Collaboration to demonstrate the potential use and value of electronic identification and DNA testing in the sheep industry

Austin R. Brown[1], Julie A. Finzel [2], Roselle Busch [2], Morgan Doran [2], John Harper [2], Dan Macon[2], Rebecca Ozeran [2], Morgan Stegemiller [3], Karissa Isaacs [4], and Alison L. Van Eenennaam[1].

[1] Department of Animal Science, University of California (UC), Davis; [2]University of California Agriculture and Natural Resources; [3]University of Idaho; [4]Superior Farms, LLC.

Austin R. Brown
M.S. Candidate
Van Eenennaam Lab
aubrown@ucdavis.edu
https://www.linkedin.com/in/austin-brown-94669a173
@Some_Shepherd

INTRODUCTION

The dearth of individual performance records typically resulting from an extensive range production system, coupled with impracticality of utilizing reproductive technologies, makes commercial genetic improvement challenging in small ruminants. Generally, producers obtain data on their flock in aggregate with their management fixated towards the average performing individuals, with occasional focus on low-performing individuals. Radio-frequency identification ear tags (RFID, or Electronic ID, EID) facilitate rapid and accurate data collection that can be used for informed decision making on several aspects of flock management. Individual record keeping allows producers to identify poorly-performing animals and remove them from the flock to increase overall flock performance. The introduction of EIDs has the potential to decrease the time and labor needed to track performance traits of individual animals within a flock. The use of EID has proven to be cost-effective in sheep production systems in other countries. However, despite the known benefits, Western sheep producer adoption of this technology remains low. Genomic selection (GS) for meat sheep has been effectively implemented by only a few countries. This is because the accuracy of sheep sire genetic evaluations tend to be low due to the limited use of artificial insemination making it difficult to compile reference populations, and the cost of genotyping is high relative to the value of the animal [1]. Thus, genomic selection is not always cost-effective in meat sheep.

OBJECTIVES

Table 1. Summary of Operational parameter & objectives of each Ranch

	Ranch A	Ranch B	Ranch C	Ranch D	Ranch E
Flock size	Large	Large	Small	Large	Large
Sire Breeds	Black and White-face	White-face	Black-face	Composite	Black & White-face
Average Lamb Crop	145%	130%	140-150%	145-150%	115%
Length of Breeding Season	75 days	75 days	62 days	120 days	185 days
Avg. Weaning Weights (Kg)	39 - 50	32 - 43	27 (~3 mos.)	48-50 (4-7 mos.)	50-52
Methods to Measure Maternal Traits	Informal observation	Tag problem ewes	Yes - EZ Care System	Mark poor mothers	No
Track Twins	Yes	Yes	Yes – EID's	No	Yes – paint brand
Yearly cost to keep a ewe	$113	$120	$99 (no labor costs)	$210	$150
Breeding Objectives	Major focus on twinning	Cull the bottom (10-15%) of flock	EID data are more actionable	Cull bottom 1/3 of flock	N/A

In this demonstration project, we collaborated with five California producers to assess how EIDs and genetic testing could inform ram selection and provide value to producers. Our objective was to determine how the data collected from these technologies could provide value to commercial ranches. Familiarity of EID technology at the start of the research varied, allowing for a qualitative reflection on the participant`s perceptions of the usefulness of this technology. Moreover, we partnered with Superior Farms (Dixon, CA) to **1)** *genotype the animals using a targeted genotyping panel*, **2)** *assign parentage*, and **3)** *link individual animal ID to camera-graded carcass measurements.* This enabled the collection of individual progeny carcass data and provided insight into sire performance, providing for the identification of prolific sires that were also producing lambs with significantly more saleable meat.

DISCUSSION

- If sheep numbers continue to decline, there`s risk that the U.S. sheep industry may reach a point that sheep numbers will no longer support key pieces of the industry's infrastructure.
- Utilizing EIDs alone doesn`t result in production gains. This tool enables the implementation of strategies for achieving desired objectives that may otherwise be prohibitively difficult or time-consuming.
- The U.S. sheep industry needs a flexible software to help manage producers` goals efficiently and compensates for a lack of IT knowledge. The results from the genetic testing in this study reveals why managing this data is so valuable. Variation in sire prolificacy ranged from 0-135 lambs per sire. Comparable variability was also observed in a similar study in the United States called "The Mickel Project", funded by the American Sheep Industry Association [4]. In that study with 42 Suffolk rams, 12 sired 10 or fewer progeny with 2 having none, and 7 sired more than 55 lambs with 2 siring over 100 lambs. These authors wrote, "*such variability in ram serving capacity deserves much greater study*."

Common EID Readers

METHODS

1.) Preliminary Interviews

We interviewed producers at the start of the project to get data on their operations and appraisals of operational parameters and costs in their management system (Table 1).

2.) Tissue Sample Collecting and Tagging of EID Tag

Tissue samples were collected from 305 rams & 2,658 lambs for DNA testing. Rams were sampled using AllFlex tissue sampling units & lambs were sampled using a combination of docked tails and ear notches.

AllFlex TSU sampling kit

Ear notch & tail collection (Premier1 Supplies)

EID ear tag & reader

Each animal sampled then received an EID ear tag that was scanned using an electronic reader. The timestamp from the reader provided a time estimate for the added steps to collect genetic samples and apply ear tags during processing.

3.) Samples Sent for Genetic Analysis

Submitted tissue samples to the Superior Farms (Dixon, CA, USA) Flock54 genetic testing program [2] for further insight on parentage and the presence of specific markers linked to disease resistance and fecundity. [3]

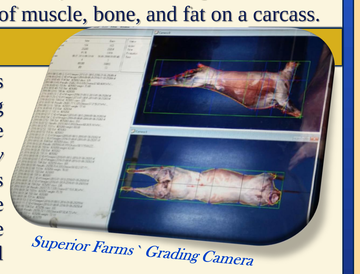
If poor rates of paternity matching occurred with Flock54, we used a software called SireMatch to obtain paternity based on raw SNP data (E. J. Pollak, personal comm.). Paternity based on SNPs was determined by comparing genotypes of all potential sires amongst each lamb`s genotype. An exclusion was listed if a ram and a lamb had no allele(s) in common at an identified marker. No more than three exclusions between the SNP genotype of a potential sire & offspring was allowed.

3.) Progeny sent to Superior Farms for Carcass Data Acquisition

Data was collected on 524 processed lambs at Superior Farms using a VSS2000 camera grading system to collect carcass data and match it to EIDs. Superior Farms measured hot carcass weight, and the camera grading system was used to predict yield grade, quality grade, common cuts, Ovine Cutability Calculation (OCC) and OCC yield. OCC estimates the raw yield of edible product on the carcass. OCC yield indicates the proportion of muscle, bone, and fat on a carcass.

4.) Carcass Data Analysis

Dollar difference in edible product was calculated using the USDA Ag Marketing Service Report`s net carcass cutout value (*13.39/kg * average progeny contemporary group deviations for OCC*). Each ram's offspring (based on SNP genotyping) were evaluated as a "progeny group" and an average OCC was calculated to define the potential carcass merit that a ram offered his offspring.



Superior Farms` Grading Camera

Dollar deviation of edible product sold was calculated as the deviation from the mean OCC of all carcass data collected on a given ranch multiplied by $13.39/kg.

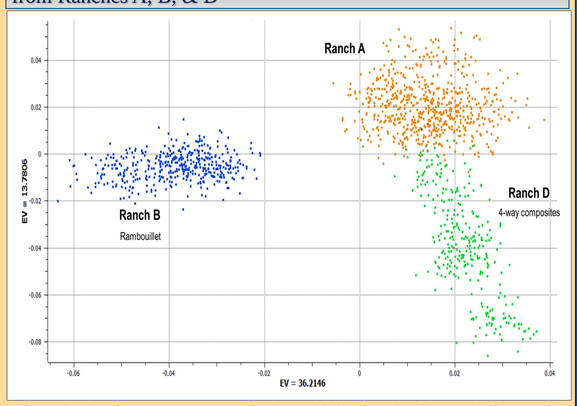
RESULTS

Table 2. Summary of Paternity Assignment Analysis

	Ranch A	Ranch B	Ranch C	Ranch D	Ranch E	Summary of all Ranches
Ram to Ewe Ratio	1:10	1:35	1:32	1:50	1:40	1:33 (Average)
Total Lambs	669 (Males only)	829	80	622	222 (Females only)	2422
Total Lambs w/an Identified Sire	606	796	80	622	149	2253
Total Sires	62	37	6	12	11	128
Sires with Progeny, %	98	60	100	32	100	78 (Average)
Parentage ID Rate, %	91	96	100	100	67	90.80 (Average)
Standard Deviation	12.5	19.8	12.6	41.7	25.0	22.32 (Average)
Average Progeny per Sire	9.9 (Males only)	21.5	13.3	51.9	20.1 (Females only)	23.34 (Average)
Max Progeny from a Sire	61 Males	65	33	135	59 females	70.69 (Average)
Min. progeny from sires with offspring	1 Male	1	1	4	2 females	1.80 (Average)
Med. progeny among all rams w/ offspring	4 Males	19	11.5	43.5	4 females	16.40 (Average)

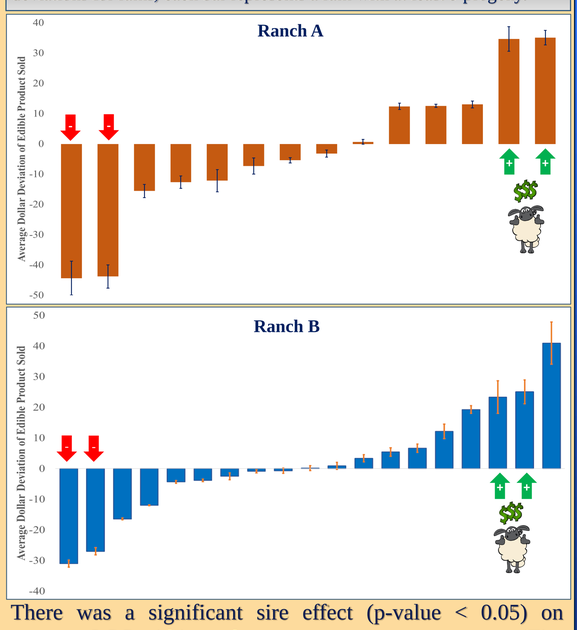
Assignment results varied from ranch to ranch, but, overall, *90.8%* of lambs were successfully matched to their sire (Table 2). Due to funding limitations, only male lamb samples from Ranch A, and only female lamb samples from Ranch E were submitted for genotyping. Ranch E, had the lowest match rate at *67%* of lambs matched to sires. Yet, it was learned that clean-up rams without collected DNA were turned out with the flock. Of note, there was a significant ranch effect on the average progeny number per ram (*p-value < 0.05*). There was also a large range in the number of lambs per sire (*0-135*) within each ranch. Ranch A with a ram to ewe ratio of *1:10*, one ram sired 66 male progeny. Assuming this represented half of his progeny as female lambs were not genotyped, this suggested he likely sired ~ *122* lambs. Ranch D, with a ram to ewe ratio of *1:50*, had two rams that sired over *100* lambs and the top producing ram which sired *135* lambs.

Fig 1. Principal component analysis of the SNP panels collected from Ranches A, B, & D



The principal component analysis (PCA) plot in Figure 1 shows the proportion of variation (POV) explained by PC1 is 36.2% and PC2 is 13.8%, emphasizing some of the breed variation found among participating flocks. Ranches C & E overlapped with Ranches A & D and were excluded from the plot.

Fig 2. Deviation in edible product avg. progeny contemporary group (CG) deviations for rams; each bar represents a ram with at least 5 progeny.



There was a significant sire effect (p-value < 0.05) on average OCC within each progeny contemporary group (Fig. 2), meaning some sires were producing offspring with significantly more or less saleable meat.

CONCLUSIONS

- Jointly, genetic testing combined with the use of EIDs offers an approach to manage individual production and parentage data required to improve flock health and reproductive management through genetic selection for more productive and profitable individual animals.
- Electronic ID could also offer the added benefit of enhanced traceability for disease prevention and management.
- Unavoidable delays between ram turnout and collection of progeny phenotype data reinforces how seedstock producers offering EBVs as a selection tool at ram purchase offers value. High-merit genetics produced at the seedstock sector can propagate to other sectors of the production system.
- Ideally, all this data would go into national genetic evaluations to develop and aid the accuracy of GEBVs – such as the National Sheep Improvement Program.
- Block chain management offers further opportunities for sheep producers by providing consumers with information on where and how their food was produced while they are at the meat counter. Consumers are increasingly interested in knowing where their food comes from, and with less than 1.5% of the population directly involved with or exposed to food production, supporting consumer access to information about food production practices provides an important outreach opportunity for sheep producers.

REFERENCES

1. Rupp R, Mucha S, Larroque H, McEwan J, Conington J. 2016. Genomic application in sheep and goat breeding. Animal Frontiers. 6(1):39-44. doi: *https://doi.org/10.2527/af.2016-0006.*
2. Job RJ, Duan M, Hunter SS, Davenport KM, Rodriguez AM, Eidman L, et al. Development of Flock54: a targeted genotyping panel for the sheep industry. 2019. Plant and Animal Genome XXII Conference. Available from: *https://pag.confex.com/pag/xxvii/meetingapp.cgi/Paper/37381*
3. Heaton MP, Smith TPL, Freking BA, Workman AM, Bennett GL, Carnahan JK, et al. 2017. Using sheep genomes from diverse U.S. breeds to identify missense variants in genes affecting fecundity. F1000Res. 6:1303. Epub 2017/09/21. doi: *https://doi.org/10.12688/f1000research.12216.1.*
4. Leymaster KA, Chitko-McKown CG, Clawson ML, Harhay GP, Heaton MP. 2013. Effects of TMEM154 haplotypes 1 and 3 on susceptibility to ovine progressive pneumonia virus following natural exposure in sheep. J Anim Sci. 91(11):5114-21. Epub 2013/08/31. doi: *https://doi.org/10.2527/jas.2013-6663.* PubMed PMID: 23989875.2020.
5. The Mickel Project. Available from: *https://www.sheepusa.org/wp-content/uploads/2020/03/leading-edge-final.pdf.*

ACKNOWLEDGEMENTS

The authors wish to acknowledge Western SARE (Grant OW19-339) for funding this research. We also wish to thank the producers who participated in this study, Dr. Brenda Murdoch from University of Idaho, and Superior Farms for their participation and support of this research.