Genomic Selection in livestock

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Abstract

Genomic selection is a fast-growing field in dairy sector for rapid and large genetic gain which ultimately improves the hereditary potential of current as well as future livestock generation. Initially suitable animals for desired traits and breeding objectives gets selected and interactions such as genotype environment will be predicted on the basis of information on causal variants by using more robust approaches.

Introduction

The recent innovation of genomic selection provides huge opportunities for traits difficult to select or yet selected for genetic gain at a similar or lower cost for sustainable production and for a better management of long-term genetic variability. This method is revolutionary by reducing the genotyping costs, phenotyping tactic, designing for replacement of reference populations, increase in strength and persistency of genomic predictions from genome sequences or genetic environment interactions. McEwan (2007) indicated the importance of genomic resources such as DNA technology for whole genome selection increases information surge back probable genetic worth of individuals, provides parentage information and allowing better breeding assessments as an method to audit traceability. The data analysis steps such as processing, storage, analysis and interpretation of results will be of much concern rather than the marker measurement technology for increasing industry adoption. Breeding goals of livestock species remains dynamic and become more specific and balanced in terms of economics and production aspect of the rearing personnel from time to time. Traditional breeding goals were limited for achieving better quality in growth, yield and efficiency. While current breeding goals are more diversified in considering traditional goals as well as incorporating other measures of value addition such as fitness, fertility, behavioral flexibility, food quality, food safety, disease resistance, sustainable animal welfare, climate

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resilience, managing diversity with suitable advance tools such as DNA diagnostics and genomic selection.

Genomic selection can be defined as the form in which genetic markers from the whole genome are used for marker-assisted selection to ensure at least one marker in linkage disequilibrium with all quantitative trait loci (QTL). The approach of genomic selection is to estimate the effects of all genes or chromosomal positions so that it can substantially replace the significance testing methods (Meuwissen, Hayes and Goddard, 2001). The estimates of the effects can be decided as the genes with small effects are expected to have small estimates and vice a versa. Similar prediction equation(s) needs to be applied for calculating all comparable genomic EBV (Goddard and Hayes 2007). The national genetic evaluation system provides a single country specific EBV system through its database for estimation of the prediction equation which hinders commercialization of genomic selection in terms of the investment needed to develop and market a set of markers. The substitute solution would be to have its own markers, database and EBV for each company. The fundamental evaluation system can remain more unbiased and gain wider acceptance within the whole industry by providing universal database and keeping it outside the realm of marketing.

Steps in Genomic selection: Genomic selection can be achieved by using standard steps in selected herd.

1. Genotyping and phenotyping information of training population are combined to get trained model for genomic selection.
2. Selected breeding population has to be genotyped for prediction of estimated breeding values (EBVs) for this population using the same trained model which was used for training population.
3. Finally animals will be selected on the basis of these resulted breeding values.

System of genomic evaluation: Genomic Best Linear Unbiased Prediction (or GBLUP), (VanRaden *et al.*, 2009) is the relationship matrix, efficient for very polygenic traits is based on marker information instead of on pedigree which is simply extension of the polygenic BLUP. Model considered the marker's effects as a random because of large number of markers, one whose value comes from a prior statistical distribution. The statistical models give the genomic breeding values with a covariance structure for all genotyped animals. The model gives the same weight to all markers, ignores the true genetic determinism of the trait and the covariance between the genomic breeding values of two animals is proportional to their proportion of genome.

From the selection candidates animals must be separated into the reference population to estimate the prediction equation in genomic selection (Goddard and Hayes, 2007). The selection candidates need to have marker genotypes while the animals in the reference population need to have both phenotypes and genotypes information. Traditional stud breeders could be produced as cheaply as commercial marker animals, the cost consideration part is only for genotyping. Enough degrees of freedom are mandatory to know the effect of all alleles on our breeding goal and this shortage of degrees of freedom emerged as the most important constrain. To overcome this enormous shortage of degrees of freedom problem there are three ways:

1. **Least Squares (LS):** Statistical significance can be tested for all the genes one by one and estimating the set the effects of the significant and non-significant genes. All genes cannot be tested simultaneously due to the degrees of freedom shortage, this resembles the QTL mapping /conventional MAS approach.
2. **Best Linear Unbiased Prediction (BLUP):** The allelic effects should be considered as random effects not as fixed effects. All allelic effects can be estimated simultaneously as the fitting of random effects does not require degrees of freedom this also require an estimate of the variance of the allelic effects. Since the majority of the genes will have very little effect on the trait and they will dominate the estimate (close to zero) of the variance but the same variance for every gene is problematic.
3. **Bayesian estimation (Bayes):** This approach is advantageous than BLUP as the estimates include prior distribution for variance and the allelic effects are assumed different for every gene.

Evaluation methods select closely located causal variants for the most predictive markers. Many Bayesian methods gives larger weights to SNP assuming causal small variants have a non-zero effect. These methods are also very efficient for multi-marker QTL mapping (Van Den Berg *et al.*, 2013). In most approaches, each SNP treated individually, ignoring their linkage disequilibrium. Compared to biallelic SNPs, haplotypes (combinations of neighboring SNP) are more informative and better imitate identity-by-descent situations.

Conclusion

The Genomic Selection in animal breeding is a paradigm shift for structural changes in the genetic improvement for various livestock species. When this approach is combined with reproductive technology such as multiple ovulation and embryo transfer (MOET), it will be impactful by decreasing generation length and also used to select the best embryos to produce the next generation (instead of random embryos). The prediction equation can be established on

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commercial animals for the relevant traits. This method entails a reduction of costs for useful interpretation even for the traits which are not measured in young animals such as meat quality and disease resistance.

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