

Advancing Sustainable Livestock Production

The ARS food animal production research program improves food animal production efficiency, sustainability, animal welfare, and product quality while safeguarding animal genetic resources. Animal production is a critical component of the U.S. economy, yielding \$440.7 billion in economic output, with \$76.7 billion in earnings, \$19.6 billion in income taxes, and \$7.4 billion in property taxes in 2014. The following accomplishments highlight ARS advances in animal production research in FY 2020.

A high-quality cattle gene atlas. The goal of genomic analyses in livestock is to make sense of the genome to understand and improve important livestock traits. With modern technologies, it is possible to localize variation in traits to regions of the genome, but it can be difficult to determine the gene, and the change in the gene, responsible for the trait. For some genes where the functions are not well characterized, it can also be difficult to determine what parts of the body are involved in controlling the trait. ARS scientists in Beltsville, MD, developed a comprehensive tissue-gene atlas for cattle by integrating their own information with publicly available information on gene regions associated with traits, genes expressed by tissues, and changes in gene chromosome structure that are known to control gene function. This high-quality cattle gene atlas links these three data sources for the first time and provides an important tool for discovering the tissues, genes, and genome structure that control traits in cattle.

New, affordable method for conducting genomic analyses of crossbred cattle. Detecting all the DNA variation in each individual animal can be done by genome sequencing, but is too expensive for routine genomic analyses of traits. The full DNA variation of individuals is necessary to effectively predict trait differences caused by DNA variation. Methods to correctly assign complete sequence-level DNA variation of key ancestors to offspring using low-cost genotyping would improve genomic predictions and save industry the expense of sequencing every animal. ARS researchers in Clay Center, NE, assembled genomic sequences from individuals with many descendants in a crossbred population representing the eighteen most predominant beef breeds in the United States, and combined it with publicly available sequences representing beef and dairy breeds. In collaboration with Gencove, Inc., these sequences were analyzed to determine DNA variants that typically occurred together. Those relationships were then used to predict all the variants in the genome from a low-cost, low-coverage genome sequencing to generate a low number of initial genotypes. The low-cost sequencing approach for generating initial genotypes results in better accuracy of DNA variation assignment than genotypes obtained using SNP chips, the most common approach to genetic marker detection. This new method will enable more effective trait-genome associations at a lower cost than currently available SNP chips. Producers will include a larger portion of animals, at low cost, for genetic evaluation programs, and predict genotypes up to the genome sequence level. This will improve selection accuracy and increase genetic gain, and lead to a faster rate of improvement in valuable beef traits for the industry.

New method to improve the identification of genetic markers for feed efficient pigs. Typical studies to identify genetic markers for livestock traits include several thousand animals and thousands of genetic markers. Genotyping, analysis, and interpretation costs associated with the large resulting data set is a challenge to producers wanting to implement genomic selection. To reduce genomic selection's cost and complexity, an improved ability to narrow genotyping to the most appropriate markers to test for association with specific traits is needed. Using tissues relevant to digestive processes from high and low feed efficient pigs, ARS scientists in Clay Center, NE, developed a methodology that used gene expression data to rank the likelihood that the genes contribute to feed efficiency. To provide a reduced

set of markers for analysis, scientists selected 10 different groups of genes and markers for separate trait association analyses based on different relationships to criteria related to feed efficiency. Scientists found 36 markers were associated with feed efficiency; 29 were linked with genes already known to have associations with feed efficiency, demonstrating prescreening helps select for relevant genes and markers. A less targeted approach using thousands of genes and markers evaluated many markers, most of which had no influence on the trait. Though they did raise the threshold for statistical significance, the analysis resulted in identifying only two markers associated with feed efficiency. Neither of those markers were in genomic regions previously associated with feed efficiency and, despite using stringent criteria, may be spurious. The novel strategy for using gene expression information to preselect markers for genomic analysis is a powerful approach for identifying economically important livestock traits markers. The markers identified in this study are available to commercial genotyping companies for producers to improve pig feed efficiency.

Weaning-associated fungus *Kazachstania slooffiae* likely has positive role in piglet growth and health.

Weaning is a period of stress and environmental change for piglets, and they experience a greater incidence of diarrhea and other digestive problems. Recent studies indicate there are dramatic changes in fungal microorganisms after weaning, and this change may contribute to the growth and health of weaned piglets. ARS scientists in Beltsville, MD, isolated *Kazachstania slooffiae*, the most dominant post-weaning fungus in healthy piglets, and sequenced its genome. Genes identified from this sequence suggested that *K. slooffiae* has positive interactions with beneficial bacteria in the piglet gut, signifying a strong beneficial role. Sequencing this genome is a critical first step for investigating the effects of this microbe in piglet growth and health. These results support the concept that *K. slooffiae* can be used as a naturally derived probiotic to enhance piglet growth.