

## Small Ruminant Symposium: Genetic improvement in small ruminants for the future

**714 National Sheep Improvement Program.** David Notter\*, *Virginia Tech, Blacksburg, VA.*

The US National Sheep Improvement Program (NSIP) was established in 1987 and is supported exclusively by US sheep breeders and their organizations. In 2010, limited options for sustainable involvement with US institutions led NSIP to establish a partnership with Meat and Livestock Australia to merge genetic evaluation activities with LAMBPLAN, the Australian sheep genetic evaluation system. Outsourcing genetic evaluation services to LAMBPLAN expanded NSIP resources and increased the frequency of updating of EBV. The operating philosophy of NSIP correspondingly evolved to become a proactive force for genetic improvement of US sheep. LAMBPLAN offers EBV for 85 different traits. NSIP provides EBV for a subset of these traits including body weights from birth through adulthood, reproductive and ewe productivity traits, ultrasonic predictions of fat and loin muscle depths, fleece weight and quality measurements, and worm resistance. LAMBPLAN offers selection indexes for various breeds and production objectives, and NSIP offers indexes specific to US breeds and conditions. NSIP serves all US sheep breeds, and also offers genetic evaluation services for meat goats, but is dominated by 4 groups: (1) Western range breeds (mainly Targhee, Rambouillet and Columbia), (2) terminal sire and other meat breeds (mainly Suffolk, Hampshire, Dorset, and Shropshire), (3) maternal wool breeds (mainly Polypay), and (4) hair sheep breeds (mainly Katahdin). In 2013, 123 flocks submitted data to NSIP. The 4 breed groups each submitted records on 2,700 to 3,200 lambs, and the 9 breeds listed above accounted for over 85% of NSIP flocks. Genetic trends in US breeds document the effectiveness of selection. Use of genomic strategies to increase accuracies of EBV is a major focus of LAMBPLAN research and development, providing opportunity for corresponding activities in NSIP. Detailed phenotypic records of animal performance are increasingly recognized as essential for discovery and validation of genomic markers, and NSIP is increasingly recognized as the most comprehensive repository of sheep data in the US. Storage of DNA from all progeny-tested NSIP sires and a sample of lambs in each major NSIP breed is intended to allow NSIP to make a larger contribution to meeting the research needs of the sheep industry.

**Key Words:** sheep, estimated breeding value, genetic evaluation

**715 Genomics and marker-assisted selection in small ruminants.** Brian L. Sayre\*, *Virginia State University, Petersburg, VA.*

As the world climate and population levels evolve, high demands are placed on livestock production systems. Small ruminants, especially goats, are critical to the small-scale producer as they are easy to acquire and maintain in sparse pasture and marginal crop regions that cannot easily sustain other livestock. Current small ruminant production systems around the world depend heavily on locally adapted breeds. While indigenous small ruminant genetics are relatively uncharacterized, most have undergone generations of adaptation and genetic isolation or bottlenecks, creating a large genetic reservoir of variation in genes and genetic markers. Identifying genes and genetic markers associated with disease susceptibility and resistance in locally adapted breeds is necessary to preserve local germplasm and to apply state-of-the-art genomic-based strategies to meet global food security challenges. Of particular interest are the genes or genetic markers involved in resistance to internal parasites and disease, and resilience to climate differences.

The aim of the current small ruminant genetics and genomics research is the development and utilization of state-of-the-art genomic-based evaluation tools for characterization of sheep and goat populations, development of sustainable strategies for improved production, and increased education and research opportunities. International collaborations have led to the development of de novo genome assembly projects, Illumina SNP panels and, for goats, a collaborative database for submission and access to goat SNP and re-sequencing data for breeds and populations worldwide (ADAPTmap). These tools establish the baseline necessary for the development and application of marker-based selection to the sheep and goat industry.

**Key Words:** genomics, marker-assisted selection, small ruminant

**716 Genetic improvement for internal parasite resistance.**

Daniel J. Brown\*, *Animal Genetics and Breeding Unit, University of New England, Armidale, NSW Australia.*

Internal parasites impose a huge financial burden for small ruminants across the world with recent estimates in Australia suggesting the cost could be as high as \$10AUD per breeding ewe per year. Genetic improvement has to be a key part of any integrated pest management plan for internal parasites. The number of worm eggs per gram of feces (WEC) is known to be a good indicator of internal parasite burden and is moderately heritable in both sheep and goats ( $h^2 = 0.2$  to  $0.3$ ). Breeding for internal parasite resistance is complicated by the fact that several different worm species can be present depending on the location, time of year, management practices and prevailing environmental conditions. In Australia, the national genetic evaluation system (Sheep Genetics) only uses data from *Haemonchus contortus* and *Trichostrongylus* spp. to reduce some of the complications caused by these multiple worm species. It is also known that WEC is genetically not the same trait across ages and thus there is benefit in breeders recording multiple assessments throughout the animal's life. Furthermore, research in Australia suggests that the genetic correlations between different sites across Australia may also be significantly less than one, and thus making it important for breeding animals to be assessed in similar environments to those in which their progeny are expected to exhibit their resistance. These issues make the estimation of breeding values and genetic improvement of this trait more challenging. Despite these challenges ram breeders in Australia have managed to make significant genetic improvements in WEC. Some breeders have reduced WEC by up to 5% per year for the last 15 years, while simultaneously improving other production traits. On-farm, these breeders have reported reduced requirements for drenching, less scouring and greater production. Genomic information has also been incorporated into the routine Sheep Genetics evaluations. Breeders now have the ability to obtain moderately accurate ASBV predictions for WEC (plus a range of other traits) via a simple blood test.

**Key Words:** internal parasite, worms, sheep

**717 Breeding strategies in sheep for low-input management systems.**

Ronald M. Lewis\*<sup>1</sup>, Napoleón Vargas Jurado<sup>1</sup>, and Kreg A. Leymaster<sup>2</sup>, <sup>1</sup>*Department of Animal Science, University of Nebraska, Lincoln, NE,* <sup>2</sup>*Roman L. Hruska US Meat Animal Research Center, USDA-ARS, Clay Center, NE.*

Profitability of sheep enterprises increasingly depends on using low-input, pasture-based management systems where costs can be curtailed without sacrificing productivity. Their success rests on using maternal genetics well adapted to such systems yet with attributes to produce a quality product. In historically medium-wool industries, fleece has become a cost rather than a source of revenue. Therefore, hair sheep germplasm has been incorporated into maternal lines to facilitate wool shedding (WS), and to enhance health (e.g., internal parasite resistance) and fitness (e.g., vigor, aseasuality, longevity). Yet, there are caveats. Hair sheep are smaller in mature size and typically lighter muscled. Within the US, carcass weights are traditionally at least 30 kg, a challenge to achieve with smaller breeds. The Katahdin breed reflects that concern, where Caribbean hair sheep were combined with wool breeds and Wiltshire Horn, a larger mature size breed that sheds. Markets for hair sheep lambs of lighter weight have evolved, allowing greater flexibility. Crossing with terminal sires offers another option, although its impact on overall productivity needs attention. The definition of a maternal breed-type ideal for low-input systems is equivocal. At the US

Meat Animal Research Center, a 1/4 Katahdin, 1/4 White Dorper and 1/2 Romanov composite has been established to attain an intermediate optimum. The inclusion of Romanov increased prolificacy, allowing identification of ewes able to produce, nurture and rear twin and triplet lambs in a low-input system. The composite retains 62.5% of heterosis benefiting health and fitness. Data on WS, color, horns, major genes affecting disease, and rearing status have been collected, and used independently in selection. Genetic analyses of WS data have been conducted. Among 3345 autumn WS records on ewes, 64% had less than 25% wool coverage; WS was moderately heritable (0.26) and repeatable (0.40). This composite is early in development, and further generations of *inter se* mating would benefit its evaluation. A breeding program for low-input systems necessitates combining breeds. A strategy capturing key attributes of a maternal breed-type, as defined through a selection index, is needed to sustain its role in the sheep industry.

**Key Words:** sheep, low-input, maternal composite