Small Ruminant Symposium: Advancements in Genetic Selection of Small Ruminants for Performance and Parasite Resistance

795 **Advancements in genetic selection of small ruminants for performance and parasite resistance: Introduction and purpose.** K. Andries*, *Kentucky State University, Frankfort.*

Small ruminant production has steadily increased over the past 10 to 15 years. Most of this increase has been in the area of meat goat production and started with the introduction of the Boer breed in the 1990 ′s. This growth has led to an increased need for basic and applied research into meat goat production. There has been an increasing need for information on genetics and breed differences in meat goats and re-evaluation of many sheep breeds due to changes in selection focus and breed types being used. There is a vast amount of genetic information available on cattle; however, little information is available for sheep and little to no information is currently available for goats, especially meat goats. The cattle industry has been able to utilize research in genetics to make tremendous advancements in productivity in the past 30 years. The Sheep Improvement Program has also moved forward using similar information through the calculation of flock expected progeny differences. Dairy goats also have genetic selection information available through the national dairy improvement program. However, meat goats do not have these types of programs readily available today. The use of molecular genetics as seen in the beef industry demonstrates the potential for small ruminants to find major genes for economically important traits. The sheep industry has implemented some of this research already but research in the goat industry is lagging behind. The one trait that seems to be achieving more research than others is parasite resistance. These efforts will play a major role in the future of small ruminant production. The purpose of this symposium is to show some of the history of genetic research and use of the information in other species and in small ruminants today. The hope is that this will help inspire future research and extension efforts in small ruminants to move both sheep and meat goats into more use advanced animal breeding methodology to improve production in these industries.

Key words: small ruminant, genetic

796 **Genetic evaluation: Lessons learned in the beef industry.** J. K. Bertrand*, *University of Georgia, Athens.*

The goal of the presentation is to provide a history of US beef cattle genetic evaluation programs and the lessons learned from their implementation. Initially, visual appraisal was to sole criteria for selection of beef cattle. In the 1950s and 60s, State Beef Cattle Improvement Associations and Performance Registry International were formed for the collection of objective phenotypic information. In 1968, The Beef Improvement Federation was formed to provide a framework for standardized record collection and systematic genetic evaluation procedures. During the late 1960s, beef breed associations became the "keepers" of phenotypic and pedigree information in the US During the 1970s and 80s, the beef breed associations began partnerships with Land Grant Universities, where the universities supplied the research and development and also conducted the genetic evaluations for the breed associations in return for grant dollars. In the end, this model was not sustainable due to insufficient funding to cover personnel and equipment. The National Beef Cattle Evaluation Consortium was formed in 2001 with a federal special grant that provided funds to the universities involved in servicing beef genetic evaluation programs to help supplement costs over and above those provided by the breed associations. Beginning in 2007, there was movement toward universities divesting themselves from the servicing of genetic evaluations to allow them to concentrate solely on research. Entities have formed or are still forming, usually at a breed association, to conduct genetic evaluations using the software/methodology provided by universities. Based on the experience of the beef industry, a sustainable industry-wide genetic evaluation program is dependent on 1) use of common sires across herds to provided the proper data infrastructure, 2) a system that allows for the collection of on-farm performance records, 3) a centralized system that maintains both phenotypic and pedigree information, and now genomic information, 4)) a national organization that provides leadership for record and procedure standardization, 5) a well funded group of research scientists and servicing personnel.

Key words: genetic evaluation, beef cattle

797 **National Sheep Improvement Program's current impact and future potential.** D. F. Waldron*, *Texas AgriLife Research, San Angelo.*

Since implementation in 1987 the US National Sheep Improvement Program (NSIP) has evolved to take advantage of developments in technology. The methods used in NSIP make use of all available performance records along with pedigree information to predict genetic merit for economically important traits. Statistical methods employed in NSIP were first developed for, and applied to, dairy cattle and later to beef cattle and other meat-producing livestock. Beef cattle breeders in the US increased adoption rates of the technology through the 1980s and 1990s. The US sheep industry's use of NSIP is expanding. Although NSIP is available to all breeds of sheep, many of the NSIP participants are from a small number of breeds. Targhee, Suffolk, and Polypay are the breeds that have had the most NSIP participation. Estimates of genetic trends are indicators of the impact of using NSIP for selection decisions. The impact of NSIP in the US sheep industry has been limited by low adoption rates. Costs of performance recording, perceived value of genetic evaluation, and lack of a consensus, within a breed, on breeding objectives are all factors that have limited the use of NSIP in the US sheep industry. Adoption of a national genetic improvement program by US sheep breeders has lagged behind that of US beef breeders. An adaptation of NSIP was developed first for Boer goats (Boer Goat Improvement Network) and then for Kiko goats. Participation in NSIP by breeders of meat-producing goats is lower than it is for sheep. As the impact from use of NSIP becomes more evident, participation is expected to increase. Recently implemented NSIP evaluations for fecal egg count as an indicator trait for resistance to parasites may lead to increased participation. Advances in genomic evaluation, as implemented in dairy cattle genetic evaluation, may be feasible to use for small ruminants in the future. However, the substantial numbers of recorded animals required to develop effective genomic evaluations are not currently available. If breeders of small ruminants will realize the potential of genomic evaluation, increased participation in NSIP is necessary, so that the records are available.

Key words: sheep, goats, genetic improvement

798   Advancements in genomics: Application and potential for small ruminant research. P. K. Riggs*, *Texas A&M University, College Station.*

Genome science and genomic tools have led to revolutionary biological breakthroughs that dramatically affect and continue to advance animal agriculture. In a short period of time, costs have fallen while technology has improved to make possible the reality that assembled genome sequences can be produced for any species of interest, particularly agricultural species. Research focused on small ruminant genomes will be able to make rapid progress by leveraging resources, tools, and knowledge gained from bovine and other species' genome projects. The cattle and sheep genome research consortia have recently completed high density gene maps, genome assemblies, haplotype maps, and related analyses. Research in goat genomics can take advantage of comparative genome similarity, as well as lessons learned from bovine and ovine studies, to make progress toward development of caprine-specific genome tools. Currently, several efforts are underway for construction of radiation-hybrid gene maps, SNP discovery, and genome sequence assembly. All of these projects present challenges for production of high quality data, storage and management of data, and bioinformatic analyses, but goat genome research can potentially move quickly as a result of previous findings. The future availability of genomic resources for goat provides great opportunity for application in the goat industry.

Key words: genomics, goat, molecular genetics

799   Sheep and goat genetic resources: Recent findings and potential for future development. H. Blackburn*, *National Animal Germplasm Program, National Center for Genetic Resources Preservation, Agricultural Research Service, Ft. Collins, CO.*

Genetic variability underpins the ability to manipulate sheep and goat populations for increased productivity and profitability. An assessment of the genetic variability of 28 sheep and 5 goat breeds using microsatellite marker panels has been made. The sheep analysis was extended to determine genetic distance and variation for US vs 5 Kazakhstan (KAZ) breeds. For US sheep the average number of alleles per locus and heterozgousity varied (3.7 to 8.2 and 0.42 to 0.65, respectively) suggesting some breeds (Rambouillet, Suffolk, Polypay, Dorper) possess substantial genetic variability for utilization. Nei′s genetic distances (GD) for US and KAZ breeds generally showed small genetic distances among KAZ breeds and moderate to large GD when compared with US breeds. The greatest GD was among US breeds. Analysis of Angora (AG), Spanish (SP), Myotonic, Boer, and LaMancha goat breeds showed high levels of heterozygousity (0.58 – 0.73) and large GD (0.21 – 0.57). The SP and AG breeds have undergone contractions in population sizes but ranked highest for genetic diversity measures. For sheep and goats these results suggest US breeds have substantial neutral genetic variability which might translate into important variability for traits of interest. But, to fully utilize genetic diversity at the genomic level or via quantitative methodology, development of substantial phenotypic databases that contain economically relevant data in addition to pedigree information must be initiated and utilized. Employing such databases will facilitate combining phenotypic and genomic information; which in turn will provide producers across breeds with an opportunity to improve sheep and goat performance and profitability.

Key words: sheep, goats, genetic resources

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