

Animal Breeding in the Genomics Era

Natascha Vukasinovic, Ph.D.
Monsanto Company

Abstract:

Milk and meat production, reproductive performance, disease resistance, specific behavior patterns, and other traits that farm animals are kept and selected for are complex quantitative traits, controlled by many genes and environmental factors. For more than 50 years, selection and breeding of farm animals relied on quantitative genetic methods. Although substantial improvement in animals' performance had been achieved, little was known about genetic architecture of selected traits. However, recent advances in molecular genetics and the explosion of DNA technology, along with new developments in statistical genetics and genomics, have created new opportunities for better understanding of quantitative trait genetics. In particular, development of dense marker maps in many livestock species has facilitated search for genes affecting quantitative traits – known as quantitative trait loci (QTL).

This talk will focus on how molecular data are used in mapping QTL in farm animals. We present strategies to detect and characterize QTL in different livestock species, from a rough genome scan to pinpointing causal mutations. We discuss statistical and computational challenges researchers face in situations that are specific for livestock populations. Examples of QTL mapping experiments in cattle and pigs and applications of findings in a commercial setting will be presented.