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ORAL PRESENTATION

Contrasting and Assessing Genome-Wide Association Studies and Marker-Assisted Selection Applications in Animal Breeding

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Abstract

The application of genomic studies in livestock species aims to comprehend the genetic underpinnings of specific traits, fortify disease resistance, and elevate product quality and production efficiency. The outcomes are integrated into animal breeding initiatives, which adopt a methodology aimed at enhancing economic attributes within livestock through heightened selection efficacy. Given the understanding that yield-related characteristics result from the additive influence of multiple genes, the identification of Quantitative Trait Loci (QTL) is employed to delineate chromosomal regions governing these traits. The shared objective of QTL identification techniques, along with genomic assessment methodologies, is to juxtapose markers and phenotypic values related to the specific trait. The intricacy inherent in the desired attributes has spurred the development of genomic selection methodology, which is rooted in predictive approaches rather than empirical testing. The utilization of selection strategies, coupled with genotyping for production-related traits and marker identification, has accelerated the pace of genetic advancement. Given that numerous genes contribute to the manifestation of most economic traits, the mere identification of a limited subset of these genes through DNA markers will merely account for a fraction of the overall genetic variance. Furthermore, individual genes are inclined to exert modest effects, necessitating a substantial volume of data to estimate their impact accurately. This challenge becomes more pronounced when utilizing a haplotype of markers to track QTL, as the need to estimate numerous haplotype effects arises. While the markers employed for Marker-Assisted Selection (MAS) may be associated with QTL, they might also exist in linkage equilibrium rather than linkage disequilibrium (LD) with the QTL. In instances of LD, it is plausible that either the QTL or the marker itself could indeed function as the QTL. In this work, our aim was to compare these methodologies, evaluating their efficacy in the context of pivotal selection practices integral to livestock breeding.

Keywords: Genetic marker, Genomic selection, GWAS, MAS, QTL

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