

Livestock Efficiency

CASE STUDY: USE OF DNA FOR SIRE DETERMINATION IN ANGUS CATTLE BRED IN A MULTI-SIRE MATING SYSTEM

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THE STORY IN BRIEF: DNA technology is being implemented in the beef industry for several uses, such as parent or sire verification and prediction of performance traits using genetic markers within important genes. Parent or sire verification tests have become a requirement of many breed associations for AI sires and embryo transfer dams. The technology can also be used to determine the sire of a calf from a multi-sire mating system. Using DNA technology for this scenario assist a breeding program as it eliminates the need to place a gap-in-time (usually two weeks) between an AI date and start of natural service mating with clean-up bulls. Errors that incur from this process include (i.e., sire of an AI calf miss-recorded due to long gestation of the dam, sire of a natural-service calf miss-recorded due to a short gestation of the dam, sire of a calf mis-recorded due to bulls wandering from pasture to pasture, and (or) human error in recording data or thawing the correct straw of semen during an AI program). Without DNA testing within the NMSU system in 2006 and 2007, 3% of the calves would have had incorrect sire recordings. Another benefit of using DNA technology for sire identification is that sire of a calf can be determined from a multi-sire mating system. This procedure has several economic benefits (Gomez-Raya, 2008), such as enhanced productivity of the herd from sire selection, reduction in the length of a breeding season, and being able to manage seedstock cows similar to a commercial herd as is the case with purebred Angus cows at CRLRC. There are multiple venues for collecting DNA (i.e., hair, blood cards, Typifix® ear tags, etc.) and several companies that can provide the service of genotyping and parent verification. Some of these companies have contracts with breed associations for paternity testing. It appears the most important part of the process is to work with a company that provides quality customer service and has the expertise and the ability to use the genotypes to sort the sires into groups prior to multi-sire mating, so the genotypes of their calves can be quickly and accurately used to determine the sire. In 2006, failure to pre-sort registered Angus calves for paternity testing yielded additional effort for 50% of the calves to determine the sire (i.e., DNA samples from the Dam or sorting of the calves by pastures, etc.). Genotypes from DNA were used to pre-sort the sires for the 2007 Angus calf-crop and sire of all calves (100%) were determined with the initial effort from the DNA company. In summary, DNA technology can be used to accurately determine the sire of Angus calves bred in a multi-sire mating system. Presorting the sires into mating groups using their genotypes assists this process.

THE PROBLEM: Feasible DNA collection and accurate prediction of the sire of an Angus calf from a multi-sire mating system.

OBJECTIVE:

Use the CRLRC Angus herd to evaluate DNA collection procedures and genotype-based sire prediction success to facilitate the transfer of these technologies to beef producers.

EXPECTED OUTCOMES:

For the CRLRC, a reliable procedure for collecting DNA will be developed and learning more about the procedures to pre-sort the sires will improve accuracy of the predicting the sire of a calf from a multi-sire mating system.

DURATION:

Breeding seasons and calf crops from 2006, 2007, to present.

APPROACH:

2006: Angus cows were AI ~May 15 of 2005 and clean-up sires placed with the cows for 45 days. Angus heifers and cows were grazed in 3 to 4 different pastures and were exposed to ≥ 3 bulls, which included AI sires. Calves were born in the spring of 2006 and a jugular blood sample was collected from each calf at spring branding while the calf was tilted in a calf-chute/table. Quickly after the blood sample was collected, the circle on a blood card obtained from the American Angus Association (AAA) was spotted with blood. The card was then mailed to the DNA service provider of AAA, MMI Genomics. A DNA sample of each of the sires had to also be mailed to MMI, if the sire had not previously tested and included in the AAA genotype database. Subsequently, genotypes were determined and results returned to NMSU via U.S. Postal Service. However, since only 50% of the calves could the sire be determined, the data/calves had to be sorted based on potential sires within a pasture and some of the calves required a DNA sample from the dam. Calves were then registered with AAA and the sire determination was based on DNA results.

2007: AI sires and clean-up bulls were presorted using genotypes of each potential sire before the breeding season in 2006. This process required that a DNA sample of each sire be sent to Merial-Igenity®, so genotypes could be used to sort the sires into the breeding groups. Note: sire sorting for this process does not always infer familial relation among the bulls. Cows and heifers were AI ~May 15 of 2006 and clean-up sires placed with the cows for 45 days (as per their pre-breeding sort). Angus heifers and cows were grazed in 3 to 4 different pastures and were exposed to ≥ 3 bulls, which included AI sires. Calves were born in the spring of 2007. A Typifix tag was used to collect a tissue punch from the

ear of each calf at spring branding while the calf was tilted in a calf-chute/table. The tissue vial of the tag was then mailed to Igenity®, genotypes determined, and results returned to NMSU via email. This same procedure is being used for the 2008 Angus calf crop at CRLRC. Calves were then registered with AAA and the sire determination was based on DNA results.

RESULTS: Table 1 describes the results of DNA collection procedures and the success of the processes involved in assigning the sire of each Angus calf

Table 1. Results of assigning the sire of Angus calves bred in a multi-sire mating system at CRLRC in 2006 and 2007.

Item	2006
2007	
Number of calves	33
DNA collection procedure	blood card
Typifix® tag	
Success of obtaining DNA	100%
96.3%	
Sires were pre-sorted base on genotype	No
Yes	
Initial success of determining the sire	50%
100%	
Overall success of determining the sire	100%
100%	
Cost, not including postage	~\$20.00
~\$20.00	
Time required to obtain results, weeks (wk)	12
3	
Error rate of assigning sires in the NMSU seedstock program without use of DNA (n = ~130 Angus, Brangus, and Brahman calves).	3%

Note: Typifix® worked with a high success rate for NMSU in 2007; however, one other beef producer in New Mexico experienced repeated high failure rate obtaining DNA with this device.

POTENTIAL APPLICATION: DNA can be collected from cattle and used to determine the sire of each calf from a multi-sire mating system. Pre-sorting of the sires based on their genotypes appears to improve the time and effort required to complete the procedure.

EDUCATIONAL PLAN: These data will grow each year and results will continue to be published in field day reports and the on-line catalogue and information for the Annual

Cattle and Horse Sale of NMSU.

REFERENCES:

Gomez-Raya, L., K. Priest, W. M. Rauw, M. Okomo-Adiambo, D. Thain, B. Bruce, A. Rink, R. Torell, L. Grellman, R. Narayanaan, and C. W. Beattie. 2008. The value of DNA paternity identification in beef cattle: examples from Nevada's free-range ranches. J. Anim. Sci. 86:17-24.

<http://www.angus.org/>

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