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### 376 Genetic Approaches to Improve Reproductive Performance in the U.S. Sheep Industry.

Thomas W. Murphy<sup>1</sup>, <sup>1</sup>USDA-ARS, U.S. Meat Animal Research Center

Abstract: The U.S. sheep industry has experienced many changes over the last 50 years, the most prominent being a 75% reduction in the national breeding ewe inventory. Wool now accounts for ~10% of enterprise returns compared to ~80% from the sale of market lambs. Most breeding objective work indicates greatest emphasis should be placed on traits associated with ewe reproductive efficiency [e.g., number of lambs born/weaned (NLB/NLW), lamb survival]. Still, average NLB across the U.S. (1.07 lambs/ewe) and within geographic regions (East = 1.13, Midwest = 1.25, West = 1.09, Southwest = 0.79 lambs/ewe) remains low. Several genetic technologies are available to improve reproductive performance. Introgression of large effect gene variants, such as those within BMPR-1B, have increased NLB by ~1.0 and ~1.5 lambs in heterozygous and homozygous ewes, respectively. However, without joint improvement in maternal ability and/or husbandry, advantages in NLW are less pronounced and few U.S. producers utilize such variants in practice. Reproductive efficiency traits present challenges in selection programs as they are lowly heritable (< 0.15) and sex-limited. Previous single-trait selection experiments had modest improvement in NLB (0.01 – 0.02 lambs/yr). Selection accuracy is greatly improved by including pedigree and/or genomic relationships when deriving estimated breeding values (EBV). Since 2000, NLW EBV have increased by 0.01 lambs/yr with concurrent improvement in direct (0.02 kg/yr) and maternal (0.04 kg/yr) weaning weight for Polypay flocks enrolled in the National Sheep Improvement Program (NSIP). Still, NSIP flocks represent < 1% of production-oriented U.S. flocks so considerable expansion is needed to realize within-breed genetic improvement at a national level. Perhaps most importantly, large differences in reproductive efficiency traits exist across breeds and should be utilized to a greater extent in strategic crossbreeding systems. Optimizing reproductive performance for specific production environments is essential for the sustainability of the U.S. sheep industry.

**Keywords:** genetics, reproductive efficiency, sheep

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### 377 Derivation and Use of Genomic Enhanced Estimated Breeding Values for Selection in Sheep.

Ronald M. Lewis<sup>1</sup>, Daniel J. Brown<sup>2</sup>, <sup>1</sup>University of Nebraska-Lincoln, <sup>2</sup>AGBU, a joint venture of NSW Department of Primary Industries and University of New England

Abstract: The efficacy of selection programs in sheep depends on accurate evaluation of genetic merit. Globally, genetic evaluations are based on best linear unbiased prediction (BLUP) in which fixed effects and breeding values are estimated simultaneously. With genotyping becoming increasingly routine, pedigree, performance, and genomic data are being combined in single-step genomic BLUP (ssGBLUP) evaluations to generate genomic enhanced estimated breeding values (GEBV). Since GEBV are more accurate, younger animals can be selected more reliably; a corollary benefit is a shortened generation interval. Traits that are lowly heritable, expressed in one sex, measured late in life, or difficult and/or expensive to measure benefit most from genomic evaluation. Adoption of this technology has lagged in sheep most likely due to the higher cost of genotyping compared to the value of an animal. Nevertheless, genomics has been successfully incorporated in sheep breeding programs in several countries (e.g., Australia, France, New Zealand). Increases in accuracy of EBV of up to 60% have been reported. In 2021, the efficacy of genomic selection in a U.S. sheep breed (Katahdin) was tested by comparing predictive ability and bias of EBV using ssGBLUP and pedigree BLUP for weight and fecal egg counts at weaning. Approximately 5,000 animals, most born within the last 5 years, were genotyped with a 50k array. Nearly 70k body weights and 14k fecal egg counts were available. Genomic information improved predictive ability for both traits by as much as 10%, and reduced bias in the evaluation of fecal egg counts. Accuracies of EBV improved appreciably in younger genotyped animals (by as much as 1.81 times). An outcome was release of GEBV in the evaluation of U.S. Katahdin sheep. With integration of genomics into genetic evaluation, there is clear opportunity to augment the reliability of genetic evaluation and thereby rates of selection response in sheep.

**Keywords:** breeding value prediction, genomic selection, sheep