Tools Available to Wisconsin Sheep Producers for Genetic Improvement of Their Flocks

David L. Thomas
Extension Sheep Specialist
Department of Animal Sciences
University of Wisconsin-Madison
dlthomas@wisc.edu

The Genetic Revolution

One of the greatest scientific revolutions of our times has happened during the past 25 years with the elucidation of the genetic codes of living organisms. Several genes are now known in man that affect specific diseases or result in certain physical defects, and there are almost daily reports from the news media on new human genetic discoveries.

Agricultural plants and animals have not been left behind in this genetic revolution. In fact, agricultural research has often been ahead of human medical research in the understanding and application of genetics; partly because genetic research is easier to conduct with non-human organisms than with humans.

Much of the crop acreage in the U.S. is planted to transgenic or genetically modified crops; some examples are Round-Up Ready soybeans, corn, sorghum, cotton, canola, and alfalfa that contain a gene from a petunia that makes the plants resistant to the herbicide Round-Up and BT cotton, corn, and potatoes that contain a gene from a bacterium that results in the production of a toxin that protects the plant from several insect pests. Unless a person specifically purchases organic or non-GMO (non-genetically modified organism) products, a U.S. consumer is very likely to consume products from genetically modified crops on a regular basis.

Transgenic livestock also have been produced; for example sheep that produce human clotting factor IX in their milk and pigs with the human growth hormone gene. Most of the livestock species also have been cloned. However, due to both animal welfare and food safety concerns among the public, potential food products from transgenic and cloned animals have been controversial. The U.S. Food and Drug Administration is (was) expected to announce by the end of 2006 that food from cloned animals is safe and will be allowed for human consumption, but approval of food from transgenic animals is still further off even though a positive ruling from FDA on a transgenic salmon was initially anticipated in 2001.

Molecular Genetics and Livestock

Molecular genetics is the study of the molecular structure and function of genes. Developments in the field of molecular genetics have led to the production of transgenic animals and, to a lesser extent, to the production of cloned animals. However, a greater impact of molecular genetics on livestock production has been (and will continue to be in the future) through the identification of different forms (alleles) of native genes that have differential effects on traits of economic importance to a livestock species. Once these alleles can be identified, selection can be practiced to increase the frequency of the desired allele(s) and to decrease the frequency of the undesired allele(s) in subsequent generations.

Some of the best examples of the use of molecular genetics for improvement of livestock have been the identification of recessive alleles causing genetic defects in cattle. As examples, animals that are carriers of bovine leukocyte adhesion deficiency (BLAD), deficiency of uridine monophosphate synthase (DUMPS), complex vertebral malformation (CVM), and Weaver can be identified through a DNA test. Artificial insemination companies routinely test bulls for these and other known genetic defects and either reject carrier bulls or make the carrier status of bulls known to potential customers so that matings of carrier bulls with carrier cows can be avoided. As a result, the incidence of these genetic defects decreases.

There are fewer examples of the use of molecular genetics to improve the production traits of livestock. This is because most production traits are due to the action of many genes, each with a relatively small effect, and it takes large and costly experiments to identify these genes. However, this is where the greatest future benefits of molecular genetics for livestock improvement are to be found. We want to be able to identify animals through a DNA test that have alleles for greater or more efficient growth, better meat palatability, greater litter size, greater milk production, etc. Some currently known genes with DNA tests for production traits include: 1) several genes for litter size in sheep (The Fec^B gene is discussed later.), 2) an estrogen receptor gene in pigs for litter size, 3) casein protein genes in cattle, 4) meat tenderness genes in cattle, and 5) extreme muscle development genes in cattle, sheep and pigs.

Selection of Livestock on Performance

Molecular genetics holds great promise for improvement of livestock production in the future, but an effective and powerful genetic improvement tool is already at our disposal. This is selection on estimates of genetic value generated from the recorded performance (phenotype) of the animals in our herds and flocks. Performance of an animal is due to both its genetic makeup (genotype) and the conditions under which the animal is raised or managed (environment); Phenotype = Genotype + Environment. Since phenotype is due partly to genotype, the two are correlated, and the genotype can be estimated from the phenotype. The problem is that phenotype is also due partly to the environment, and it may be difficult to separate the portion of the phenotype which is due to the genotype and the portion which is due to the environment. We want to select animals to be parents of the next generation that have high levels of performance due to superior genetics and not those that have high levels of performance due to an above average environment. Fortunately, statistical animal geneticists have developed mathematical and statistical techniques over the past 50 years that can produce very accurate estimates of animal genetic values (genotypes) from phenotypic (performance) records on animals or their relatives.

The genetic or genotypic value is called a Breeding Value (BV). An animal's BV is the sum of the individual effects of all genes possessed by the animal that have an effect on the trait in question. Since a single parent only passes one half of its genes to an offspring, the parent passes, on average, one half of its BV to its offspring. One half of a BV is called a Progeny Difference (PD), and PD is the expected performance of the progeny of one parent when the other parent is of average BV and when environmental effects are average. Since we never know the true genetic make-up of individuals, BV and PD are estimated from performance records, and we use the terms EBV for Estimated Breeding Value and EPD for Expected Progeny Difference. Both EBV and EPD are expressed relative to some average for the flock/herd or breed and can take on negative and positive numbers.

Using Estimated Breeding Values and Expected Progeny Differences

The ram Topper has an EBV for fleece weight of +1.2 pounds. This means that Topper is estimated to have genes that result in 1.2 pounds more fleece weight than a ram of average genetic value from the same population (i.e. a ram with an EBV = 0.0). Topper's EPD is +0.6 pounds (EPD = 1/2 EBV). If Topper is mated to a group of ewes of average genetic value (EBV = EPD = 0.0), his progeny are expected to produce fleeces that are 0.6 pounds heavier than the fleeces from a ram of average genetic value (EPD = 0.0) (Expected Performance of Progeny = EPD of sire + EPD of dam = EBV of progeny).

The ram Signal has an EBV for fleece weigh of –0.8 pounds and, therefore, an EPD for fleece weight of –0.4 pounds. If Topper and Signal are both mated to a group of ewes of average genetic value, Topper's progeny are expected to produce fleeces that will weigh 1.0 pound more than the fleeces of Signal's progeny (Expected difference in performance between the progeny of Topper and the progeny of Signal = Topper's EPD – Signal's EPD = 0.6 – (-0.4) = 1.0 pounds).

If the ram Topper is mated to ewe Acorn (EBV = +0.5, EPD = +0.25), their progeny are expected to have fleece weights that are 0.85 pounds heavier (Topper EPD + Acorn EPD = 0.6 + 0.25 = 0.85 pounds) than the fleece weights of progeny from the mating of a ram and ewe of average genetic value

There are dramatic examples in all of our livestock species of rapid genetic improvement by selection of parents on EBV or EPD. One of the most successful examples is the U.S. dairy cattle industry. Regional Dairy Herd Improvement (DHI) centers collect performance information on dairy cows throughout the U.S., the performance records are processed by USDA in a central facility to calculate very accurate EBVs, and bulls with high EBVs are selected and used to produce several hundred or even thousands of progeny through artificial insemination. Figure 1 presents the EBVs for milk production for Holstein bulls (upper line) and cows (lower line) born from 1957 to 2004. There has been a dramatic change over this 47-year period from an EBV of -6,804 pounds of milk in 1957 to an EBV of +681 pounds of milk in 2004 for a total genetic improvement of +7,485 pounds of milk or +160 pounds of milk per cow per year. Just due to genetic selection, cows born in 2004 are expected to produce 7,485 pounds more milk per lactation or 24.5 pounds more milk per day than cows born in 1957. Increases in milk production due to improvements in feeding, health, and management over this same 47-year period would be added to the 7,485 pounds of milk from genetic improvement.

Dairy cattle have a long history of an organized program for genetic improvement that has included the broad use of artificial insemination and substantial direct financial assistance from USDA in the calculation of EBVs. The meat producing species were slower to implement genetic improvement programs, partly because there was very little or no public assistance for genetic improvement programs and less use of artificial insemination in these species. However, even with these liabilities, the meat animal species have instituted self-funded genetic improvement programs that have been very successful. The STAGES (Swine Testing and Genetic Evaluation System) program for the Duroc, Hampshire, Yorkshire, and Landrace breeds of swine has been especially successful. The program is supported by swine breeders using the program, and the EPDs are calculated by animal geneticists at Purdue University, West Lafayette, IN.

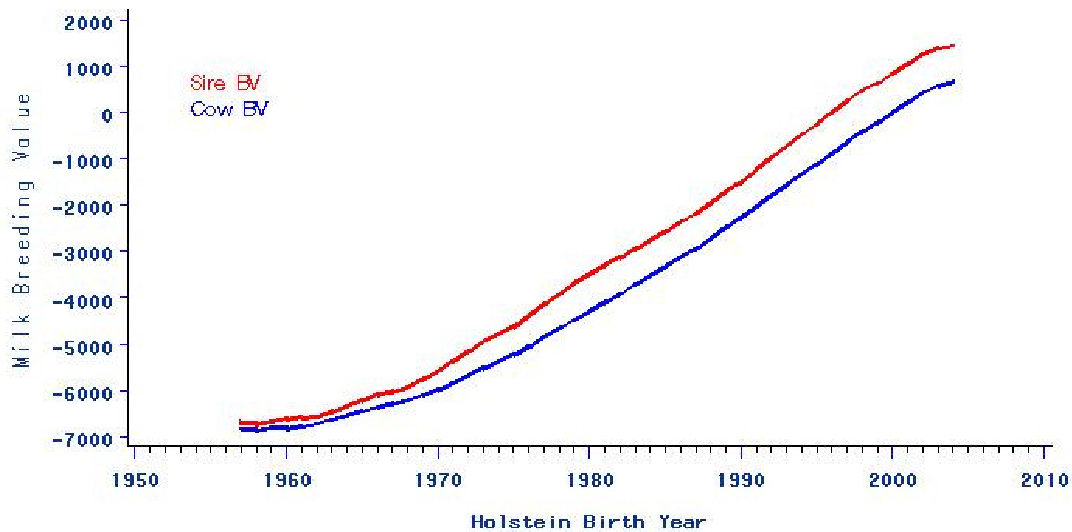


Figure 1. Estimated Breeding Values (EBVs) for 305-day milk production of U.S. Holstein dairy cattle born between 1957 and 2004. Sires on top line and cows on bottom line. (From: http://aipl.arsusda.gov/).

Presented in Figure 2 is an example of genetic change in pigs from herds enrolled in STAGES. The figure shows the change in EPD for estimated pounds of lean in a 185 pound carcass of Duroc pigs born between 1985 and 2006. The EPDs have increased from about –5.0 pounds in 1985 to about +0.8 pounds in 2006 for a total change in EPD of 5.8 pounds or +0.28 pounds per year. Since these estimates of genetic values are EPDs, we must multiply them by 2 to determine EBVs and expected performance of the pigs. Using the EBVs, pigs born in 2006 were expected to have 185 pound carcasses with 11.6 pounds more lean than pigs born in 1985.

It is interesting to note the shape of the curve in Figure 2. During the first 8 years from 1985 through 1992, there was very little genetic change. This probably was due to reluctance of the breeders to use the EPDs in selection of their breeding stock. They were accustomed to selecting on visual appraisal and not on EPDs, so the animals did not change much in genetic value during these early years of STAGES. From 1992 through 2001, there was a linear increase in EPD; probably as a result of the realization on the part of the breeders that EPDs were useful tools for genetic improvement. Since 1992, EPDs for pounds of lean has continued to increase but at a slower rate than before; probably due to breeders realizing that they need a balanced selection program where some emphasis is placed on additional traits.

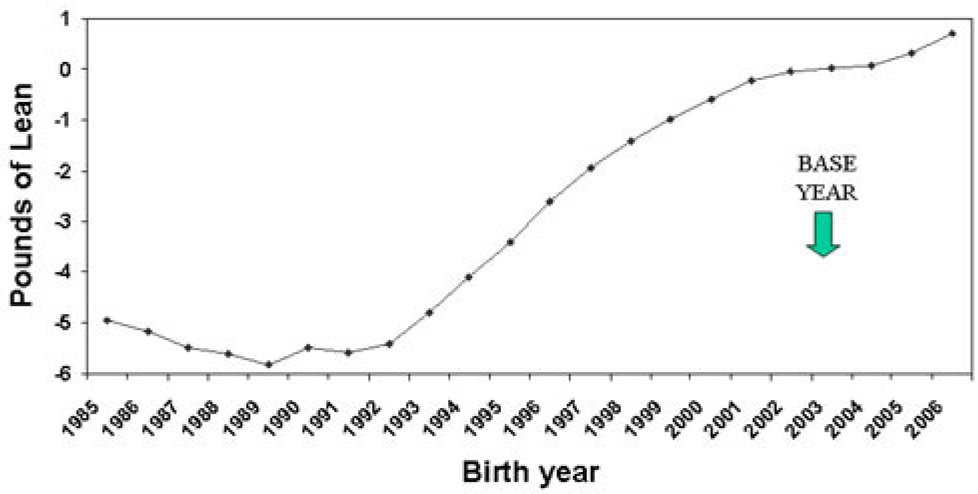


Figure 2. Expected progeny differences (EPDs) for pounds of lean in a 185 pound carcass for Duroc pigs born between 1985 and 2006.
(From: http://www.ansc.purdue.edu/stages/).

The use of EPDs for the selection of bulls and replacement females is well accepted throughout the dairy and beef cattle industries in both purebred and commercial herds. All dairy bulls in artificial insemination studs carry detailed and very accurate estimates of genetic value, and it is almost impossible to sell a commercial or purebred beef bull without above average EPDs. A majority of boars going into commercial swine operations come from private breeding companies such as PIC. While these companies do not publish EPDs on the animals they are selling, the companies are using EPDs and molecular genetics to select their parent stock in an attempt to stay ahead of their competition in the production of genetically superior breeding stock. Many of the purebred swine producers who still have a commercial boar market have adopted the use of EPDs in their selection programs in order to compete with the private breeding companies.

Genetic Improvement in the U.S. Sheep Population

The sheep industry in the U.S. lags behind dairy cattle, beef cattle, and swine in the adoption of genetic improvement tools and as a result, has slower rates of genetic improvement for traits of economic importance than these other species. Primary selection emphasis in most purebred flocks is on visual appraisal with some attention paid to limited production records such as type of birth of the animal.

Conformation is a highly heritable trait so it is possible to make reasonable genetic progress for body shape, and the main selection trend among sheep in the U.S. has been for taller animals. However, there has been little genetic improvement in litter size, growth rate, feed efficiency, or wool production and quality through selection. There have been some improvements in these traits, but they largely have been through the introduction of new breeds with superior performance for these traits and crossbreeding, and not through selection.

The slow adoption of technology in the U.S. sheep industry, including genetic technology, may be due to the fact that sheep are often found in very small flocks that return very little net income to their owners. In 2002, 92% of the flocks were composed of fewer than 100 sheep (http://usda.mannlib.cornell.edu/usda/nass/SheeGoat//2000s/2003/SheeGoat-01-31-2003.pdf). Many of these small sheep flocks are maintained as show flocks, 4-H projects, or hobbies. Since the flock is not maintained as a source of income, there is little incentive to invest in technology that will improve the efficiency of production and net income.

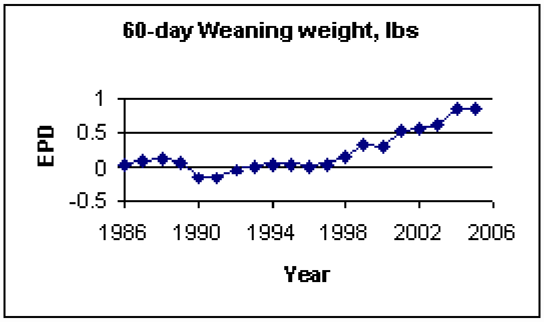
Even though the U.S. sheep industry is characterized by small flocks where economic returns are not of primary importance, there exist larger sheep producers who depend upon all or part of their incomes from sheep and some smaller sheep producers who are sincerely concerned about the genetic improvement of their breed and the national flock. What genetic tools are available to these producers with a vested interest in the sheep industry?

Sheep EPDs. The same statistical technology used to calculate EPDs in the dairy cattle, beef cattle, and swine industries is available to the sheep industry through the National Sheep Improvement Program (NSIP). NSIP can produce EPDs for fleece weight, staple length, fleece grade, direct weaning weight, indirect weaning weight (milk), postweaning weight, and number of lambs born. In addition some breeds have developed specific EPDs for traits with special importance to their breed such as ewe productivity (weight of lamb weaned per ewe lambing) and fecal egg count (indicator of internal parasite resistance). Access to NSIP is through a sheep breed association or a group of breeders of a particular breed who will take responsibility for collection of the performance data, put it in a form needed by NSIP, and submit it to NSIP for analysis. The earliest users of NSIP were the Targhee, Suffolk, and Polypay breeds. More recently, the Dorset, Hampshire, Katahdin, Rambouillet, Columbia, and Romney breeds have joined NSIP. In 2005-2006, records from approximately 110 flocks, 7,000 ewes, and 11,000 lambs were processed by NSIP across all breeds. The Katahdin breed was represented with the most flocks (34) and four of the breeds had 5 or fewer flocks represented (Hampshire, Rambouillet, Columbia, and Romney) (Dr. David Notter, personal communication). These numbers indicate that NSIP is not widely used by the U.S. sheep industry.

Flocks enrolled in NSIP have shown positive genetic changes over time. As an example, Figure 3 presents the EPDs for 60 day and 120 day weights from 1986 to 2005 of Polypay sheep enrolled in NSIP. If changes in EBVs (2 x EPD) are considered, Polypay lambs born in 2005 were expected to be about 2 pounds heavier at 60 days and 4 pounds heavier at 120 days than Polypay lambs born in 1986 due to genetic selection. Most of this gain came in the past 8 years; probably because the breeders had more confidence in the use of EPDs when making selection decisions in later years after they had some experience in their use and value.

Purebred breeders interested in joining NSIP should contact their NSIP coordinator through their breed association. If your breed is not yet enrolled in NSIP, contact NSIP directly to determine how your breed can join at:

Jim Morgan
NSIP President
Phone: 479-444-6075
Fax: 479-444-8441
email: info@nsip.org
web site: http://www.nsip.org/



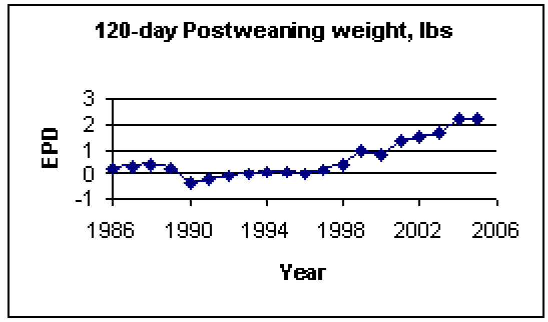


Figure 3. EPDs for 60 day weight and 120 day weight of for Polypay lambs enrolled in the National Sheep Improvement Program and born between 1986 and 2005. (From: http://www.members.aol.com/ovineepd/ovineepd.htm).

At least one U.S. sheep breed association and a few individual U.S. sheep breeders have joined the Australian sheep genetic evaluation system, LambPlan. Further information on LambPlan can be accessed at:

LambPlan, Sheep Genetics Australia
P.O. Box U254
University of New England
Armidale, NSW 2351
AUSTRALIA
Phone: (02) 6773 2948
Fax: (02) 6773 2707
http://www.sheepgenetics.org.au/lambplan/

A major advantage of the EPDs generated by both NSIP and LambPlan is that the EPDs are comparable across flocks within a breed as long as there are a sufficient number of genetic ties among flocks (related animals in different flocks). These across-flock genetic evaluations allow breeders to compare their genetic progress relative to other breeders, and it allows ram buyers the ability to fairly compare rams in different flocks on genetic values before a purchasing decision is made. The only negatives about NSIP and LambPlan is that not all breeds participate, and even among participating breeds, a minority of breeders participate. Greater participation in programs like NSIP and LambPlan is needed in order for the entire U.S. sheep industry to benefit from the genetic tools of EBVs and EPDs.

Badger Sheep Improvement Program (BSIP). The first on-the-farm performance recording program for sheep in the U.S. was started in Wisconsin in 1950 by Dr. Arthur B. Chapman, an animal geneticist in the Department of Meat and Animal Science at the University of Wisconsin, and was known as the Wisconsin Sheep Improvement Program (WSIP). The WSIP was operated by UW Cooperative Extension for over 35 years and then was discontinued when NSIP was developed. However, due to a demand for an on-the-farm performance testing program that was less costly and, in some people's opinion, less complicated than NSIP, WSIP was resurrected and renamed BSIP and operated privately as a service to Wisconsin sheep producers by Rudy Erickson and his family in the 1990's.

The BSIP provides each ewe and lamb in the flock an index based upon 90 day lamb weights, type of birth of the lamb, and ewe fleece weight (optional). It also produces a predicted producing ability of ewes in the next lambing season based upon their average production in previous lambing seasons. These indexes are only comparable within a flock, so across-flock comparisons can not be made. However, the BSIP indexes are an excellent tool for selection and culling decisions of animals born and raised within the flock.

An advantage of BSIP over NSIP is that individual producers, both purebred and commercial, can submit data directly to BSIP without belonging to a formal group as required with NSIP. BSIP is ideally suited for the commercial sheep producer. A commercial producer can use the BSIP indexes to cull the ewe flock and to select replacement ewe lambs. The commercial producer, ideally, would then purchase rams based upon their EPDs generated by NSIP in order to obtain rams with the highest possible EPDs across a number of flocks enrolled in NSIP. Most of the genetic improvement in the commercial flock would come from the selection of rams with NSIP EPDs and a minority of the genetic improvement would come from the selection of replacement ewe lambs on indexes from BSIP.

Further information on BSIP can be obtained from:

Rudy Erickson
633 Hwy 128
Wilson, WI 54027
715-772-4798
rumarfarm@wwt.net

Wisconsin Ram Test Station. Central test stations of swine, beef cattle, and sheep have existed in the U.S. for approximately 60 years. The basic operation is to bring young males from several farms to a central facility where they are fed and managed under the same environmental conditions. Growth rate while at the central test station is the performance record that is common to all test stations across species. The premise behind the central test station is to standardize environmental effects so that performance differences among males from different farms are more indicative of genetic differences.

The Wisconsin Ram Test Station (WRTS) was started in the late 1960's at the UW-Madison, Agricultural Research Station. Within a few years, it moved from UW-Madison facilities to locations on private farms in Wisconsin. The WRTS currently is located at Nelson Crest Farm, Janesville, WI and is sponsored by the Wisconsin Sheep Breeders Cooperative with assistance from the UW-Madison Department of Animal Sciences and UW-Extension, Cooperative Extension.

Three tests are conducted each year; one each for January-, February-, and March-born ram lambs. Ram lambs arrive at the station when they are approximately 60 days of age. They have a one-week adjustment period and then are on official test for 8 weeks. Performance data collected or calculated include average daily gain, scrotal circumference, ultrasound measurement of loin eye area and fat thickness, estimated percentage of boneless closely trimmed retail cuts in the carcass, and estimated lean gain per day. Fleece diameter can be determined for an additional cost.

The WRTS provides an excellent opportunity for breeders to compare rams from their breeding program with rams produced by other breeders. It also provides a source of rams for buyers where comparative data is available on several rams of several breeds. Additional information on the WRTS can be obtained from the test station manager:

Nils E. Nelson
10919 W. Mineral Point Rd.
Janesville, WI 53548-9444
608-876-6928
scrapbooknan@earthlink.net

Molecular Genetics and DNA Testing. A DNA map of the sheep genome constructed by an international group of scientists from Australia, France, Kenya, New Zealand, the United Kingdom, and the U.S. was announced in November 2006. While having the DNA map of the sheep is an important step, there is still much research to be done before DNA testing can be an integral tool for the selection of sheep with improved levels of performance. With the new sheep DNA map, we know more about the physical order of the components of DNA in each of the 27 pairs of chromosomes. However, we still have relatively little knowledge about which of these DNA fragments are the genes that control performance traits. It is estimated that we currently have knowledge of the location in the genome of about 200 functional genes and only a handful of these functional genes have been related to performance traits. However, every year will bring new results from research where a specific piece of DNA on a specific chromosome will be identified as a gene that has a major effect on another performance trait in sheep. Such information will allow breeders to select animals on the basis of a DNA test at a young age with a high degree of accuracy for desirable genes.

We already have some examples of the application of molecular genetics and DNA testing for the improvement of sheep performance for scrapie resistance, spider syndrome, and litter size.

Scrapie Resistance. Scrapie is an infectious disease of sheep that attacks the central nervous system and is always fatal. It is a type of transmissible encephalopathy found in a number of animal species including humans. Upon necropsy, infected animals will have holes or vacuoles in the tissue of the brain. Scrapie has a very long incubation period of several months to a few years so the disease is seldom seen in animals less than 1½ years of age. While scrapie affects relatively few sheep, it is a disease of major concern to Federal animal health officials because it is related to BSE (mad cow disease). Consumption of meat from BSE-infected cattle has been implicated as a cause of an encephalopathy in humans (new variant CJD). Presence of the disease in North America limits the opportunities for breeding sheep exports.

Certain alleles at the prion protein locus have an effect on scrapie susceptibility. Differences in amino acids of the prion protein in at least two positions or codons appear to have an effect on susceptibility of sheep to scrapie. At the 136 codon, two amino acids have been identified in sheep populations: alanine (A) decreases susceptibility and valine (V) increases susceptibility to scrapie. At the 171 codon, the amino acid arginine (R) is associated with decreased susceptibility, and the amino acid glutamine (Q) is associated with increased susceptibility to scrapie. Therefore, animals that are homozygous for alanine at codon 136 (AA) and homozygous for arginine at codon 171 (RR) would be the most resistant to scrapie and would produce progeny with the greatest probability of resistance.

Spider Syndrome. Spider syndrome is a condition that was first reported in Suffolk and Suffolk crossbred sheep in the United States in the popular press and the scientific literature in the mid-1980's. Spider lambs have severe bone deformities throughout the entire skeleton that are manifested at birth or within 30 days of age. The most noticeable condition is an outward bending of the front legs from the knees, with many lambs also having a crooked spine in the thoracic area and a marked Roman nose. Spider syndrome is due to a single allele (**n**) that is completely recessive to the dominant allele (**N**) for normal skeletal development. Sheep that are homozygous for the spider allele (**nn**) exhibit spider syndrome and are so deformed that no producer would retain one for breeding, and even if retained, the probability of a successful mating would be very low. Therefore, spider syndrome lambs almost always result from mating two normal appearing, but heterozygous, individuals. The Spider locus is found on Sheep Chromosome 6. There is a DNA test that can identify the presence or absence of the spider gene and this test is used to differentiate between normal appearing animals that are carriers (Nn) or non-carriers (NN) of the spider syndrome gene.

Booroola Gene for Litter Size. The Booroola Merino is a highly prolific strain of Australian Merino that was discovered and propagated by the Seears brothers on their "Booroola" property in New South Wales, Australia and later studied by the Australian government research organization, CSIRO. Their exceptional reproductive performance is due to a major allele, denoted as Fec^{B}. Each copy of the allele has been found to increase ovulation rate by approximately 1.5 ova. The related increase in litter size is partially dominant. The first copy of the allele increases litter size by .7 to .9 lambs, and the second copy results in an additional .4 to .5 lambs. Therefore, if ewes in a flock of sheep without the Fec^{B} allele (genotype = Fec^{++}) had an average litter size of 1.50, ewes in the same flock that were heterozygous (genotype = Fec^{B+}) or homozygous (Fec^{BB}) for the Booroola allele would be expected to have an average litter size of approximately 2.30 and 2.75, respectively. The Fec locus is located on Sheep Chromosome 6, the Fec^{B} allele was sequenced in 2002, and there is a DNA test for the Fec^{B} allele. The DNA test allows breeders to differentiate among FEC^{++}, Fec^{B+}, and Fec^{BB} ewe and ram lambs prior to them reaching sexual maturity.

Callipyge. In 1983, a Dorset ram exhibiting an abnormally large amount of muscling (muscle hypertrophy) was identified in a flock in Oklahoma. It was reported that the muscle hypertrophy of this ram was passed to some of his progeny, and descendants with the trait passed it to some of their progeny in later generations. These observations suggested the muscle hypertrophy was of genetic origin. Subsequent studies have shown that the callipyge condition is inherited. The callipyge allele has been mapped to chromosome 18 of sheep, and the gene was sequenced in 2002. It is possible to DNA test individuals for presence of the gene, but no company has offered the test commercially.

DNA Testing. Commercial DNA tests for the spider and scrapie alleles have been developed and are available in the U.S. A large proportion of the black-faced purebred sheep in the U.S.

are tested for the spider and scrapie alleles, and genotypes for these alleles have a strong influence on the price paid for breeding animals, especially rams. The DNA test for the Booroola allele is not offered commercially in the U.S. but is available in New Zealand. The DNA is generally extracted from a blood sample. The following labs conduct these DNA tests and should be contacted for blood sampling procedures and pricing information. Cost of a DNA test for one gene in the U.S. will range from $12 to $20 per sheep.

Scrapie resistance gene testing: A list of approved labs for official USDA testing can be found at (http://www.aphis.usda.gov/vs/nahps/scrapie/). Following are two labs from that list:

GenMARK
3591 Anderson Street, Suite 104
Madison, WI 53704
Contact: Karen Van Beek
Phone: 877-766-3446 ext 0
Toll-Free: 877-766-3446
Fax: 608-310-9512
Web: www.genmarkag.com

GeneCheck, Inc.
1629 Blue Spruce Drive
Suite 106
Ft. Collins, CO 80524
Contact: Ms. Tresea Mulqueen
Phone: 800-822-6740
Fax: 970-472-9956
Web: www.genecheck.com

Spider gene testing: The two labs listed above also conduct DNA test for the spider gene.

Booroola gene testing:

GenomNZ
AgResearch, Invermay Agricultural Centre
Private Bag 50034
Mosgiel, New Zealand
Contact: Rayna Anderson
phone: 64-3-489-9124
fax: 64-3-489-9032
email: rayna.anderson@agresearch.co.nz
website: http://genomnz.co.nz

Summary

Selection of sheep on the basis of a DNA test will become an important tool for genetic improvement in the future, and it eventually may become the predominant tool. However, there are too few genes that currently can be identified by a DNA test for it to have a large impact on genetic improvement of sheep now, especially for the performance traits of lamb, wool, and milk production. Sheep breeders should take a lesson from the cattle and swine industries where selection on estimates of genetic value based on measures of performance of an individual and its relatives (EBVs and EPDs) have resulted in large and consistent increases in performance over time. The EBV/EPD tools are on the “shelf” and awaiting use by the U.S. sheep industry.