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Importance of Genomic Studies in Livestock Improvement

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The animal products are proving 18 percent of total calories and 39 percent of the protein in human diets worldwide. To meet future demands, animal production need to be enhanced maintaining or reducing its requirements for land, water, and feed adjusting climate change. The genomic technologies needed to be exploited to realize the potential of genomic technologies for improving animal production efficiencies. The research work was broadly classified into following areas viz. i) Science to Practice focused on research intended to implement genomic selection in commercial animal production. ii) Discovery Science described the basic knowledge of animal genomes that would be needed to realize genome enhanced animal selection and iii) Infrastructure described the computing, data analysis, and enhanced training that would be needed to advance the field. The genomes of livestock species viz. cattle, swine, sheep, goats, chickens and catfish had been defined as generation of complete genome sequences. Technologies and analysis methods have been developed for the comprehensive genotyping of individual animals at a variety of scales using including complete genome sequencing. This led to prediction of more accurate genomic breeding values for enhancing the efficiency of Animal Breeding and provided the groundwork for future studies. The Animal Genomic Research exploited to achieve to the following main goals for animal production: 1) Providing Nutritious Food for a Growing Human Population, 2) Improving Sustainability of Animal Agriculture, 3) Increasing Animal Fitness and Improving Animal Welfare, and 4) Meeting Consumer Needs and Choices. The research and analysis of WGS aid in to maintaining the genetic diversity at ecosystems level, between and within species level and between breeds and within breeds level. The optimum maintenance of genetic diversity is essentially required to balance ecosystems and to avoid catastrophic situations. The understanding of genetics based on WGS leads to developments of various prophylactic measures including effective vaccine development. It is clearly evident and realized during COVID 2019 Pandemic. WGS have still very application in following areas.

A) Personalized medicine: - Whole genome sequence data may be an important tool to guide therapeutic intervention. and hence may lay the foundation for predicting disease susceptibility and drug response.
B) The sequence of Genome may be used identify genes and further allow SNP detection. This SNP is also used to pinpoint functional variants from association studies
C) Evolutionary biology: WGS improve the knowledge available to researchers interested in evolutionary biology. It gives more light on adaptability of different organisms in ever changing climates.

Genomic prediction of breeding values is increasingly widely used in livestock breeding programs for dairy, beef, sheep, chickens and pigs. Till date, most of these predictions have been based on arrays of approximately 50K, 80K SNP chips across the world. However, Selection of animals based on Genomic breeding value predictions is far away from achieving of this target in many developing countries of world including India. The developed countries practicing genomic selection of animals due to fact that they have started systematic progeny testing since approximately 100 years back and possess organised large with phenotypic data in easily retrievable form. The genomic selection practicing countries jumped next higher level in accuracy of Genomic prediction of breeding values using SNPs variations based on sequence of Whole Genome Sequences instead of information generated from various 50K, 80K SNP chips etc. The genomic prediction of breeding values based SNP chips involves. As a result, the accuracy of the prediction equation will rapidly decay over generations as large chromosome segments break up due to recombination. The advantage of using whole genome sequence data for genomic prediction of breeding value over such SNP arrays arises from the fact that with the sequence data, the actual casual mutations responsible for trait variation are now in the data set. This could have at least three benefits:

1. Better persistence of accuracy of genomic predictions over generations and less erosion of accuracy in genomic predictions for individuals that are less related to the reference set.
2. Higher accuracy of genomic predictions. One issue with the current SNP arrays (eg. 50K, 800K for cattle) is that the SNP have been selected to have a high minor allele frequency. This means that the SNP arrays are less likely to have SNP in linkage disequilibrium with casual mutations where one of the alleles is at low frequency in the population. If this variation from rare alleles could be captured with the whole genome sequence data, and exploited in genomic predictions, accuracy of genomic

breeding value may be able to be improved in the order of 2-30%, depending on trait.

3. More accurate genomic predictions across breeds. For a breed like Holstein dairy cattle, large reference populations have been assembled, leading to high accuracies of genomic predictions. For other breeds, assembling such large populations is challenging, so using genomic information across breeds would be appealing. However, the accuracy of genomic predictions across breeds with the Bovine 50K array is close to zero, and this improves slightly when the 800K array is used. With the whole genome sequence data, at least the causative mutations which do segregate across breeds could be captured and this information used in multi-breed genomic predictions. A multi-breed reference population would be required to achieve this. A multi-breed reference would also have the benefit from the fact that linkage disequilibrium across breeds is lower than that within breeds, so that causative mutations could be mapped more precisely. So multi-breed reference combined with sequence data should be the best approach to achieve the potential benefits from sequence data.

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