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Genomics Symposium: Translational genomics to improve fertility of animals

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In 2010, the USDA National Institute of Food and Agriculture (NIFA) launched the Agriculture and Food Research Initiative (AFRI) Food Security Challenge Area program. The goal of this program was to support integrated research, extension, and education projects directed at increasing the agricultural production of plants and animals (Mirando et al., 2012) needed to feed a burgeoning global population that is expected to be almost 9.8 billion people by the year 2050 (United Nations, Department of Economic and Social Affairs, Population Division, 2017). One program area in the 2010 AFRI Food Security Challenge Area request for applications (RFA) focused on increasing production efficiency in livestock through funding of integrated research, extension, and education project grants that fostered collaboration of scientists and educators working in the field of genetics and genomics with those in other disciplines, including animal nutrition, health, and reproduction. Animal-focused AFRI programs to be offered over the next 2 yr were also described. In 2012, the AFRI Food Security Challenge Area RFA solicited grant applications for the “Translational Genomics for Improved Fertility of Animals” program, and NIFA subsequently awarded 4 grants totaling US$10,125,583 to project directors originally located at the University of Nebraska (D. C. Ciobanu), the University of Missouri (J. F. Taylor), Texas A&M University (P. J. Pinedo), and Washington State University (T. E. Spencer).

Results emanating from grants awarded in the 2012 “Translational Genomics for Improved Fertility of Animals” program were presented at the Genomics Symposium titled “Translational Genomics to Improve Fertility of Animals” held at the Joint Annual Meeting of the American Dairy Science Association, the American Society of Animal Science (ASAS), the Canadian Society of Animal Science, and the Western Section of the ASAS in Salt Lake City, UT, July 19 to 24, 2016. The symposium began with a presentation by D. C. Ciobanu, who discussed results from his AFRI grant titled “Translational genomics for improving sow reproductive longevity” (Wijesena et al., 2017). He described work in which genetic variants associated with age at puberty and litter size traits were identified using genome-wide association studies and transcriptional profiling. Results indicated that gilts attaining puberty at an earlier age were more likely to have increased reproductive longevity as sows. The long-term goal is to identify functional SNP with large effects on fertility traits that can be used to select replacement gilts for improved reproductive performance and increased longevity.

The next presentation, by J. F. Taylor (University of Missouri, Columbia), focused on identifying variants in the bovine genome that are lethal to embryonic survival. Taylor et al. (2016) reported on the development of the first generation of a bovine functional assay containing 170,000 variants, of which >120,000 have the potential to be functional and 34,000 are common variants present on many of the genotyping assays currently used for genotyping in the cattle industry as part of their AFRI grant titled “Identification and management of alleles impairing heifer fertility while optimizing genetic gain in Angus cattle.” The assay, GGP-F250, is now pub-
licly available from GeneSeek (Neogen Corporation, Lansing, MI). Using this assay, the authors have geno-
typed 18,300 cattle representing Holstein and 9 U.S. beef
breeds. Results from this research will assist with mating
decisions and lead to improved fertility in both the dairy
and beef cattle industries.

The third presentation, by G. L. M. Rosa (University
of Wisconsin-Madison), described results from the AFRI
grant “Genomic selection for improved fertility of dairy
cows with emphasis on cyclicity and pregnancy” (Rosa
et al., 2016). Holstein cattle (12,000) from 7 states were
monitored for uterine health, estrous cyclicity, estrus,
pregnancy rate, pregnancy loss, metabolic disorders,
and milk yield. Extensive analysis of the phenotypic
data using pedigree information has been performed to
estimate genetic parameters, such as heritability of each
trait and genetic correlations between them. In addition,
a reproductive index, predicting probability of pregnan-
cy at first AI after calving, was developed and used in se-
lective genotyping of high-fertility cows (i.e., pregnant
after first AI) and low-fertility cows (i.e., not pregnant
after 2 AI). The project team described plans to continue
identifying fertility indicators as well as detect genomic
regions affecting fertility in dairy cattle.

The final presentation was made by T. E. Spencer
(University of Missouri, Columbia), who discussed the
AFRI grant titled “Improving fertility of dairy cattle us-
ing translational genomics” (Spencer et al., 2016). The
overarching goal of this project is to improve the fertility
of lactating dairy cows through marker-assisted genetic
selection for maternal fertility in both heifers and cows
combined with use of sires with high daughter pregnancy
rate. The project team members have identified genomic
loci associated with fertility in heifers and primiparous
lactating dairy cattle and contributed educational content
on the genomics of reproduction in both English and
Spanish to the DaireXNET website (http://articles.exten-
sion.org/dairy_cattle; accessed 9 July 2017).

In summary, presentations at the Genomics
Symposium at the 2016 Joint Annual Meeting de-
scribed results of research funded through the 2012
AFRI Food Security “Translational Genomics for
Improved Fertility of Animals” program and thus pro-
vided a constructive forum for discussing the applica-
tion of translational genomics to improve fertility in
swine, beef cattle, and dairy cattle. Although projects
are still ongoing, the presentations revealed substantial
progress toward application of genomic approaches to
enhance reproductive performance of animals.

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