

UF-Gainesville Beef Cattle News Corner

Genomic research on Brahman influenced cattle presented during the Plant and Animal Genome conference

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The International Plant and Animal Genome conference is the largest Ag Genomic Conference in the world where approximately 4,000 genomic researchers and industry representatives gather each year to present the latest genomic findings across all animal and plant species as well as present the newest upcoming genomic technologies. I have been attending this conference for the last 16 years ever since I was a postdoc at Cornell University because it is such a unique experience to be able to hear and see in action the latest technologies in the field of genomic research but also hear about the applied research and how these new technologies can be applied toward the genomic improvement of economically important traits in a variety of species.

I always ask my graduate students if they want to present their work, which is the only way I would take them to attend the conference. The only oral presentations at this conference are the invited ones, so there is less pressure on the students knowing they will only have to present a poster. This year however was different. My graduate student Kaitlyn Sarlo Davila applied for the travel award and she was selected to receive a NRSP8 Bovine Genome Coordinator funding award. As the recipient of the award, she was invited to give an oral presentation of her research during the Cattle Workshop, in addition to her poster presentation.



Photo: Kaitlyn Sarlo Davila presenting her research on genetics of thermotolerance in beef cattle during the International Plant and Animal Genome conference.

Kaitlyn presented on her genome-wide association study for hair length in Brahman-influenced heifers conducted to identify genetic variants associated with the length of the topcoat and undercoat of cattle. The coat is important because a shorter, slicker hair coat is a key thermoregulative adaptation that allows cattle to lose heat more efficiently through conductive, convective, and evaporative cooling at the hair-skin interface. Hair samples were collected from the shoulder, 4 inches down from the spine and halfway along the horizontal axis from 1,456 heifers in 2016 and 2017. The length of the topcoat and undercoat were evaluated for each individual by averaging five long and five short hairs, respectively. DNA was extracted from blood samples and genotyped with the Bovine GGP F250 array (this allows us to look at 250,000 SNPs or genetic markers throughout the genome of each individual animal). Under very stringent conditions, Kaitlyn was able to identify four genetic markers in the prolactin receptor gene as significantly associated with topcoat length. The *SLICK* mutation in the prolactin receptor gene has previously been demonstrated to have a significant impact on hair length in tropical cattle. Seven genetic markers in a different gene (*PCCA*) were also found to be significantly associated with undercoat length. *PCCA* belongs to the biotin transport and metabolism pathway. Biotin deficiency has been widely reported to cause hair loss. Kaitlyn concluded that these genetic variants may contribute to a shorter, slicker hair coat and more thermotolerant animals.

Kaitlyn did a fantastic job presenting her work and representing the Department of Animal Science and University of Florida in front of a room packed with genomic researchers from around the world. She answered the questions she got at the end in great detail, showing a great understanding and knowledge of the biology underlying the traits she is working on. We also received many positive comments the days following her presentation regarding our work with Brahman and Brahman-influenced cattle and the importance of this research as we continue to improve the productivity of our beef populations in a continuously warming climate.