

RESEARCH ROUNDUP

Researchers put bull fertility, BRD under microscope

Compiled by Shauna Hermel, editor, and Megan Silveira, Angus Journal assistant editor

Fertility in the future

Understanding and predicting fertility in bulls is helping achieve reproductive efficiency.

In discussions of fertility, the cow often takes precedent. Francisco Peñagaricano, assistant professor of qualitative genetics at the University of Wisconsin, said the bull rather than the cow should be at the forefront of these conversations.

“A single bull will have a larger impact than a single cow on genomics,” Peñagaricano said during his presentation,

“Genomic Discussion and Prediction of Bull Fertility,” at the 2021 Beef Improvement Federation (BIF) Research Symposium & Convention in Des Moines, Iowa.

Peñagaricano reminded producers a cow typically produces only one calf each breeding season, whereas a bull can sire numerous calves. A vast majority of beef producers share the goal of improving reproductive efficiency, so, Peñagaricano said, it’s important for members of the beef industry to understand fertility in bulls.

Based on past research on dairy bulls, Peñagaricano said genetic factors do explain part of the variation in bull fertility.

However, he explained, genes with the ability to influence fertility do so with minuscule effects. Often, it’s novel regions, genes or variants in genetic data that Peñagaricano finds have large nonadditive effects on the next generation of livestock. For this reason, pathways, rather than single genes, are often the primary targets of selection for fertility.

Homozygous bulls are also often seen to possess lower genetic

diversity, Peñagaricano said, warning producers that homozygosity might be an important risk factor for bull fertility.

With all this in mind, Peñagaricano said, the next question producers have is, “Can

fertility in a bull actually be predicted?” His answer: Yes.

“Genomic prediction works,” he said. “It is outstanding. There is no discussion.”

In fact, genomic prediction is so strong that for smaller breeds of cattle, Peñagaricano said, it will even be able

to be used to produce across-country evaluations.

Peñagaricano described genomic prediction as a black-box tool and said it has great potential application to the subject of fertility. With Peñagaricano’s research focusing on dairy bulls, he encouraged future research and evaluation to focus on calves from beef-on-dairy crosses to help scientists continue to better understand the fertility of beef bulls.

As technology continues to

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advance and producers push the industry forward, Peñagaricano said, research on both genomics and bull fertility will continue to be on producers’ minds.

Eventually, the focus of the fertility conversation might start to naturally shift to center on the bulls rather than just the cows.



Francisco Peñagaricano



PHOTO BY SHAUNA HERMEL

Poor health, viruses, and environmental stress can leave young calves susceptible to secondary bacterial infections that cause BRD. These severe infections commonly result in pneumonia, and treatments can be costly. Research is looking to identify unique proteins that can be used for future interventions against this disease.

Find more coverage of the 2021 BIF Symposium in the Newsroom at www.bifconference.com.

Feed efficiency and bull fertility

Will selection for feed efficiency affect bull fertility? That’s what researchers at California State University–Chico set out to discover.

In their summary in the Nov. 30, 2020, *Journal of Animal Science* (Vol. 98, Suppl 4, pp. 474-475), Taylor Lacey, Stephen Doyle and Kasey DeAtley

reported findings from two feeding trials monitoring a total of 28 Angus and Red Angus bulls.

For each trial the bulls were randomly assigned to 7x8-meter pens equipped with GrowSafe® feeders. They were fed a 15.6% crude protein (CP) ration containing 56.22% total digestible

nutrients (TDN) *ad libitum* for the respective 87- and 84-day trials.

The bulls were given a breeding soundness exam (sometimes referred to as a BSE) at 18 months of age. Residual feed intake (RFI) was categorized as low [0.5 standard deviation (SD) above the RFI mean], marginal (± 0.5 SD of the mean) or high (0.5 SD below the RFI mean).

The researchers report there were no significant differences among breeds or RFI groups for start weight, end weight, metabolic mid-weight, residual gain, scrotal circumference or sperm motility. Also, no interaction was detected between breed and RFI group, with the exception of sperm morphology for which low-RFI Red Angus bulls had poor morphology compared to marginal and high-RFI groups.

The black bulls were superior to the reds in average daily gain (ADG), feed conversion and RFI. High- and marginal-RFI groups had

greater dry-matter intake than the low-RFI group.

The researchers concluded there were no significant correlations between phenotypic growth and efficiency measures with regard to scrotal circumference and sperm morphology, and that, cumulatively, scrotal circumference and sperm motility were not affected in efficient bulls.

Studying a possible BRD intervention

Poor health, viruses, and environmental stress can leave young calves susceptible to secondary bacterial infections that cause bovine respiratory disease (BRD). These severe infections commonly result in pneumonia, and treatments can be costly.

To identify unique proteins that can be used for future interventions against this disease in cattle, USDA Agricultural Research Service (ARS) scientists took a closer look at the genetic material of multiple subtypes (strains) of three groups of bacterial species commonly implicated with BRD.

In a study recently published in *Genome*, U.S. Meat Animal Research Center (USMARC) Microbiologist Emily Wynn and Molecular Biologist Mike Clawson examined DNA sequences from bacteria commonly found in cattle exhibiting signs of BRD. These bacteria are known as *Histophilus somni* (*H. somni*), *Pasteurella multocida* (*P. multocida*) and *Mannheimia haemolytica* (*M. haemolytica*), which has a variable genotype (strain types). The scientists have sorted the variable genotypes of *M. haemolytica* into two strain types (type 1 and 2).

It is not uncommon to find all three groups of bacteria, along with communities of “good” bacteria, living in the upper respiratory tract of cattle with no signs of BRD. When a calf’s immune system becomes weakened by viruses or due to stress caused by environmental factors (such as weaning, transportation, poor ventilation, etc.), these three bacteria (*H. somni*, *P. multocida*,

and type 2 *M. haemolytica*) multiply in the upper respiratory tract and invade the lungs, where they cause disease.

Yet this multiplication in calves with weakened immune systems does not happen as frequently with type 1 *M. haemolytica*. Therefore, it was important for the scientists to compare gene content across the three groups of disease-causing bacteria and to identify differences between the groups and the more benign strain, type 1 *M. haemolytica*.

Scientists focused on the differences in the proteins that exist in the outer membrane of each of the bacterial groups, as these outer-membrane proteins can be very important for either bacterial survival or its recognition and targeting by the host’s (calf’s) immune system.

“Part of our research aims to use very high precision in targeting unique proteins, or antigens, in the outer membrane of the BRD-causing bacteria. These antigens induce an immune response and can protect the animal. We anticipate these proteins can be used in future preventative measures without disrupting other ‘good’ microorganisms coexisting within the same environment or host,” said Wynn. “One of the most exciting discoveries in this study was to find the outer membrane protein W, or OmpW, in all three harmful bacteria but not in the type 1 *M. haemolytica*. We look forward to investigating that further.”

Wynn and Clawson found other proteins present in the outer membrane of all these groups of bacteria, giving them additional preventative targets.

Insights from this study open doors for the use of antibody recognition of outer membrane proteins to develop preventive strategies against bacteria that cause BRD. The scientists plan to expand their study with larger populations of BRD-associated bacteria, and to use the same approach to specifically target additional disease-causing bacteria. ■