The Breeding and Genetics Symposium titled “Systems Biology in Animal Breeding: Identifying relationships among markers, genes, and phenotypes” was held at the Joint Annual Meeting of the American Society of Animal Science and the American Dairy Science Association in Phoenix, AZ, July 15–19, 2012. The primary goal of the symposium was to demonstrate the use of high-density SNP genotypes to determine the complex regulatory relationships among genotypes and phenotypes but also to present methods for studying complex relationships among phenotypes. Case studies from mammalian and avian species were included to emphasize the broad applicability of these methods.

Modern systems biology attempts to explain how variations in DNA markers relate to phenotypes through transcription, protein, and regulatory networks. Systems biology is a rapidly growing field of study, and many animal breeders are unfamiliar with this area. Still, resources for such work are rapidly becoming available, including high-density SNP genotypes for thousands of phenotyped dairy cattle collected by the North American dairy industry in the National Dairy Database maintained by the Animal Improvement Programs Laboratory (Beltsville, MD), and several multi-institutional and some international projects are genotyping and phenotyping animals for novel traits such as efficiency of production. In addition, a number of competitive grants recently awarded by the USDA National Institute of Food and Agriculture’s Agriculture and Food Research Initiative competitive grants program include 1 or more objectives incorporating systems biology approaches in several species, including cattle, swine, and poultry. There is substantial evidence that most QTL in the cattle genome explain only small proportions of additive genetic variance for important phenotypes (e.g., Cole et al., 2011). Recent papers, such as Fortes et al. (2011) have shown that gene network analysis can provide powerful insight into the genetic architecture underlying complex phenotypes.

Fortes et al. (2010) presented a method that combined genomewide association analysis using SNP genotypes with gene network theory using it to dissect a complex trait, age at puberty. The symposium’s first speaker, Toni Reverter (Commonwealth Scientific and Industrial Research Organisation, Brisbane, Australia), presented 2 examples of how to use that approach to identify gene networks, with particular emphasis on the use of complexes formed from the intersection of multiple networks (Reverter and Fortes, 2013). In both illustrations, the results from SNP-based association analyses were used to perform inference on gene regulatory networks. The presentation also included details about available tools for performing such analyses.

In the second presentation, Warren Snelling (USDA-ARS U.S. Meat Animal Research Center, Clay Center, NE) accentuated some of the important points.