Abstract by Brian Meredith - Investigation of the genetic basis of bovine somatic cell score and milk production traits using genome-wide association data

The Irish dairy industry is an integral part of Irish agriculture contributing 28.1% of national agricultural GDP. To compete on the international stage manipulation of milk yield and composition traits tailored to the specific product requirements will be required. In addition, animal health and welfare allied with mastitis-related production costs ensure focus remains on mastitis control and treatment. Permanent and cumulative improvements in these aforementioned traits can be achieved through selection of genetically superior animals. However, although progress has been made with dairy cattle selection programmes, our knowledge of the intricate biology underlying these traits is limited. Therefore this study aims to identify genomic regions associated with milk production and mastitis resistance using genotypic data from 914 Holstein-Friesian AI sires and 493 Holstein-Friesian cows genotyped on the Illumina BovineSNP50 Beadchip. Phenotypes were based on national genetic evaluations. Two statistical models were used to quantify the associations, 1) a linear mixed model and 2) a Bayesian model. The linear mixed model yielded p-values corrected for multiple testing while the Bayesian analysis provided posterior probabilities of association for each single nucleotide polymorphism (SNP). Numerous significant associations were identified for milk yield (401), fat percentage (341), protein percentage (242) and somatic cell score (10) across all analyses. Haplotypes were generated which allowed significantly associated SNPs to be linked to nearby genes which may have a role in the expression of the particular trait. Ultimately the utilisation of such genome-wide association data may help elucidate the biological pathways underpinning phenotypic differences in bovine mastitis resistance and milk production.