NSIP Meeting

Thursday – March 12, 2015

7 p.m. CST

Minutes submitted by Lisa Weeks

Attendees: Matt Beals, Matt Benz, Rusty Burgett, Carl Ginapp, Cody Hiemke, Rodney Kott, Ron Lewis, Jim Morgan, Dave Notter, Reid Redden, Bill Shultz, Lisa Weeks

Agenda:

- Board Communication Forum:
  - Rusty Burgett a lot of interest from new members in the NSIP programs.
  - Bill Shultz (Terminal rep) the group is reviewing what reports they want available from Lambplan.
  - Carl Ginapp (Hair rep) a lot of interest in the free membership for 1<sup>st</sup> year members.
  - Rodney Kott (Range rep) The Columbias want some appearances changes to the reports. The report should look more like the AUS report does. Cody commented that we need to define a protocol for custom reports and change requests.
  - Jim Morgan (Katahdin rep) working to get all enrolled flocks submitting data.
  - Matt Beals (Suffolk rep) there will be additional flocks enrolling soon.
  - Matt Benz (Ramboillett rep) there is a lot of interest in the Western US from seedstock producers. There is concern that Fact Sheets couldn't be found on the NSIP website. Jim Morgan made the suggestion to offer some webinars for each of the four groups (Maternal, Terminal, Hair, and Range) after a data run to help producers interpret results.
- Committee Reports (all reports included as .pdf attachments)
  - Technical Jim Morgan began a discussion on the Genomic Project. We (NSIP) need to commit to collecting this data. Dave Notter stated that we do not have discovery populations in the sheep industry today. At a minimum blood should be collected on sires and blood cards should be collected from lambs of those sires. This discussion was tabled for future discussion.
  - Executive Bill Shultz moved to allow the Executive Committee to hire a part time director at their discretion while we seek funds to hire a full time director. Carl Ginapp seconded and motion passed.
- Meeting adjourned.

Next meeting scheduled for April 9, 2015 at 7 p.m. CST.

### Appendum A

Sheep Genomics Work in the US: Sampling DNA from Industry Populations. James Morgan & Lynn Fahrmeier (for the ad hoc subcommittee **Work With Industry for Sample Collection** that came out of the **Sheep Genomics Workshop** in Lincoln, NE November 13-14 2014)

(committee also includes Dr Reid Redden, NDSU & NSIP, Dr Harvey Blackburn, USDA-ARS-NAGP; While not on the committee, Dr Dave Notter has been key in the discussions) Benefits for the US sheep industry from genomics work will come from evaluating DNA from populations of a breed that have wool or meat production phenotypes. Depending on the trait, number of genes involved and heritability, it is expected that researchers will need DNA samples from populations of 1,000 to 10,000/breed.

The goals of US sheep genomic work include but are not limited to the following: a) identify DNA markers that can be used to develop Genomic Breeding Values (GBVs) that supplement currently provided Estimated Breeding Values (EBVs). (note: In beef cattle, GBVs provide the accuracy of 50 progeny at birth)

b) develop a new Ovine SNP (single nucleotide polymorphism) chip with increased relevance for the US sheep industry. This chip will be used on USDA-ARS & University flocks for discovery of markers. Included in this work will be a run on 20,000 to 40,000 US sheep industry DNA samples (from sheep with NSIP phenotypes) for validation of markers and potentially some discovery work.c) identify disease resistance and susceptibility DNA markers

d) develop new SNP (single nucleotide polymorphism) chips that can test for multiple current DNA markers for under \$25 a sample (Prion genotypes, parentage, myostatin, Spider gene, TMEM154 genotype (OPP susceptibility) .....

e) focus on identifying DNA markers that have across-breed value

To provide this number of samples for most breeds, the US sheep industry will need to step up and provide DNA from sheep with phenotypic information on production traits. The system in place that is already collecting and storing key phenotypic data for the US Sheep Industry is the National Sheep Improvement Program. Of special interest are samples from progeny-tested sires in NSIP, since these sheep have the most accurate predictions of genetic. The goal of Sheep Genomics work in the US will **also** be to provide value to breeds that have smaller numbers of animals with phenotypes. For analyzed DNA samples from sheep to have value for predicting genetic merit for traits, the samples need to be from sheep that have collected data (some subset of the following: birth weight, 60 day weight, 120 day weight, 240 day weight, yearling weight, fleece weights, staple length and diameter, litter size born and reared, fecal egg counts and ultrasound carcass data among others). These are the commonly collected phenotypes from sheep in NSIP. The Sheep Genomics working group has suggested that disease resistance data be collected by University and USDA research flocks.

The Sheep Genomics working group in November said that DNA samples are also needed from all lambs and dams with NSIP phenotypes as well as progeny tested sires. These samples can be used for validation of DNA markers and in some cases, discovery of markers associated with production phenotypes. The DNA samples will be used either on current ovine SNP chips (Single Nucleotide Polymorphisms) or as proposed by the Sheep Genomics working group on a newly developed US ovine SNP chip designed by USDA-ARS. The industry collected samples will i) foster development of genomic breeding values that complement, but not replace classic estimated breeding values (EBVs), ii) provide DNA for validation of DNA markers identified in USDA and University research flocks and iii) provide samples of DNA for future research projects.

This is investment of collection of DNA samples by producers will begin having benefits in 2-5 years.

1) Starting in 2015, NSIP will have producers submitting phenotypic data to collect three FTA blood cards per sheep in NSIP. This includes all sires, dams and lambs.

2) USDA-NAGP in Ft Collins Colorado will provide blood collection kits for NSIP progeny tested sires (with at least 5 progeny) including shipping coolers, gel packs and labels covering shipping. The Sheep Genomics committee will work with NAGP to help cover costs in the future.

3) Sires from non-NSIP flocks or NSIP flocks that have sires without phenotypic data can ship blood to USDA-NAGP, but it will be at their expense.

4) There are several factors that can facilitate blood collection and make it easier and more economical for producers.

a. First we applaud USDA ARS-NAGP for offering to help with

i. providing blood collection kits for progeny tested sires with blood tubes, gel packs, styrofoam coolers and pre-paid shipping labels

ii. processing and storing blood from these sires

iii. storing FTA blood cards in a facility with temperature and humidity control.

Collection notes.

1) It is easier to collect blood following shearing or when hair sheep have shed

2) For those needing help with collecting tubes of blood, we suggest the following. Most NSIP producers are shipping rams or ewes interstate health papers or have health professionals out to their operations. When having interstate health papers or other procedures, it would be an opportune time to also have your DVM collect blood. USDA-NAGP will work with NSIP flocks to have blood collection kits on hand at these times.

3) NSIP will be developing YouTube videos demonstrating how to properly collect samples for FTA Blood Cards and to collect blood tubes. For FTA Blood Cards;

a. The drop of blood needs to be the size of a quarter and rounded.

b. Following collection the cover of the card is loosely inserted without sealing.

c. After storage in an open tub for several days to allow blood on the card to dry, the cover can be pressed down.

d. After collecting, the blood cards need to be moved out of the heat and humidity. They shouldn't be stored in the sun or in a pickup. They should not be stored in a ziplock bag, since that will facilitate sample degradation and mold growing on the samples.

4) information needed on samples

a. 16 digit Lambplan ID

b. Flock ID

c. Breed Registration # if available.

5) Blood cards can be purchased for \$1 each from Neogen.....

6) For blood tubes from sires that do not have a 16 digit ID and thus are not in NSIP, the following information is needed.

a. Breed

b. Flock ID

- c. Breed Registration # if available
- d. ID & Registration # of the sire of the Sire collected
- e. ID & Registration # of the dam of the Sire collected

f. DOB of sheep that sample is submitted for

### Appendum B

#### NSIP Technical Committee Report David Notter

Tasks and Priorities, March 12 through June 1: The following tasks will be completed prior to installation of a new Chair of the Technical Committee on June 1.

1) Produce a fact sheet on Terminal Sire Indexes for the web site: an article on breeding objectives for Terminal Sire breeds has been accepted for publication in the ASI Sheep and Goat Research Journal. Several indexes were developed based on research from the U.S. Sheep Experiment Station and extended to address alternative harvest endpoints (constant time on feed, constant body weight, constant fat thickness). A breeding objective was also developed to address potential (currently largely unrealized in U.S. markets) for increased levels of value-based pricing based on carcass fatness and muscling and was shown to correspond closely to the LAMBPLAN Carcass Plus Index. Carcass Plus is thus an acceptable breeding objective for Terminal Sire breeds that wish to place moderate positive emphasis on fatness and muscling in anticipation of greater emphasis on value-based marketing in U.S. markets were dominated by differences in Postweaning Weight EBVs. A Fact Sheet for the web site will be developed to present these alternative breeding objectives and discuss their use in selection and pricing of terminal sires.

2) Produce a fact sheet on ultrasound scanning EBVs for the web site: our work on breeding objectives for

Terminal Sire sheep breeds revealed some misunderstanding regarding interpretation of EBVs for scanning traits. The main issue is interpretation of the EBV for Backfat Depth. In both Australia and the U.S., this EBV is based on ultrasound scans taken over the loin muscle between the 12th and 13th rib, and EBVs from the LAMBPLAN analysis are based on this measurement. However, because there is very little variation in this measurement, the resulting EBV is multiplied by 3 before reporting. This conversion is designed to convert the backfat depth EBV to a body-wall thickness EBV. The body-wall measurement is known in Australia as the "GR" fat measurement and is the primary predictor of lean-meat yield. This is different from the U.S., where backfat depth is the primary predictor of Yield Grade. So EBVs and genetic trends for Fat Depth are based on predicted differences in the GR measurement (i.e., body wall thickness), not the actual ultrasound backfat depth, and actual differences in EBV for ultrasound fat depth between animals are only one third the reported differences is needed to accompany and assist in interpretation of the fact sheet on Terminal Sire breeding objectives in 1). It will include some diagrams of where the fat measurements are taken, a discussion of interpretation and use of the Fat Depth EBV is different breeds and production systems.

3) Finish analysis of Cornell University accelerated lambing data: Mike Thonney provided data from the Cornell STAR Dorset flock to test possible indicators of genetic merit for lambing performance in accelerated lambing. Analysis of these data will be completed and compared to results obtained from the Tisdale accelerated Polypay flock. LAMBPLAN is still committed to updating their EBVs for reproductive traits to provide separate EBVs for ewe fertility, litter size and some measurement(s) of lamb survival. However, no timeline has been developed for implementation of the new reproduction modules, so this is not a pressing issue, but it is one that is very important to a few of our NSIP breeders.

4) Work with LAMBPLAN to evaluate alternatives for adjustment of body weights: analyses of adjustment

factors for effects of birth-rearing type and dam age on weaning and postweaning weights in NSIP Terminal breeds have shown that existing multiplicative adjustment factors over-adjust weights of twin and triplet lambs in flocks that utilize high-levels of concentrate feeding and under-adjust weights of twin and triplet lambs in flocks that manage their lambs with lower levels of concentrate feeding. This observation was initially interpreted as a breed effect on the adjustment factors and breed-specific adjustment factors were implemented in the analysis of body weights for NSIP Termimal breeds. However, it has become obvious that there is a systematic negative association between the feeding level and the magnitude of the body weight adjustments, especially for effects of birth-rearing type. This relationship (high-performance flocks have smaller absolute effects of birth-rearing type) is, in fact, exactly opposite that assumed by using multiplicative adjustment factors. Results of these analyses were reported (via Skype) to the LAMBPLAN Technical Committee on March 5, 2015 and received a sympathetic hearing. Consideration of this problem has been added to the LAMBPLAN Work Plan, and I will work with LAMBPLAN to consider possible improvements to adjustment protocols. For the moment, our breed-specific adjustment factors allow adjustment factors to be customized to the breed-mean performance level, but differences among flocks within breeds are not handled properly. This issue has implications for development of across-breed EBVs using data from flocks that differ widely in feeding level. Our report to the LAMBPLAN Technical Committee is being circulated with this Report.

## Appendum C

Because of tables and already in PDF format would not move with formatting so it is the PDF listed below this one.

# Appendum D

March NSIP Executive Committee Report

- The "Vision for Genetic Improvement" was sent to leadership for NSIIC, ALB, and ASI (Lets Grow).
- It prompted a conference call among these groups, without NSIP on the call
- Reports indicate that they were in agreement that our vision is sound and needed by the industry
- Unofficially, we were asked to submit grants as follows:
- $\circ~$  \$50,000 to Let's Grow for development of the leading breeders groups and national genetics education program spring funding cycle
- $\circ~$  \$50,000 to NSIIC and ALB for NSIP membership consultation and program director summer funding cycle
- Funding salary as we suggested was not a restriction based on the source of these funds
- They understand that we are requesting a three year funding cycle but no one has the option to do that. We were encouraged to document progress and resubmit in subsequent years. However, it was encourage that NSIP develop a plan to internally fund staff within 3 years.
- The executive committee wants to get started now and suggest to the board that we hire a fulltime or part-time program director on a monthly contract basis. This would allow us to train and mentor a program director during the spring and summer season, when lambing data is submitted and ram sales are being held/organized. If we wait until the summer funding cycle, these funds won't be available until the fall. This puts us a full year behind. The job description for a program director is in the Demeter report, under the organizational recommendation section. However, we'd like to find a program director who can also take on the membership consultation role.
- o Full-time \$4k per month
- o Part-time \$2k per month

• ~\$5K signing bonus, when funding is secured for full-time position

• As of the last financial report, NSIP has \$79K of equity. And we wish to keep ~\$45K to operate on and a rainy day fund. Therefore, we have \$34K to spend on personnel and other matters to improve the sustainability of this program.