Don't Stack Problems

Abnormal progeny and embryonic death are among the implications of improper management of known genetic anomalies.

*by **Kasey Brown,** associate editor; & **Troy Smith,** field editor*

Perhaps you have heard the story about a respected animal breeder whose reputation was founded on the successful raising and marketing of linebred stock. When asked to explain the difference between linebreeding and inbreeding, the veteran stockman said, "When it doesn't work, it's inbreeding."

Whatever you prefer to call it, according to geneticist Alison Van Eenennaam, inbreeding is the mating of animals more closely related than the average relationship of animals in a population. It is applied to produce progeny that are more uniform and homozygous for superior genes. In the vernacular of our storied breeder, that's what you get when it works. However, genes associated with abnormal phenotypes or embryonic death also may become homozygous. That's what you don't want.

A University of California–Davis (UC–Davis) beef cattle specialist, Van Eenennaam explained to attendees of the Applied Reproductive Strategies in Beef Cattle (ARSBC) symposium Oct. 8-9 in Stillwater, Okla., why genetic abnormalities occur. She also discussed ways to avoid problems through management of what she called "loss-of-function alleles."

Van Eenennaam explained how many genetic abnormalities are associated with recessive genes. Alternative forms of the same gene (alleles) may not function normally, or at all. Mutant alleles that "don't work" are called loss-of-function alleles. An abnormality occurs when an individual inherits a loss-of-function allele from both parents. If an individual inherits the loss-of-function allele from just one parent, that individual will appear normal, but will be a carrier of the loss-of-function allele and is capable of passing it on to progeny.

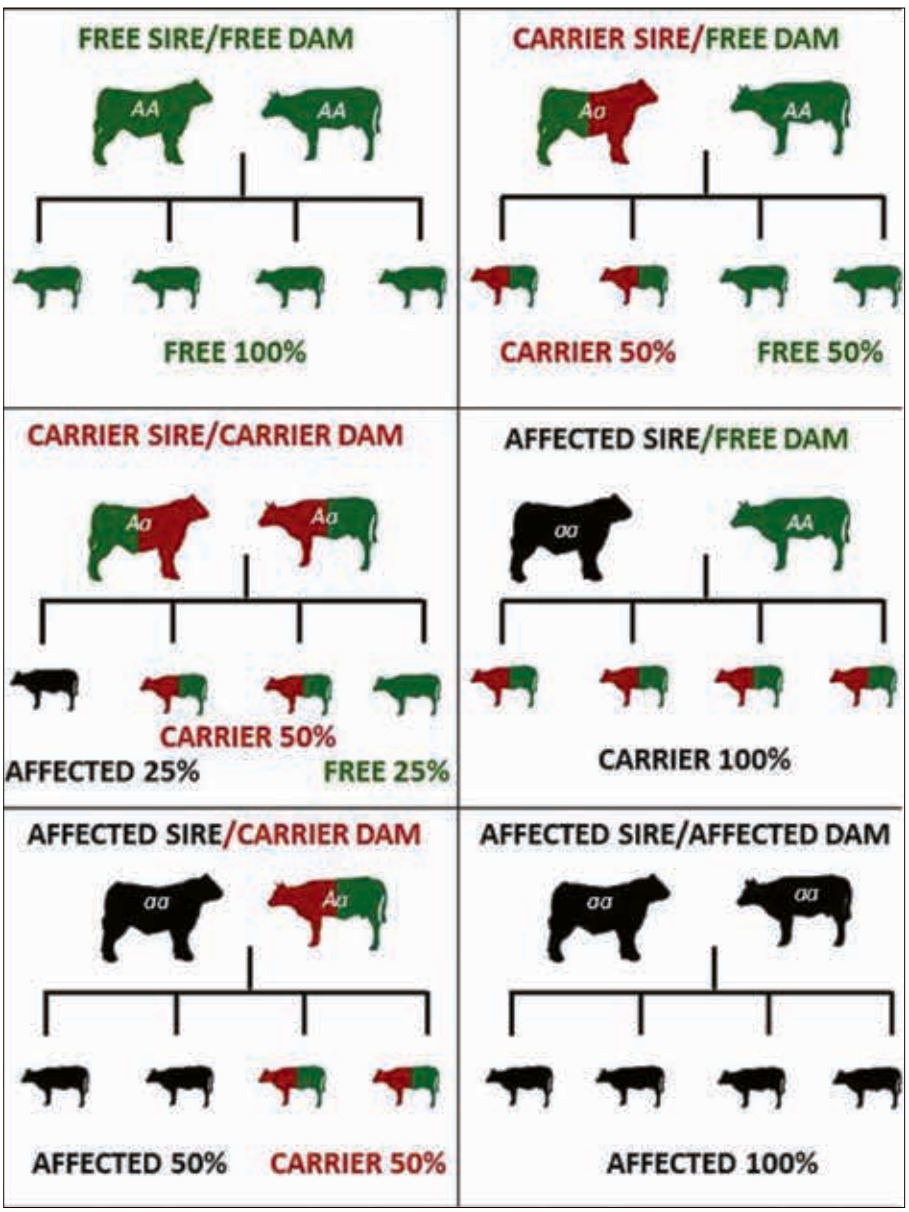
With inbreeding, one or more common ancestors contribute alleles to both sides of an animal's pedigree. Van Eenennaam said that is the reason why deleterious recessive alleles often are identified with widely used sire lines. She emphasized that it is not because these sires carry more deleterious alleles. Rather, it is because these sires are so widely used, through artificial insemination (AI), that they are more likely to appear on both sides of a pedigree. That increases opportunity for an individual to inherit a deleterious allele from both sire and dam.

"Because carriers appear normal, recessive alleles can increase in frequency in a population more easily than undesirable dominant or additive alleles. It is only when two carriers mate that there is the possibility of producing offspring that have, by chance, inherited both of the nonfunctional alleles from their parents," explained Van Eenennaam.

She further explained how it is likely that all

CONTINUED ON PAGE 236

Fig. 1: Demonstration of loss-of-function alleles in mating decisions



Reproductive Strategies

Don't Stack Problems CONTINUED FROM PAGE 234

animals carry recessive genetic conditions in their DNA. Genomic technology has allowed for the discovery of recessive alleles associated with specific physical abnormalities. It is likely that more will be discovered. Other recessive conditions are lethal, resulting in fertility problems such as increased calving interval or missed heat periods.

Van Eenennaam said genotyping of individual animals allows determination of whether an individual possesses alleles

PHOTOS BY TROY SMITH

►Alison Van Eenennaam explained why genetic abnormalities occur. She also discussed ways to avoid problems through management of what she called "loss-of-function alleles."

associated with known abnormalities. Their occurrence can be managed by avoiding the use of sires identified as carriers. However, this strategy does not allow their use for genetic improvement of traits for which the sires have superior merit. Another way to manage the occurrence of deleterious genetic conditions is to avoid matings between animals identified as carriers.

For implementing the latter strategy, said Van Eenennaam, a decision-making tool, called MateSel, has been developed. This software program is designed to optimize mating selections, showing the tradeoff between genetic gain achieved by mating the very best sire to the very best dams irrespective of their relationship to each other, and genetic diversity, which is maintained by avoiding or minimizing inbreeding.

According to Van Eenennaam, its Australian developer, Brian Kinghorn, is in the process of modifying MateSel so that it can be used to optimize the rate of genetic gain with a key objective being to reduce both affected offspring and frequency of the lethal alleles. Thus, it should help ensure that the value of carriers with otherwise high genetic merit is

CONTINUED ON PAGE 238

35 Keys to Success
Reproductive Efficiency

Parentage testing: Implications for bull fertility and productivity

Cow-calf producers weighing the potential advantages of implementing estrus synchronization and artificial insemination (AI) may want to consider the results of a study that evaluated the breeding performance of bulls used for natural service. During the Applied Reproductive Strategies in Beef Cattle (ARSBC) symposium hosted Oct. 8-9 in Stillwater, Okla., University of California–Davis (UC–Davis) extension beef cattle specialist Alison Van Eenennaam provided an overview of the California Commercial Ranch Project. She explained how DNA parentage testing was applied to more than 5,000 calves during a period of three years to evaluate sires for prolificacy and economic return.

According to Van Eenennaam, the participating ranches managed from 700 to 900 cows each, which were divided into breeding groups that were exposed to multiple sires. Breeding season varied by ranch, from 60 days to 120 days. The number of bulls turned into breeding pastures varied from two to nine head, but all ranches maintained a breeding ratio of one bull per 25 cows. Sires were predominantly Angus, but bulls representing several other breeds also were involved. All bulls had passed a breeding soundness examination prior to use.

Van Eenennaam said the results showed a wide variability of individual reproductive performance. The number of progeny per sire ranged from zero to 64 calves per calf crop. On average, about 4% of bulls sired no calves, regardless of breed. Results also showed that the most prolific bulls sired the greatest number of early-born calves, which generally posted the heaviest weaning weights.

When each bull's contribution to ranch income was evaluated, sire prolificacy was the most significant factor. Bulls siring the most calves returned the most income, but tools for selecting sires for prolificacy remain elusive. Van Eenennaam cited a positive correlation between bull scrotal circumference and prolificacy, but the trait explains only about 12% of variation among bulls.

"Based on the results of this study, the high cost of herd bulls, and the development of reliable and fixed-time AI protocols," opined Van Eenennaam, "it may be time for commercial producers to re-evaluate the economics of using elite genetics available via AI sires versus the exclusive use of natural-service bulls."

— by Troy Smith, field editor

Editor's Note: *Van Eenennaam spoke during Thursday's ARSBC session focused on use of genomics for reproductive improvement. Visit the* www.appliedreprostrategies.com *Newsroom to view her PowerPoint, read the proceedings or listen to her presentation. Compiled by the* Angus Journal *editorial team, the site is made possible through sponsorship by the Beef Reproduction Task Force and provides comprehensive coverage of the symposium.*

Don't Stack Problems CONTINUED FROM PAGE 236

maintained and those genetics are available to appropriately utilize in breeding programs.

"Using mate selection software to avoid carrier matings achieves a better outcome than just indiscriminately avoiding the use of carriers," concluded Van Eenennaam.

— by Troy Smith

Opportunities for embryo genotyping

Genetic defects are becoming a prevalent issue in today's beef industry and will continue to be as we learn more about genotyping. Kirk Gray, veterinarian with Cross Country Genetics, explained the process of genotyping via embryo biopsy.

Gray explained that the challenges of genetic defects are to overcome the "rules" within an operation's breeding program and to salvage affected bloodlines. Identifying defects has gotten easier as technology has improved. Rather than reviewing pedigrees, investigating by talking to breeders or progeny testing, Gray said DNA testing has made testing quicker and easier. It is possible to genotype embryos to identify carrier females and breed them to noncarrier bulls.

►**Genotyping embryos offers opportunity to determine defect status before embryos are implanted in a recipient, said Kirk Gray, Cross Country Genetics.**

To do so, Gray explained that seven days after breeding, the embryo is collected and has a compact inner cell mass. Viable embryos are identified and moved to the biopsy station at the clinic.

The embryos are rinsed as a group in accordance with American Embryo Transfer Association (AETA) certification. Then they are moved to well-A of a Nunc working plate. Gray said older embryos are the best.

Once they remove the media, the embryos are prepared for the biopsy and loaded into individual petri dishes. Then they are moved to the micromanipulator and biopsied. The embryos are manipulated and then frozen similar to conventional transfer. They are then sent for a DNA test. Gray said the goals of embryo biopsies are to biopsy all embryos from a suspect collection, accomplish at least 90% genetic status determination with DNA testing, and maintain an acceptable pregnancy rate with biopsied embryos.

He shared testing results of biopsied embryos since 2009 at Cross Country Genetics. There have been 198 collections and 1,499 embryos analyzed. Only 8.33% have come back as "non-determined" whether the embryo was a carrier or not. There has also been much success in gender determination from biopsied embryos, he added.

— by Kasey Brown

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