentage identification can reduce inbreeding (Hsu *et al.,* 2015; Weng *et al.,* 2016) in genomic selection. In addition to which, it is known that generation interval can be reduced from 12 months to 6 months (in layers) which is a promising opportunity especially for males (Wolc *et al*., 2015; Chatterjee *et al.,* 2019) as breeders do not need to wait for the birds to obtain certain age to observe and identify the phenotypes for all the young birds.

In layers

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 selection programme and resulted that the genomic based selected birds outperformed those selected as per classical method. Other companies also obtained similar results and thus, reported genomic selection as a relevant option against conventional breeding for rapid genetic improvement in layer chickens (Sitzenstock *et al.*, 2013). A study (Druet *et al.,* 2020) was conducted for genomic evaluation of 5 egg quality traits in pure line layers *i.e.* egg weight, eggshell colour, eggshell strength, albumen height and eggshell shape index to judge the reliability of the method and observed a clear advantage of shifting the conventional selection to genomic selection at least in males. Furthermore, the increased accuracies were also observed to be trait dependent among the different traits studied and with the greater reference population, higher accuracy was observed. There was greater increase in accuracy of genomic evaluation with restricted phenotypic information.

In broilers

The first genomic selection implementation in 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 genomic selection still plays a significant role in the traits of reproduction and disease resistance. When selection candidates were genotyped with less than 400 markers and imputed up to 42K, the accuracy of imputed genotypes lies in the range of 97%, for moderately heritable traits whereas, fertility and egg production traits obtain 20-45%, (Wang *et* *al.*, 2013), and in case of high heritable traits (feed intake traits) (Wolc *et al.*, 2014) it can achieve greater than 50% further by means of enhancing the number of the haplotype marker up to 600K the accuracy can gain up to 99%. However, collectively all the large-scale evaluations resulted for the GEBV's superiority over the conventional EBV in broiler populations.

Gradually, with the sequencing of the turkey genome (Dalloul, 2010), subsequently, the discovery of whole genome SNP in turkey was also presented (Aslam *et al.*, 2012). And the genomic selection in turkeys has been carried out aligning the conceptual, theoretical as well as the applied front (Baes *et al*., 2019). The accuracy in the programme was assessed for feed efficiency, body weight, egg production, breast meat yield and walking ability using four two steps model i.e. GBLUP, Bayes A, Bayes B, Bayesian Lasso models against the pedigree based BLUP approach. The two step models showed increased accuracy of genomic predictions against the pedigree based by 9%, 13%, 33%, 19% and 56% for feed conversion ratio, residual feed intake, body weight, walking score and breast meat yield respectively. Although it is still a developing area in turkey, the technology can be widely spread in turkeys and further other birds with the proven model studies of chicken and need to be evaluated against the pedigree-based method.

Applications

1. As we know, most of the layer traits of interest can be measured only in the female and after the maturity being sex-limited. Although, both the males and females have the gene variants, it is only expressed phenotypically and measured directly by matured 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 the highly reliable genomic selection (Druet *et al.*, 2020).
2. Genetic variations can be measured right after hatch genetically, instead of waiting for sexual maturity or even later in life. Thus, selection of the superior bird can be done at a much earlier age in the lifecycle of the chicken unlike the time-consuming conventional method saving the expenses of rearing undesirable birds till maturity. The genomic selection can greatly be applied with high benefit for traits that cannot be measured directly during selection eg. carcass traits, growth traits, etc. (Liu *et al.*, 2014),
3. With the availability of huge number of SNP chips of chicken, genomic selection programme can predict the total genetic value of an animal based on data from genome wide dense marker maps (Meuwissen *et al.*, 2001)
4. Through the application of genomic selection, we can also perform rapid selection of desirable trait of interest and increase the frequency of favorable traits (Siegel, 2006). For instance, pathogenic resistance gene or immune response genes eg: MHC (Major Histocompatibility Complex), cluster of genes that play a role in resistance against the oncogenic herpes virus that causes Marek's disease in poultry (Bacon *et al.*, 1981), could be identified through genomic selection.
5. Further, we can also identify and eliminate undesirable traits. However, enough expertise is required to avoid eliminating the surrounding favorable genes. Eg. the gene that involves in producing fishy taint in chicken was determined and eliminated (Honkatukia *et al.*, 2005).
6. Genomic selection can detect pathogen in the poultry using pathogen specific marker (Charlton *et al.*, 2005). It can further improve the immune response and antibody response (Liu *et al.*, 2014). Thereby, it can be applied in disease resistance which is one of the urgent needs as disease outbreak is one of the major factor in huge economic loss to the industry.
7. Genomic selection can also be applied against mortality for socially affected traits such as cannibalism for instance to avoid practice of the beak trimming which is undesirable from a welfare point of view (Alemu *et al.*, 2016). Few recent genomic selection studies carried out in poultry are summarized in Table 1.

Table 1: Summary of few genomic selection (GS) carried out in poultry

References	Traits studied	Chip size	Models	Accuracy of prediction	Interpretation
Liu *et al.* (2014)	Antibody response trait to avian influenza and new castle disease in chickens.	Illumina 60K beadchip	Single trait GBLUP, Multiple trait GBLUP	0.318 in family scenario, 0.430 in random scenario	Indicates promising genomic predictions in the trait with a little higher accuracy of multiple trait GBLUP model
Alemu *et al.* (2016)	Survival time trait in brown layer with cannibalistic behaviour	60K SNP chip	ssGBLUP	0.42	Improvement of the trait was revealed.
Liu *et al.* (2017)	Feed efficiency (FE)trait: Feed Conversion Ratio (FCR), Residual Feed Intake (RFI) in meat type chicken	Illumina 60K beadchip	GBLUP	0.371 in family scenario, 0.322 in random scenario	Selection for FCR is suitable for improving carcass traits; leg muscle and breast muscle. Selection for RFI can effectively reduce feed cost.
Druet *et al.* (2020)	Egg quality traits in layers	600k Affymetrix Axiom HD	ssGBLUP	0.56 - 1.39 for Collective Cage traits and 0.65 - 1.01 for Individual Cage traits	GS was reported to be of much advantage than pedigree based, in respect to the trait especially in males.

Challenges

1. The high cost of genotyping with respect to the value of the chicken
2. The need for large reference population
3. Continual refinement of the reference population is required
4. Most of the poultry species genome are yet to be fully sequenced

Strategies

1. The existing genetic diversity of the poultry should be routinely monitored and thus, managing the expected diversity of their future progeny by using genome-based mating programs (Hayes *et al.*, 2009).
2. The importance of whole genome sequencing needs to be executed to all the breeds of poultry because, decoding the entire genome sequence has led to the discovery of numerous important genetic regions attributable to the variation in traits. The availability of large amount of generated genomic data has enabled access to the extensive bioinformatics tools available for genomic studies (Fulton, 2012). In addition, the issue of decay in the association between the causative mutations and the SNP over generations due to recombination, which results in a decrease in accuracy over time, can be overcome by the use of genomic predictions from the whole genome sequence data, considering that the causative mutations are present in the sequence data. (Meuwissen & Goddard, 2010; Hayes *et al.*, 2013; Wolc, 2014; Boichard *et al.*, 2015).
3. Genomic selection is routinely applied in chicken, similar genetic improvement programme is ventured with recent genome sequencing of Turkey species (Dalloul, 2010) which could achieve faster genetic progress in the population.
4. Continual refinement of the prediction equation to avoid erosion of accuracy in the selection (Meuwissen, 2009) over generations.
5. Approaches of developing phenotyping strategies for new important traits.
6. Sufficient genetic variation is required to carry out any DNA based methodologies. It has been reported that there has been a huge genetic loss in poultry (Fulton, 2012), especially as a result of numerous research carried out on genetic resources, so strategies such as the development of well-established germplasm conservation centres for poultry genetic resources should be developed, although there only a few of them.

Outlook

Through the use of genomic technology, we can encounter the global climate change in animal welfare. To mitigate the global environmental issues, mainly the manure in the environment in areas characterised by dense production, poultry industries needs to adopt standard methodologies, the major waste emission gas include: ammonia, methane, carbon dioxide, phosphorous and nitrogen (FAO/OECD). During 1980s and early part of 2000, there was decrease in those emissions made possible by exploiting the broiler's genetic potential at various levels (*i.e* 20%, 23%, 10% for methane, nitrous oxide, and ammonia respectively) (Hume *et al.* 2011). With the alarming negative environmental impact from agriculture and allied sector, the poultry industry stands as one of the largest next to Cattle, producer of greenhouse gases and various other waste emissions (FAO/OECD), and with respect to the growing population of broilers the reduction of wastes is still an important challenge. Selection for feed efficiency (FE) traits could be one of the striking strategies to follow in poultry breeding to address the problem. More studies can be explored on identifying genomic regions in relation to FE related traits; residual feed intake traits, feed conversion ratio traits, etc. Although, numerous studies have revealed that selection to improve FE has drastically reduces the emission of greenhouse gases and other wastes in poultry meat production and enhanced accuracy by four times (Liu *et al*., 2017). So, optimization of feed efficiency (Kubiak *et al.*, 2017) for instance by improving the feed digestibility so as to decrease the wastes and subsequently lowering greenhouse gas emission following appropriate feeding strategies accompanied by effective standard breeding methodologies like genomic selection which provides estimates of breeding values to non-phenotyped candidates or traits that is expressed later in life such as FE which deemed economically important could reduce the negative global environmental impact of poultry production. Additionally, feed accounts for about 70% of the total chicken production cost (Liu *et al.*, 2017), thus, genomic selection on FE related traits and traits that affect the utilization of different nutrients in particular will definitely reduce the cost of production coupled with degradation of greenhouse gas emission. To run such strategy successfully, we need to first understand the host-microbial interactions as it affects the key traits. For instance, in case of ruminants, with the application of technologies like Next Generation Sequencing it has overcome the limitations of ruminal bacterial culture (Hayes *et al*., 2013) and has been investigated as this is where the methanogens reside.

Conclusion

Genomic selection could provide rapid genetic progress through enhanced accuracy in selection and genetically identifying superior individual at a young age reducing generation interval and subsequent improvement of the individuals in the following next generation. Genomic selection dominates traditional method by an overall faster rate of genetic gain in the livestock and poultry improvement programme. Although, it is still a developing area in poultry, unlike the pronounced dairy cattle sector, being an industry it is, exclusively involved in generating a profitable and sustainable income source while responding the global demand of protein rich meat and eggs through the production traits. Therefore, with the introduction of genomic selection, its application in the poultry industry is viewed as a wise and promising means to overcome past limitations and most importantly achieve the goal of rapid and efficient genetic progress resulting to significant increase in production.

However, poultry industry being a highly competitive sector, the efficiency and the success rate of implementing the genomic selection programme will depend on how well and correctly it is applied in the breeding strategy.

Conflict of Interests

There is no conflict of interest.

Publisher Disclaimer

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