# ABSTRACTS FROM FRANK BAKER AWARD-WINNING ESSAYS

## GENETIC ANALYSIS OF LONGITUDINAL DATA IN BEEF CATTLE

Scott Speidel, Colorado State University

Currently, many different data types are collected by beef cattle breed associations for the purpose of genetic evaluation. These data points are all biological characteristics of individual animals that can be measured multiple of times over an animal's lifetime. Some traits can only be measured once on an individual animal, whereas others, such as the body weight of an animal as it grows, can be measured a multitude of times. Data such as growth has been often referred to as "longitudinal" or "infinite-dimensional" since it is theoretically possible to observe the trait an infinite number of times over an the life span of a given individual. The analysis of such data is not without its challenges, and as a result, many different methods have been or are beginning to be implemented in the genetic analysis of beef cattle data each an improvement over its predecessor. These methods of analysis range from the classic repeated measures to the more contemporary suite of random regressions that use covariance functions or even splines as their basis function. Each of the approaches has both strengths and weaknesses when it comes to the analysis of longitudinal data. Therefore, the objective of this essay is to summarize past and current genetic evaluation technology for analyzing this type of data and to review some emerging technologies beginning to be implemented in current national cattle evaluation schemes along with their potential implications to the beef industry.