

CASE STUDY: USE OF DNA FOR SIRE DETERMINATION IN ANGUS CATTLE

BRED IN A MULTI-SIRE MATING SYSTEM
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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 predicting the sire of a calf from a multi-sire mating system.

DURATION

Breeding seasons and calf crops from 2005 to present.



APPROACH

2006

- Cows AI ~May 15 of 2005, clean-up sires placed with cows for 45 days
- Heifers & cows were exposed to ≥ 3 bulls, including AI sires
- Jugular blood sample collected from calves born in spring 2006 at branding while calf was tilted in a chute/table
- After blood sample was collected, circle on a blood card was spotted with blood
- Card and DNA sample of sires were mailed to MMI Genomics as per the requirement of the American Angus Association (AAA)
- Genotypes were determined & results returned to NMSU
- Only 50% of the calves sires could be determined, therefore, data/calves had to be sorted based on potential sires within a pasture or DNA sample from the dam
- Calves were then registered with AAA and 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
- Process required DNA sample of each sire be sent to Merial-Igenity®
- Cows and heifers AI ~May 15 of 2006, clean-up sires placed with the cows for 45 days (**as per their pre-breeding sort**)
- Heifers and cows grazed in 3 to 4 different pastures & were exposed to ≥ 3 bulls, including AI sires
- Calves were born spring of 2007, Typifix tags were 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
- Typifix tags were mailed to Igenity®, genotypes determined, and results returned to NMSU via email
- Calves then registered with AAA and the sire determination was based on DNA results
- Same procedure is being used for the 2008 Angus calf crop at CRLRC



RESULTS

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	27
DNA collection procedure	blood card	Typifix® tag
Success of obtaining DNA	100%	96.3%
Sires were presorted based 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	12	3

Error rate of assigning sires in the NMSU seedstock program without use of DNA (n = ~130 Angus, Brangus, and Brahman calves).

3% 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. Gomez-Raya and co-workers (2008) demonstrated the profitability of these sire selection procedures in a range beef production 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-Adiamo, D. Thain, B. Bruce, A. Rink, R. Torell, L. Grellman, R. Narayanan, 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/>
<http://www.igenity.com/>
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