NSIP Meeting

Thursday – March 9, 2023

7 p.m. CST

Minutes submitted by Lisa Paris Weeks

Attendees: Matt Benz, Kristen Bieber, Gavin Blomquist, Rusty Burgett, Zach Meinders, Lynn Fahrmeier, Cody Hiemke, Tom Hodgman, Carol Heupel, Dylan Laverell, Ron Lewis, Devin Peterson, Brett Pharo, Brenda Reau, Bill Shultz, Curt Stanley, Jake Thorne, Todd Taylor, Robert Walker, Andrew Weaver, Lisa Weeks

Agenda:

- Brenda Reau called meeting to order and welcomed new board members:
  - Andrew Weaver – 2nd V. Chair
  - Robert Walker – Hair Rep
  - Gavin Blomquist – Terminal Rep
  - Devin Peterson – Goat Rep
  - Dylan Laverell - Targhee
- Secretary Report
  - Tom Hodgman moved to accept the November minutes as submitted, seconded by Jake Thorne. Motion passed.
- Treasurer Report
  - Presented by Bill Shultz (report attached)
  - Through February deposits we are at 167 memberships for 2023 fiscal year.
  - Curt Stanley moved to accept the report, seconded by Brett Pharo. Motion passed.
- Program Director Report
  - Presented by Rusty Burgett (report attached)
  - For 2023, 415 tissue samples have been submitted to Neogen. The high level of volume justifies moving to bi-weekly submissions. The submission due dates will align with the data run calendar on the NSIP website.
  - The Searchable Database experienced a few more outages leading to the development of a new update tool. The February 15 run validated the effectiveness of the new tool.
  - Goals for the next quarter:
    - Update breeder lists.
    - Host another NSIP webinar series for beginners.
    - Develop a schedule for webinars with more advanced topics.
    - Continue conversations with MateSel and LambPlan.
- Executive Committee
  - Presented by Brenda Reau.
  - The Technical Advisor role will be open when Dr. Ron Lewis retires in June.
  - The EC is seeking feedback from the current Technical Committee members as we work toward filling this key position.
  - Dr. Lewis will continue leading the GEMS project.
- Technical Committee
  - Presented by Ron Lewis (report attached)

- With the adoption of the new method of reporting the five genetic conditions from genomic sampling, we will need to define a reporting mechanism. Currently the report is done stateside using the program developed by Dr. Lewis. The NSIP will require a more sustainable solution long term.
- Brenda Reau requested Lynn Fahrmeier and Rusty Burgett work with Dr. Lewis to determine a plan for the long term solution including contacting LambPlan for cost projections to incorporate Dr. Lewis' program and Neogen directly to determine options for sending data directly to NSIP for processing.
- Brenda Reau requested the Genetic Conditions Results Key table be posted on the NSIP website.

- New Business
  - Goat ultrasound proposal – After being approached by goat producers to adopt a training protocol for ultrasound scanners, Chris Schauer has proposed the NSIP adopt the same certification standards for goat ultrasound training schools as are in place for the sheep training schools. Matt Benz moved to accept the recommendation, seconded by Jake Thorne. Motion passed.
  - Matt Benz proposed changing the MWWT acronym to MILK as long as the cost is <$250. Gavin Blomquist 2nd the motion and motion passed.
  - Matt Benz brought forth a suggestion of changing our EBV system which is reported in metric units to the EPD system which is reported in imperial units so that it better aligns with the cattle industry.
    - Discussion points –
      - Pro – both cattle and small ruminants would be on similar reporting systems.
      - Pro – simplifies discussion points during lectures to not have to explain an estimated breeding value vs. an expected progeny difference value.
      - Con – small ruminants are not cattle
      - Con – all our literature would have to be redone
    - Brenda Reau requested Rusty to work on gathering cost estimates of changing from EBV to EPD and report at the next meeting.
  - Devin Peterson (Goat rep) presented some proposals
    - Potential name/branding change to be more inclusive of goat producers – this is not a consideration at this time.
    - Potential discounts on NSIP fees – Rusty will poll the multiple registries to determine if discounting fees is a viable option or if this type of program could be standardized across all registries.
    - Request for Rusty to attend a function in September hosted by Pedigree International to promote the use of NSIP and EBVs.
  - NSIP ad in Suffolk Directory
    - Cost $300 for two full pages
    - Use same ad as 2022
    - Matt Benz moved to proceed with placing ad, 2nd by Caro Heupel. Motion passed.
  - Review of Committee Assignments – Brenda Reau pushed this review to the executive committee.
- Devin Peterson moved to adjourn, seconded by Cody Hiemke. Motion passed.
  - Next Meeting will be May 11 @ 7 p.m. CST.

NSIP Treasurer's Report

March 9, 2023 Bill Shultz

As we close in on the mid-point of our 2023 fiscal year (March 31st) we appear to be on budget. We currently have $42,199 in checking with another $33,868 in receivables for total equity of just over $76,000. A more complete report of year - over-year will be made at the end of our second quarter.

We are in the middle of our main enrollment period with current membership running steady to last years. Through the February deposits we have had 167 enrollments for the 2023 fiscal year totally $41,659.50 compared to 171 enrollments and $41,613 in 2022 through February deposits.

The first four months for FY 2023 of data charges from MLA was $12,332 (3,978 records processed) which is almost identical to the 1st four months of FY 2022. That comparison is more appropriate for the similarities between 2021 and 2022 membership's data processed than what we might expect in 2023.

Invoices from both MLA and Neogen remain to be both sporadic and unpredictable in their arrival which sometimes can create a short term cash flow issue which happened this winter. Larry Kincaid at ASI continues to work with us to avoid and real problems.

NSIP Director's Report
March 2023

Much of the past 2 months has been consumed with processing membership forms. Still have quite a few renewals coming in along with new members getting signed on for the first time. Also have had several genomics orders coming in. So far in 2023 we've had 415 samples come in and I have another 4 orders received yet to process as well as 2 more coming to the PO box this week. In 2023, with board approval, I'd like to try bi-weekly genomic submissions. In conversations with Ben Pejsar at the ASI convention, he feels we could possibly improve turnaround time on results by more frequent submissions which would improve efficiency on the part of the lab. This doesn't do anything to improve the response time from AGBU but if we can shave a week off the time at Neogen, we should improve the whole system.

We experienced a few more outages of the searchable database so I worked with the development team to get that back up and working. They made some improvements on the backend and we've had no issues since then. They made a new update tool for me which I just implemented for the February 15 data run and things look to have run smoothly. I also mentioned that we'd like to make some updates to the reports generated (we talked about those at our last board meeting to include extended pedigrees and more visual representations of data). Once I finalize the plan, they will generate a cost estimate for us so we can move forward.

My goals for the coming months are to update the breeder lists on the website (was hoping to have that done by now but membership renewals kept coming in) and to host another beginner to NSIP series of webinars. Those basic Pedigree Master webinars have been fairly well attended and I keep getting requests. I'd also like to develop a schedule of more advanced-topic webinars for the year to keep the membership engaged. I'll continue to design the desired updates to the searchable database and come up with a firm plan, timeline and budget for implementation. I'd also like to continue our conversations with MateSel and LambPlan as those communications have waned in the past couple months.

Thanks to everyone for all of your help.

Rusty

NSIP Technical Advisory Committee Report
Mar 2022

Reporting genetic conditions

I am pleased to report that we are there. Using genotype data made available in late February, a fully validated analysis of genetic conditions based on the Neogen GeneSeek Genomic Profiler (GGP) 50k array was completed and is ready for commercial release. It includes genomic information on 10,569 sheep, primarily Katahdin (8,657), Rambouillet (886), and Polypay (584). With Rusty Burgett's help, these results will be circulated to individual NSIP members shortly. Each report will be provided as an Excel sheet including those animals on which the producer submitted a sample.

The genetic conditions reported will be:

- Ovine Progressive Pneumonia (OPP) susceptibility (*TMEM154* gene)
- Scrapie susceptibility (codons 136 and 171)
- Myostatin
- Callipyge
- Booroola FecB

Along with the genetic conditions, two documents will be provided. The first document describes the genetic conditions (Appendix I). The second document is a disclaimer (Appendix II). As stated in the disclaimer, although we "have taken all reasonable care to ensure our methodologies are valid and results are accurate, you should be aware that genomic testing and methodologies have inherent inaccuracies which, in some cases, cause inaccuracies in the genomic results and our recommendations".

Sheep GEMS update

Each year, the scientific team needs to submit a report to the USDA-National Institute of Food and Agriculture (NIFA) as part of our federal grant supporting Sheep GEMS. It contains several sections including a summary of Accomplishments. Following is that section of the annual report, which was submitted in early January.

> The sheep industry contributes nearly $6 billion annually to the US economy and demand is growing. Production inefficiency, however, threatens this industry's ability to remain domestically and globally competitive. Resilience to climate changes and improved animal productivity and welfare are key to the priorities of the USDA and federal administration, and increasingly recognized by sheep producers as vital to their sustainability. Currently, however, robustness and climatic resilience traits are largely absent in US sheep genetic evaluations, and thereby not incorporated into selection decisions. To redress that shortfall, nearly 60 Katahdin, Polypay, Rambouillet and Suffolk breeders, all members of the National Sheep Improvement Program (NSIP), have been recruited to evaluate udder health, lamb survival, ewe longevity, and parasite resistance in their flocks. The NSIP is the organization responsible for the national genetic evaluation services provided to US sheep producers. These 60 flocks reflect about half,

and the most influential, producers within NSIP in these breeds. The performance data beginning to be collected will facilitate our understanding of the genetic background of robustness and climatic resilience in US sheep populations. Furthermore, they will generate the knowledge necessary to improve the welfare and well-being of sheep raised in variable climatic conditions in the US.

Beyond providing performance information, these same NSIP producers are obtaining genomic information on key animals in their flocks. Genotypes on nearly 3,500 additional animals, more than one-third those previously available on these breeds, have already been collected in conjunction with this project. Above their value in characterizing genomic diversity in these US sheep populations, these genotypes have been used to verify parentage and to assess genetic conditions for five disease, fecundity, and muscularity traits in the participating flocks. Given the cost, only a subset of animals can affordably be genotyped by sheep producers. Therefore, based on the structure of these flocks, optimal strategies for identifying the most valuable sheep to genotype are being investigated by simulation. The outcome will be recommendations to NSIP, and the US sheep industry generally, on best practices for collecting and using genomic information in selection programs. The process of developing these tools has ancillary benefits. It is allowing our training of highly educated graduates and is providing stakeholders with an understanding of the role of genomics and robustness and climatic resilience traits in sheep breeding.

Goal one. Our first goal for this reporting period was to begin to generate datasets for assessing genetic and genomic diversity in these breeds, which is requisite for the successful implementation of genomic selection in US sheep. Through the current and collaborative studies, genotypes are now available on nearly 9,500 performance-recorded Katahdin, Polypay, Rambouillet and Suffolk sheep. They were collected using either a moderate (50k array) or high (600k) density array.

Thus far, most of those genotypes available are in Katahdin sheep (89%), profiting from genotyping completed in a previous USDA NIFA funded grant. Consequently, our exploration of genetic diversity began in Katahdins. The effective population size (N_e) of this breed was estimated using pedigree data. It varied from 67 to 87 depending on the statistic used. Since N_e approximates the extent of allelic diversity in a population, it is useful for predicting the accuracy of genomic predictions of breeding values depending on the number of animals genotyped (genomic reference population). For a lowly heritable trait, typical to fitness-related characteristics, we estimated prediction accuracy for genomic reference populations of 10k, 15k, 20k, and 25k animals; they were 0.58, 0.65, 0.70 and 0.74, respectively. Although the accuracy increased as the reference population grew, the relatively small N_e of the Katahdin breed benefitted genomic prediction. With over 10k genotypes anticipated in this breed by the end of the project, the genetic evaluation of robustness and climatic resilience should be quite reliable. This will facilitate their incorporation by NSIP into routine genetic evaluation services.

Goal two. Our second goal for this reporting period was to begin to build reference populations for key robustness and climatic resilience traits in the four breeds. Approximately 60 NSIP flocks were recruited and have begun submitting records indicative of robustness and

climatic resilience (e.g., lamb survival, ewe longevity, gastrointestinal parasitism, udder health, coat shedding). Collaborators at three USDA ARS facilities have collected even more comprehensive measures of these traits in their own flocks.

Udder health effects both the well-being and productivity of ewes. At the US Meat Animal Research Center (USMARC), ewes were assessed for udder depth and teat placement, as in the participating industry flocks, along with many other udder traits (e.g., teat length, udder symmetry, palpation score, secondary teats). At the USMARC, the udder traits were measured within 5 days of lambing, as in the industry flocks, and at lamb weaning. A portion of ewes were milked to quantify intramammary infection and subclinical mastitis using the California Mastitis Test (CMT). A lower CMT is considered better in terms of udder health. Approximately 25% of four-year-old Katahdin ewes evaluated were clinically healthy but had subclinical mastitis. Ewes with high CMT scores also weaned over 23 pounds less weight of lamb than ewes with low CMT scores. It appears that CMT score was higher in ewes with longer teats and in those with secondary (i.e., extra) teats. Although little is known about the impact of secondary teats on ewe productivity, recent work from the United Kingdom suggests they might be a potential reservoir for mastitis causing pathogens. These preliminary results indicate that udder health substantially impacts the productivity and well-being of the ewe flock and will serve as a valuable indicator of robustness.

Goal three. Our third goal for this reporting period was to begin to evaluate genotyping strategies and methods for optimizing genomic prediction of breeding values in the main US sheep breed-types. It is too costly to genotype all the animals. Therefore, for this goal, we used AlphaSimR, an computer package frequently used for simulating genomic and phenotypic data globally, to begin to evaluate the efficacy of various genotyping scenarios.

As a first step, the underlying structure for simulating large-scale genomic and phenotypic datasets were built considering the historical development of breeds. After forming the base population, 30 flocks are being generated mimicking flocks participating in NSIP. Animals are selected directly for weaning weight (kg) and indirectly for fecal egg count, assuming a genetic correlation of -0.10 between the traits. Several selection strategies are being emulated: best (heaviest) weaning weights; best estimated breeding value for weaning weight; and at random. All animals in the base (reference) population have phenotypes, genomic data, and pedigree information. The reference population is then being divided into training and validation sets. Different genotyping strategies will then be evaluated, including different proportions of males and females genotyped (0, 10, 20, up to 100% for each sex separately). Various criteria for choosing the males and females genotyping will also be considered. All the pipelines for conducting these analyses have been developed. By comparing these scenarios, we will develop recommendations for genotyping and phenotyping strategies to reduce costs for US sheep farmers to accelerate genetic gain in their flocks while maintaining enough genetic diversity.

Ron Lewis
NSIP Technical Advisory Committee Chair
Mar. 9, 2023

Genetic Conditions Results Key

Scrapie Susceptibility		
Codon 136	**Codon 171**	**Description**
AA	RR	Complete Resistance
AA	QR	Rarely Susceptible
AV	QR	Somewhat Susceptible
VV	QQ*	Susceptible

*Animals QQ at codon 171, regardless of their genotype at codon 136, are susceptible to scrapie and can transmit the disease to susceptible flock mates.

Scrapie is a degenerative disease affecting the central nervous system, which can be debilitating to a flock. Once an animal is infected there is no treatment. Infected animals typically do not show symptoms until two to five years after the initial infection. After the onset of symptoms, animals tend to live only one to six more months. Symptoms include nervousness or aggression, obsessive rubbing, incoordination, and tremors. Because of the delay between infection and onset, control of this disease within a flock by signs and symptoms alone is ineffective.

The ability to manage a flock using genetics has made it increasingly easier to prevent Scrapie. Two locations on DNA that code for prion protein are particularly important for classical scrapie susceptibility: Codons 136 and 171. Codon 136 codes for the amino acids alanine (A) or valine (V). Codon 171 codes for the amino acids arginine (R), glutamine (Q), histidine (H), or lysine (K). The effects of H and K relative to Q and R at codon 171 on scrapie susceptibility have not been documented. Therefore, for selection purposes, consider them as equivalent to Q.

Animals with the AA at Codon 136 and RR at Codon 171 are completely resistant to the disease. This means that while other animals in the flock may have the disease, these animals will never be infected. Any animal with the QQ at Codon 171 will be susceptible to Scrapie, while other codon combinations grant varying levels of partial resistance.

OPP Susceptibility (TMEM154)	
Diplotype Results	**Description**
1,1 or 4,4 or 1,4	Less Susceptible (desirable)
*,2 or *,3	Highly Susceptible
Other haplotypes and their combinations	Unknown

Ovine Progressive Pneumonia (OPP; also known as Maedi Visna outside the US) is an infectious disease of sheep caused by the OPP virus, a very slow growing Small Ruminant Lentivirus. The disease is eventually fatal. The most prevalent signs are general wasting ('thin ewe syndrome'), decreasing milk production ('hard bag syndrome'), and pneumonia unresponsive to treatment, with labored breathing, exercise intolerance and coughing. Symptoms are usually not apparent until later in life so the infection status can only be determined by testing.

Depending on the incidence of OPP in the flock, production losses can be significant. There is no known treatment, and no vaccines are available. Variable degrees of natural resistance to infection exist and can be determined by genetic testing (TMEM154 test). Selecting replacement breeding animals carrying desirable genotypes can help decrease susceptibility to OPP in the flock.

The four most common genetic haplotypes (one inherited from the sire, one from the dam) are denoted 1, 2, 3 and 4. Haplotypes shown to confer less susceptibility are 1 and 4. Therefore, diplotypes 1,1, 1,4 and 4,4 are desirable when selecting animals for breeding, while haplotypes 2 and 3 (even in combination with desirable haplotypes) indicate high susceptibility and are not desirable.

We recommend that producers increase the frequency of haplotype 1. If producers have access to replacement animals with haplotype 4, it can be selected at the expense of haplotypes 2 and 3 but not at the expense of haplotype 1. The rationale for the last recommendation is that haplotype 1 was as effective as haplotype 4, yet only one amino acid different from the ancestral protein sequence. Thus, haplotype 1 has the best chance at retaining the natural function of the TMEM154 gene, which is presently unknown.

Regardless of TMEM154 diplotype distribution, adult sheep in infected flocks should be periodically tested for antibodies against the virus (serological prevalence) starting with the oldest animals first. A blood test that detects the presence of antibodies against the virus can be used for this (for example ELISA tests from IDEXX or VMRD). A reduction in OPP prevalence can be achieved by simultaneously selecting less susceptible animals for breeding while removing seropositive animals from the flock.

Myostatin		
Results	**Description**	The function of the normal myostatin gene is to keep muscle growth in check. A mutation in this gene, which originated in Texel sheep, reduces its function with increases in muscle growth and fiber numbers during early fetal development. Each additional copy of the myostatin variant acts in an additive manner by decreasing carcass fat while increasing carcass muscle. Meat quality is not significantly affected. Lambing ease is also not affected in litters with multiple lambs. Moreover, any differences in dystocia were not repeatably detected when US Texel sires were used in terminal crosses with different breeds.
Noncarrier	No Copies of Mutation	
Carrier	1 Copy of Mutation	
Homozygous Myostatin	2 Copies of Mutation	

Callipyge		
Results	**Description**	The causative mutation for this condition occurred in a single Dorset ram and has dramatic effects on muscle development. The genetic locus was given the descriptive name Callipyge (CLPG), derived from Greek for 'beautiful buttocks'. The phenotype is characterized by extreme muscle development due to hypertrophy during early postnatal (three to eight weeks of age) growth. Despite large effects of this hypertrophy condition on slaughter and carcass composition traits, the associated adverse effects on meat quality traits have deemed this a mutation to eliminate for the good of the US sheep industry. Due to the unusual inheritance of the Callipyge phenotype, it is important to realize the genetic testing will identify the number of copies of the mutation but will not predict the phenotype without additional parental status information. Regardless, the test can be used to eliminate this mutation from the desired populations.
Noncarrier	No Copies of Mutation	
Carrier	1 Copy of Mutation	
Homozygous CLPG	2 Copies of Mutation	

Booroola FecB		
Results	**Description**	The Booroola fecundity gene (FecB) variant is inherited as a single autosomal locus influencing ovulation rate and litter size. The effect of FecB is additive for ovulation rate. That means for each copy of FecB variant inherited, there will be an increase of about 1.6 corpora lutea per cycle. Multiple researchers identified the causative mutation within the bone morphogenetic protein IB (BMP-IB) receptor. These teams found that Booroola sheep had a mutation (Q249R) in the highly conserved intracellular kinase signaling domain of the BMP-IB receptor. Selection for multiple copies of this fecundity mutation can cause large increases in ovulation rate and litter size. Such impacts on the existing production system need to be considered before incorporating the FecB mutation into a flock.
Noncarrier	No Copies of Mutation	
Carrier	1 Copy of Mutation	
Homozygous FecB	2 Copies of Mutation	

Inconclusive test

In some cases, the result of a genotype test will be inconclusive. There are redundancies built into the testing process to validate a test. When there is a level of inconsistency among those redundant tests, the genotype call is less reliable and therefore deemed inconclusive. Such inconsistency can arise from the condition of a tissue sample, the extraction of the DNA from a sample, and the complexity of the chemistry associated with each test.

If a test is inconclusive, and a reliable genotype on an animal is needed for marketing or selection decisions, a new tissue sample should be collected and submitted for retesting.

Last updated: Jan. 6, 2023

Genetic Conditions Results Important Notice (Disclaimer)

Parentage results
The parentage results in this report are based on methodology developed by Sheep CRC Ltd and further refined by Sheep Genetics and its service provider (AGBU) which enables allocation of the pedigree of animals from the list of supplied candidate parents.

Poll results
The Poll test results are a predictive breeding value for poll status that has been based on Sheep CRC Ltd research and data from the Information Nucleus program.

This test is not the direct marker or the actual gene causing poll status, which means that the outcome of the test is not 100% accurate. There is a 3% chance that a "PP" sire will produce horned progeny. However, sires with the "PP" genotype will produce significantly more offspring with polled status than sires with a "PH" genotype or "HH" genotype.

Animals recorded with Sheep Genetics will also have their poll result included in the Sheep Genetics databases.

Genetic conditions and recessive genes
The genetic condition and recessive gene tests are based on published information about Single Nucleotide Polymorphisms responsible for specific conditions.

General
While the Sheep Genetics, Meat & Livestock Australia Ltd (MLA), Animal Breeding and Genetics Unit (AGBU), and National Sheep Improvement Program (NSIP) have taken all reasonable care to ensure our methodologies are valid and results are accurate, you should be aware that genomic testing and methodologies have inherent inaccuracies which, in some cases, cause inaccuracies in the genomic results and our recommendations.

In addition, the samples and information used to prepare this report are obtained from various parties. Neither Sheep Genetics, MLA, AGBU nor NSIP can or do verify this information and any inaccuracies in it will impact the accuracy of the results (e.g., genotypes assigned to the wrong animal can result in misleading results).

Please also be aware that the results and recommendations in this report do not consider your specific business interests and circumstances. You should check these against your/the breeder's records to verify that any suggested pedigree allocations are possible. You should also make any other relevant inquiries and consider the inherent inaccuracies of genomic testing and methodologies before making decisions concerning your interests or otherwise relying on these reports in any way.

To the extent permitted by law, this report is provided 'as is', and the Sheep Genetics, MLA, AGBU and NSIP expressly exclude all rights, warranties, and guarantees regarding the completeness or accuracy of the information in this report.

Last updated: Jan. 6, 2023