

Animal and Bioscience Department

Title

Precision cattle breeding using precision genomics

Abstract

The precision of genome wide association studies and genomic predictions to-date have generally been limited to 1) medium to high density genotype densities, 2) relatively small populations, 3) single nucleotide polymorphism markers, and 4) only on additive allelic effects. Moreover, because of the large confidence intervals in detected putative genomic regions, association studies heretofore generally terminate simply with a reported putative genomic region but no proof of causation of the polymorphism. The availability of full sequence data on >1000 animals (through the 1000 genomes project) coupled with low cost genotyping plus imputation, facilitates the achievement of the objectives of this project to undertake a statistically well-powered genome wide association using imputed sequence data for two important traits, milk yield and carcass weight, in a population of >250,000 dairy and beef cattle. The novel component of this study is that all structural genomic variants (i.e., SNPs, CNVs, indels) will be investigated, and both additive and non-additive allelic effects will be modelled. Furthermore, the ensuing results will be rapidly deployed to industry through a custom genotyping panel and associated precision genomic mating plans to maximise the exploitation of the detected additive and non-additive genetic variation.

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