

## NSIP Technical Advisory Committee Report Dec. 2015

### Technical Advisory Committee Membership

Tom Murphy, a Ph.D. student working with Dave Thomas at the University of Wisconsin-Madison, was invited to join the Technical Advisory Committee and has agreed to do so. Due to commitments associated with his doctoral program, his formal involvement with the Committee will begin in March 2016.

### Let's Grow Application

Ron Lewis submitted an application entitled *Engaging the New Biology: establishing the foundation for genome-enhanced breeding values in the U.S. sheep industry* to the Let's Grow program. In total \$9,643 in funding was requested. The application was submitted through the University of Nebraska-Lincoln. Reid Redden and Rusty Burgett provided letters of support, which confirmed the close collaboration of NSIP in the work proposed. The Executive Summary of the project follows:

The efficiency of lamb and wool production has increased substantially by applying quantitative genetic principles in sheep breeding programs. Accelerating those gains depends on **melding state-of-the-art technologies in animal genomics with quantitative genetics approaches** to more accurately identify high merit animals. This proposal focuses on three key steps for the U.S. sheep industry to combine molecular and quantitative tools in genetic improvement programs: (i) **provide producer education** clarifying the opportunities and limits of genomics, and the practices needed in order to collect molecular information to obtain more accurate estimates of genetic merit (genome-enhanced estimated breeding values); (ii) **devise efficient strategies to collect genomic data**; and, (iii) **establish a reservoir of genomic samples** (DNA) on well-chosen performance-recorded animals through collaboration with the National Sheep Improvement Program (NSIP); such is necessary to develop procedures for their incorporation in genetic improvement programs. These efforts will lead to **productivity improvement**, a goal of the Sheep Industry's Roadmap, contributing to the long-term profitability of the American sheep industry.

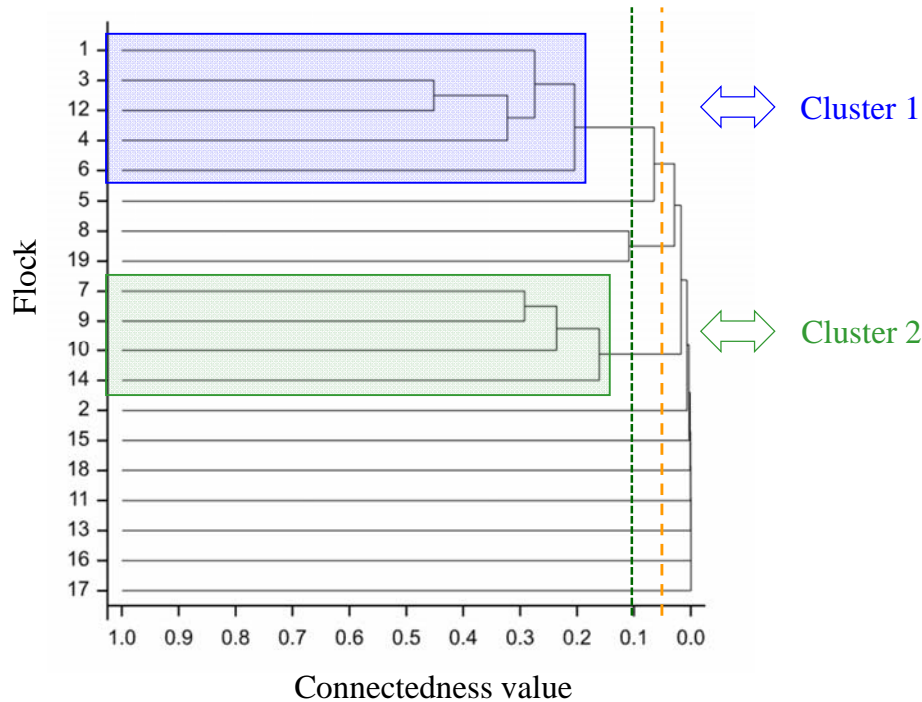
### Genetic connectedness among Suffolk flocks

The strength of genetic connectedness among flocks characterizes the reliability of comparisons of EBV of animals across those flocks. When connectedness is sufficiently strong, such comparisons are robust thereby enhancing the quality of selection decisions.

**Approach.** Similar to work undertaken previously in the Katahdin breed (Technical Committee Report, August 2015), genetic connectedness among Suffolk flocks within NSIP was evaluated. Pedigree data on 54,807 Suffolk sheep from 105 flocks born between 1960 and 2015 were considered, which included 2,965 sires and 13,436 dams. Median, average, and standard deviation (SD) in sire family size were 5, 16.7, and 29.3 progeny, respectively. One ram sired 355 lambs. Weaning weights collected between 1983 and 2015 on 35,802 lambs from 101 Suffolk flocks also were available, and contained 2,009 contemporary groups. At weaning, average age was 62.8 (SD 10.6) days and average weight was 67.6 (SD 11.7) lb. Among these flocks, 19 submitted data to NSIP in either or both of 2014 and 2015, and were classified as 'active' for this study.

Genetic connectedness was determined between all pairs of the 105 Suffolk flocks. The heritability for weaning weight used was 0.15, which is the value used by LambPlan in the genetic evaluation of this trait in the Suffolk breed. Connectedness among the active flocks was summarized using hierarchical clustering and illustrated using a tree diagram (dendrogram).

**Results and their significance.** Figure 1 is the dendrogram reflecting the strength of genetic connectedness among the 19 Suffolk flocks categorized as actively participating in NSIP in 2014 and/or 2015. There were two clusters of flocks with strong inner-connectedness (connectedness values above 0.1). Flock 5 was moderately connected to the first cluster. In addition, a pair of flocks (8 and 19) were strongly connected. Connectedness between the two main clusters, and the pair of flocks, were relatively weak (connectedness values less than 0.05). Seven flocks were weakly connected to the rest.



**Figure 1.** Cluster analysis of 19 Suffolk flocks with weaning weights recorded in either or both of 2014 and 2015. Dashed lines indicate thresholds for moderate (0.05) and strong (0.10) genetic connectedness. Two strongly inner-connected clusters are highlighted.

A very similar analysis had been run for Suffolk flocks participating in NSIP in 2005 (Kuehn et al., 2009). Eight of those flocks were among those designated as active in the current analyses. As found here, flocks 1, 3, 4 and 6 were part of one cluster while flocks 7, 9 and 10 were part of a second cluster. Flock 11 was then, and remains, distinct from either cluster. Within the individual clusters, connectedness has become stronger among these flocks over the past decade, suggested their increased sharing of rams. Between clusters there has been little change in connectedness.

In the earlier work (Kuehn et al., 2009), an explanation proposed for the formation of the two main clusters was that groups of breeders were selecting for different biological types of Suffolk sheep. Such likely remains the case today.

These results suggest that ancestries differ among the various groupings of Suffolk flocks, which also may coincide with genetic differences. If genetic connections between clusters, and among flocks generally, were further strengthened, comparisons of EBV would become even more reliable allowing for even better selection decisions.

**Opportunities.** Connectedness evaluations offer some useful diagnostic tools. Firstly, they identify groups or clusters of flocks within which EBV of animals can be reliably compared. Secondly, and particularly for those flocks that are less well connected, they can help identify rams to use from active NSIP flocks that will establish stronger genetic links. Most importantly, they provide a mechanism to improve the robustness of a genetic evaluation scheme providing the opportunity for faster rates of genetic gains within a breed.

**Reference cited.** Kuehn, L. A., R. M. Lewis, D. R. Notter. 2009. Connectedness in Targhee and Suffolk flocks participating in the United States National Sheep Improvement Program. *J. Anim. Sci.* 87:507-515.