

regulatory instruments such as zonation, institutional ownership changes, empowerment, awareness and education are mentioned as instruments of change. In general it is accepted that the rural poor and landless, especially women, could benefit from an intensification of animal agriculture, and the 'Livestock Revolution' could contribute to the alleviation of poverty. However, rapid industrialization supported

by widespread subsidies for large-scale credit and land use could harm this mechanism of income and asset generation by the poor. The goal of this presentation is to address some technologies available for the different production systems throughout the world's climate zones.

Key Words: Sustainable animal agriculture, World trade, Farm policy

Breeding and Genetics: Beef, Sheep & Swine Breeding

617 Connectedness in Targhee and Suffolk flocks participating in the U.S. National Sheep Improvement Program. L. A. Kuehn*, R. M. Lewis, and D. R. Notter, *Virginia Polytechnic Institute and State University, Blacksburg.*

Connectedness among animals in separate flocks reduces risks associated with the across-flock comparison of EBV. The objective in this study was to assess levels of connectedness in the genetic evaluation of weaning weight among Targhee and Suffolk flocks participating in the U.S. National Sheep Improvement Program (NSIP). Among flocks currently participating in NSIP, a total of 25,404 weaning weight and 35,794 pedigree records were available for 16 Targhee flocks, and 14,017 weaning weight and 18,311 pedigree records were available for 24 Suffolk flocks. Connectedness was measured using two different methods. First, numbers of progeny with recorded weaning weights from linking sires (defined as sires with progeny in multiple flocks or sires born in one flock with progeny in another flock) were counted. Second, connectedness was measured by calculating the average prediction error correlation of mean flock EBV (flock r_{ij}). Benchmarks for flock r_{ij} were established with 0.10 and 0.05 representing low and moderate risk of comparing EBV among flocks, respectively. From 1995 through 2004, 44% of Targhee lambs but only 23% of Suffolk lambs with weaning weights were born to linking sires. Average flock r_{ij} were 0.10, 0.19, and 0.28 and 0.02, 0.02, and 0.04 in 1990, 1995, and 2005 among Targhee and Suffolk flocks that participated in NSIP in all 3 yr. Among all active flocks in 2005, flock r_{ij} averaged 0.13 in Targhee and 0.03 in Suffolk. Hierarchical clustering of flocks based on flock r_{ij} revealed that all active Targhee flocks connect at a level near or above 0.10. In Suffolk flocks, two distinct clusters had formed in which connectedness was relatively high within each cluster (flock r_{ij} near 0.10) but near zero between clusters. Risk in comparing EBV among flocks in Targhee is low; however, caution should be exercised when comparing EBV between Suffolk flocks from different clusters.

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Key Words: Connectedness, Prediction error, Sheep

618 Role of sire referencing schemes in terminal sire sheep to improve carcass quality in crossbred lambs. R. M. Lewis^{1,2}, A. M. van Heelsum², W. Haresign³, M. H. Davies⁴, R. Roehe², L. Bünger², and G. Simm², ¹*Virginia Polytechnic Institute and State University, Blacksburg*, ²*Scottish Agricultural College, Edinburgh, Scotland, UK*, ³*University of Wales, Aberystwyth, Wales, UK*, ⁴*ADAS Rosemaund, Preston Wynne, England, UK*.

In sire referencing schemes (SRS) genetic links are created among flocks by sharing rams. These links allow for across-flock genetic

evaluations creating a larger pool of candidates for selection and quicker genetic progress. In the early 1990s, SRS were introduced in the Charollais, Suffolk and Texel breeds in the UK resulting in gains near 2% per annum in a Lean Growth Index (LGI). In this study, the consequence of that gain on carcass traits of terminal sire cross lambs was tested. Thirty rams from SRS in each breed, half high and half low in LGI, were mated to 4,800 crossbred ewes between 1999 and 2002. Mean LGI differed by 5 s.d. between index groups. At target finish of 11% subcutaneous fat (SCF), the 6,584 lambs were weighed and slaughtered. Cold carcass weights were recorded. The right side of 978 carcasses was processed into retail cuts including leg steaks, cutlets and chops. A linear mixed-model was fitted using REML with year, sire index category and breed, sex, birth-rearing rank, dam age and, as a covariate, estimated SCF as fixed effects. Rearing dam and residual were random effects. A sire index category by breed interaction was found ($P < 0.05$) but did not cause re-ranking. Offspring of high as compared to low index sires weighed 1.1 ± 0.10 kg more at finish yet were no older, with 0.56 ± 0.047 kg heavier cold carcass weights. High index lambs yielded 0.47 ± 0.090 kg more saleable meat with increased weights of leg steaks, cutlets and chops ($P < 0.001$). In 2004, the average value per kg carcass was £2.62 (US\$4.60) in the UK. If over its lifetime, a ram sires 240 reared lambs and each lamb produces 0.56 kg extra carcass weight, a high index ram would earn an extra £353 (US\$620). In the UK, where roughly 10.1 million terminal sire cross lambs are marketed annually, this could generate £15 million (US\$26.2 million) more income. Clearly, within-SRS selection on LGI results in crossbred lambs yielding more saleable lean meat allowing substantially higher market returns.

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Key Words: Sire referencing, Carcass quality, Crossbred lamb

619 Genetic factors influencing different body weights of Thalli sheep in Pakistan. P. Akhtar*, A. Hussain, S. Ali, and M. Younas, *University of Agriculture, Faisalabad, Punjab, Pakistan.*

Thalli is the native sheep breed of Thalli area of the Punjab, Pakistan. Data on 17030 birth records of 5421 Thalli sheep maintained at Livestock Experiment Station, Rakh Ghulaman, district Bhakkar during 1975-2004 were utilized in the present study with the objective to evaluate the performance of Thalli sheep in Pakistan. The data were analyzed using GLM procedure of SAS to study the influence of environmental sources of variation on various performance traits. The genetic parameter estimation was done using DFREML 1997 procedure fitting an Individual Animal Model. The average birth weight was 4.11 ± 0.82 kg, which was significantly affected by year, type of

birth, sex and age of the dam and season of birth had non-significant effect on birth weight. The average 60- and 90-day weights were 11.58 ± 3.57 and 14.92 ± 4.56 kg, respectively, which were affected by year, season of birth, birth weight, type of birth (60 days weight) and sex (60 days weight) and age of the dam had non-significant effect on 60 days weight. Age of the dam significantly affected 90-day weight. Sex and type of birth had non-significant effect on 90 days weight. The weaning weight averaged 18.95 ± 4.12 kg and was affected by year and season of birth, sex of lamb born. The effect of type of birth, birth weight and age of dam on weaning weight were non significant. The direct heritability estimate of birth weight was 0.067 ± 0.01 . The heritability estimates for 60- and 90-day weight were 0.116 ± 0.01 and 0.18 ± 0.01 , respectively. The heritability estimate for weaning weight was 0.03 ± 0.11 . Genetic correlation between birth weight and weaning weight was -0.045 ± 0.003 which is negatively low. The low estimates of heritability for various performance traits indicated the presence of less additive genetic variance and large environmental variances. Hence improvement in the traits through selection may be limited.

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Key Words: Genetic parameters, Body weights, Thalli Sheep

620 Estimation of breeding values of different body weights of Thalli sheep in Pakistan. A. Hussain, P. Akhtar*, S. Ali, and M. Younas, *University of Agriculture, Faisalabad, Punjab, Pakistan.*

Data on 17030 records of 5421 Thalli ewes maintained at LES, Rakh Ghulaman, Pakistan during 1975-2004 were utilized to estimate the breeding values of different economically important traits by GLM procedure of SAS to see the influence of environmental sources of variation and the genetic parameter estimation was done using REML procedure. Breeding values for various performance traits were estimated using BLUP procedure by DFREML 1997. The direct heritability estimates of birth, weaning weight, 180-day, 270-day weights and yearling weight were 0.067 ± 0.01 and 0.03 ± 0.11 , 0.07 ± 0.01 , 0.083 ± 0.01 and 0.072 ± 0.01 , respectively. The direct heritability estimates of pre- and post-weaning gains were $0.07 \pm .01$ and 0.06 ± 0.01 , respectively. These estimates are low as reported by other workers. The estimated breeding values for rams ranged from -0.447 to 0.216 for birth weight; -1.512 to 2.859 for weaning weight; -1.357 to 2.404 for 180 days weight; -1.752 to 2.621 for 270 days weight; -1.686 to 2.089 for yearling weight; -0.0144 to 0.0255 for pre-weaning gain and -0.0045 to 0.0062 for post-weaning gain. Breeding values for ewes ranged from -0.368 to 0.0302 for birth weight; -2.618 to 1.677 for 60 days weight; -5.227 to 3.209 for 90 days weight; -1.799 to 2.421 for weaning weight; -1.656 to 2.069 for 180 days weight; -1.662 to 2.407 for 270 days weight; -1.144 to 2.261 for yearling weight; -0.0142 to 0.0211 for pre-weaning gain and -0.0031 to 0.0061 for post-weaning gain. No specific genetic trend was observed for growth traits during this period. There were wide fluctuations among the least squares means for estimated breeding values. The genetic trend remained oscillating around the x-axis indicating no net genetic change for growth traits. The genetic trend for growth traits was close to zero indicating that the breeding program in the past was ineffective and almost similar trend will be expected in the presence of random mating.

Acknowledgement: to Livestock and Dairy Development Department for data and Higher Education Commission, Govt. of Pakistan for expected travel grant.

Key Words: Estimated breeding values, Body weights, Thalli Sheep

621 Performance traits of 1980 vs. 2005 pigs when fed 1980 or 2005 feeding programs. J. S. Fix*, D. J. Hanson, E. van Heugten, J. P. Cassady, and M. T. See, *North Carolina State University, Raleigh.*

The objective of this study was to assess changes over 25 years in pig performance traits. Pigs (n=162) representative of the current commercial industry were compared to pigs representative of the commercial industry 25 years ago. The 1980 genetic line was produced from dams selected to minimize genetic improvement and frozen semen from boars available in 1980. Pigs within sex, farrowing group, and genetic line were randomly assigned to a feeding program and placed 3 per pen (n=54) at an initial wt of 7 ± 0.4 kg. The 2005 feeding program included a 7 phase feeding program (Lysine from 1.51 to 0.73% and ME from 3428 to 3651 Kcal/kg), pelleted diets, and current diet formulation. The 1980 feeding program consisted of 4 meal diets (Lysine from 1.05 to 0.62% and ME from 3262 to 3317 Kcal/kg) based on formulations from the 1978 Pork Industry Handbook. Individual weights and pen feed consumption were measured every 2 wk. Pigs were slaughtered on a weekly basis when average pen weight exceeded 116 kg. Pigs from the 2005 genetic line were slaughtered 11 days sooner (162 vs. 173 d; $P < 0.05$). Pigs fed the 2005 feeding program reached final BW 12 days sooner (162 vs. 174 d; $P < 0.01$). A genetic line by feeding program interaction ($P < 0.05$) was observed for ADG where 2005 pigs and 1980 pigs showed 12% and 6% increases in ADG, respectively, when comparing 1980 to 2005 feeding programs. Pigs from 2005 genetics fed the 2005 program had the greatest ADG (885 g/d), while pigs from 1980 genetics fed the 1980 program gained the least per day (753 g/d). Pigs from 2005 genetic line fed the 1980 program (789 g/d) did not differ in ADG from 1980 pigs fed the 2005 program (799 g/d). Pigs fed the 2005 program showed 10% ($P < 0.01$) less ADFI than those fed the 1980 program, resulting in a 21% improvement ($P < 0.01$) in G:F. 2005 pigs were more efficient than pigs from the 1980 genetic line (0.41 vs. 0.37; $P < 0.01$). These results demonstrate that substantial improvements have been made in growth and efficiency over the past 25 years due to advances in both genetics and feeding programs.

Key Words: Pigs, Genetics, Nutrition

622 Some hybrid beef performances (B.taurus x B. indicus) in tropical Malaysia. A. Aman*¹, O. Ahmad², and S. Othman², ¹*International Islamic University Malaysia, Jalan Gombak, Kuala Lumpur, Malaysia,* ²*MARDI, Kuala Lumpur, Malaysia.*

Malaysian indigenous cattle (Kedah-Kelantan- KK) were bred by artificial insemination with semen from Limousin, Simmental and Charolais. The Kedah Kelantan breed is small, prolific, slow growing (ADG) and resistant to heat. By crossing KK with temperate cattle, growth (on grass and feedlot) and reproduction increased. The Charolais-Kedah Kelantan (CK) crossbred was heaviest, followed by Simmental-Kedah Kelantan (SK), and Limousin-Kedah Kelantan (LK). The CK crossbred was superior to KK by 41% at birth, 48% at weaning, 55% at yearling and 72% at 20 months. In feedlot CK was grew most rapidly (815 g/day), followed by SK (773 g/day) and

LK (750 g/day) and KK (528g/day). CK and LK crossbred calves were more efficient in converting feed to meat (6 kg. feed/kg meat). Crossbred heifers conceived earlier than KK. The crossbred calves had greater gains and better carcass quality than KK.

Key Words: Crossbred, B.indicus X B.taurus, Beef cattle

623 Use of a mathematical computer model to predict feed intake: Genetic parameters between observed and predicted values, and relationships with other traits. D. P. Kirschten^{*1}, E. J. Pollak¹, L. O. Tedeschi², D. G. Fox¹, B. Bourg², and G. E. Carstens², ¹Cornell University, Ithaca, NY, ²Texas A&M University, College Station.

The objectives of this study were to investigate the suitability of using DM required (DMR) as predicted by the Cornell Value Discovery System (CVDS) in genetic evaluations and to determine relationships between model predicted and individual DMI and other traits. Observed feed intake (F_{io}) records during the finishing phase were available from 115 individually fed Santa Gertrudis steers sired by 20 bulls. The data also contained records of ADG and mean BW (MW), carcass measurements (ribeye area, fat thickness, and marbling) and real-time ultrasound estimates (ribeye area, fat thickness, and marbling). These inputs were used in the CVDS model to predict DMR. For the purposes of parameter estimation, CVDS predictions of DMR using ultrasound (DMR_{us}) and carcass traits (DMR_{ca}) were considered surrogates for F_{io}. Genetic parameters were estimated with REML, using a sire model with fixed effects of WW contemporary group and feedlot pen. Phenotypic correlations between F_{io} and DMR_{us}, F_{io} and DMR_{ca} and DMR_{us} and DMR_{ca} were 0.78, 0.79, and 0.99, respectively. Heritabilities for F_{io}, DMR_{us} and DMR_{ca} were 0.09, 0.32 and 0.35, respectively. Genetic correlations between F_{io} and DMR_{us}, F_{io} and DMR_{ca}, and DMR_{us} and DMR_{ca} were 0.98, 0.98, and 0.99, respectively. Sire BV rank correlations were calculated for F_{io}, DMR_{us} and DMR_{ca}. BV rank correlations among F_{io}, DMR_{us} and DMR_{ca} were all 0.99. Residual feed intake (RFI) was calculated using F_{io}, metabolic MW and ADG. Phenotypic correlations between RFI and F_{io}, MW, and ADG were 0.21, 0.09, and 0.01, respectively. Heritability for RFI was 0.18. Genetic correlations between RFI and F_{io}, MW, and ADG were -0.88, -0.48, and 0.00, respectively. The strong genetic relationships between F_{io}, DMR_{us} and DMR_{ca} and minimal re-ranking of sires suggested that predicted DMR_{us} and DMR_{ca} may be used in place of F_{io} in genetic evaluations.

Key Words: Feed intake, Mathematical models, Beef cattle

624 Examination of feed efficiency traits with post-weaning growth and carcass traits in central test bulls. G. S. Hecht^{*} and L. A. Kriese-Anderson, Auburn University, Auburn, AL.

Twenty-seven years of performance test data from the Auburn University bull test was examined to determine heritabilities and genetic correlations among measures of feed efficiency, growth rate and ultrasound carcass attributes. Beginning in 1977, individual feed intake was measured on a maximum of 96 bulls per year using a Calan™ gate feeding system. Data on 2,180 bulls was collected from 1977 to 2004, among nine different breeds: Angus (n = 857); Brangus (n = 41); Charolais (n = 380); Gelbvieh (n = 103); Hereford (n = 12); Limousin (n = 106); Polled Hereford (n = 180); Santa Gertrudis (n = 106); and Simmental (n = 395). A sire-maternal grandsire model and MTDFREML was used to analyze the data. Fixed effects included test length (84, 96 and 140 days), breed and year. Covariates of age or weight were also included in the model. A⁻¹ included 3,739 animals.

Two-trait MTDFREML analyses were performed with results averaged over each trait. Traits included average daily gain (ADG) (n = 2,005; mean = 1.72 kg/d; h² = 0.58), weight per day of age (WDA) (n = 2,005; mean = 1.46 kg; h² = 0.25), feed efficiency (FE = gain to feed (G:F)) (n = 2,007; mean = 3.42 kg; h² = 0.53), fat thickness (FT) (n = 1,836; mean = 0.80 cm; h² = 0.54), intramuscular fat (IMF) (n = 391; mean = 3.20%; h² = 0.35), ribeye area (REA) (n = 927; mean = 100.00 sq cm; h² = 0.21), total gain (n = 2,005; mean = 204.74 kg; h² = 0.54), total feed intake (n = 2,007; mean = 1,534.8 kg), and residual feed intake (RFI) (n = 2,015; mean = 1.04 kg/d; h² = 0.36). Heritability estimates fall within published estimates and suggest genetic selection would be successful. Genetic correlations between FE and total gain, ADG, WDA, IMF, and REA were -0.62, -0.66, -0.16, 0.40, and -0.58, respectively with age as covariate. Genetic correlations between RFI and FT, IMF, REA, WDA, and ADG were 0.09, 0.50, -0.47, 0.06, and 0.04, respectively with age as covariate. RFI continues to show little correlation with ADG indicating cattle can be selected for improved feed efficiency without affecting growth rates or mature size.

Key Words: Feed efficiency, Performance testing, Post-weaning growth and carcass

625 Significance of cytoplasmic origin on body composition in Limousin cattle. M. M. Rolf¹, D. W. Moser^{*1}, and L. R. Hyde², ¹Kansas State University, Manhattan, ²North American Limousin Foundation, Englewood, CO.

Ultrasound carcass measurements were obtained on 7,031 yearling Limousin bulls and heifers and merged with a pedigree file containing 24,684 animals traced back to the original foundation dam of record. Approximately 25% of the measured animals traced back to a Limousin founder dam, and were categorized as being from a Limousin cytoplasmic line (LCL). The remaining records traced back to non-Limousin founder dam, and were categorized as being from a non-Limousin cytoplasmic line (NCL). The LCL versus NCL effects were evaluated using an animal model with contemporary group as a fixed effect and cytoplasmic line and animal as random effects on scan weight, rib fat, percent intramuscular fat and ribeye area. Results from MTDFREML showed that cytoplasmic line had virtually no effect on scan weight. The proportion of phenotypic variance explained by cytoplasmic line for ribeye area and percent intramuscular fat were 0.51% and 0.77%, respectively. LCL calves had .8949 sq cm larger ribeyes and .0649 percent less IMF than did NCL calves. Cytoplasmic line explained 2.2% of phenotypic variance for rib fat, and LCL calves had .0351 cm less rib fat than did the NCL calves. The magnitude of cytoplasmic line effects is small enough as to not bias current BLUP EPD predictions when such effects are ignored.

Key Words: Beef cattle, Carcass traits, Cytoplasmic origin

626 Association of microsatellite markers on bovine chromosomes 5 and 6 with carcass traits. A. M. Sanborn^{*1}, E. Casas², and A. J. M. Rosa¹, ¹South Dakota State University, Brookings, ²U.S. Meat Animal Research Center, Clay Center, NE.

The objective was to identify chromosomal regions associated with phenotypic variation in carcass traits in three crossbred families. Three half-sib families were developed from crossbred sires. Families 1, 2, and 3 comprised 29, 25, and 77 offspring, respectively (N=131). The genetic background of the sires, dams, and offspring was 1/3 Angus, 1/3 Hereford, 1/3 Simmental. Animals were housed at the South Dakota State University Beef Breeding Unit, Brookings, SD.

Calves were born between 2001 and 2004. Carcass traits collected were finished weight, hot carcass weight, marbling score, and longissimus muscle area. Microsatellite markers on chromosomes 5 and 6 were selected based on their relative position. Markers used on chromosome 5 were BM6026, RM103, BM321, RM084, BMS1216, BM315, and BM597. Markers used on chromosome 6 were ILSTS093, ILSTS090, BM1329, BMS518, ILSTS035, BM8124, and BMC4203. Individual marker analysis was conducted because homozygosity of the bulls for some markers hindered interval mapping. Family 1 exhibited allelic effects for finished weight, hot carcass weight, and marbling score on chromosome 5. Markers RM103 and BM321 were associated with finished ($P < 0.01$) and carcass ($P < 0.05$) weights. An association with marbling score was identified with BM6026 ($P < 0.05$), RM103 ($P < 0.01$), and BM321 ($P < 0.01$). On chromosome 6, BMC4203 was associated with longissimus muscle area in family 1 ($P < 0.05$) and family 2 ($P < 0.001$). No association was detected ($P > 0.05$) on family 3. Association of these markers with carcass traits on chromosomes 5 and 6 are consistent with findings from independent studies.

Key Words: Markers, Bovine, Carcass

627 Associations between single nucleotide polymorphism in the Dgat2 gene and several economic traits in commercial feedlot steers.

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DGAT2 was found to be a new diacylglycerol acyltransferase gene family in 2001. It plays more important role in mammalian triglyceride metabolism than DGAT1 does, but associations between DGAT2 and beef cattle economic merits have not been reported. The objective of this study was to try to find single nucleotide polymorphisms (SNP) with PCR-SSCP method in bovine DGAT2 gene and evaluate the

association of that with carcass and meat quality traits from 157 commercial feedlot steers distributing to 3 Chinese local breeds and 4 cross breeds. In this study, 15 SNP have been discovered in the Dgat2 Intron3 (GenBank Accession No. AY589091) at positions 65, 128, 178, 210, 241, 255, 270, 312, 328, 334, 365, 366, 371, 415 and 437 (Named as their position in PCR amplified fragments). Only 7 of them were analyzed (128, 178, 241, 270, 312, 328 and 371), because three groups (65-128-255, 178-210-365 and 241-334-366) were in complete linkage disequilibrium within group, SNP at position 415bp is a mutation of deletion and that at position 437bp is a null mutation. These data were analyzed using two different models, 1) genotype, and 2) allele substitution. Contemporary groups were fit as a fixed effect and formed from feed group in feedlot plus breed type. Significant statistics are listed in table 1. An initial conclusion was that associations exist between DGAT2 gene and several beef cattle economic traits that concern with carcass fat. For the small sample size of this study, proposal is further effort should be required to validate these findings in larger populations.

Table 1. List of significant statistics

Model	Trait ¹	SNP	LSM or regression coefficient estimates	F	Pr>F		
Genotype	REA	128	AA: 62.9 ± 6.7 ^a	GG: 77.9 ± 0.9 ^b	5.4	0.028	
Genotype	KPH	270	CC: 40.1 ± 3.2 ^a	CT: 42.5 ± 2.2 ^a	TT: 47.8 ± 1.0 ^b	4.0	0.019
Allele substitution	NMP	270	270-C	0.81 ± 0.40	4.0	0.046	
Allele substitution	REA	128	128-A	-7.48 ± 3.37	4.9	0.028	
Allele substitution	KPH	270	270-C	-4.27 ± 1.53	7.8	0.006	
Allele substitution	KPH	312	312-A	3.36 ± 2.43	4.9	0.029	

¹IMF: intramuscular fat percentage (%); REA: rib eye area (cm²); KPH: kidney, pelvic and heart fat weight (kg); NMP: net meat percentage (Retail cuts weight / Live body weight, %). ^{a,b}Within a row, least square means with different superscript letter differ, P<0.05.

Key Words: DGAT2 Gene, SNP, Carcass traits

FASS Environment, Waste Management and Ecosystems: Transforming Forages to Improve Nitrogen Use by Dairy Cows and Decrease Nitrogen Emissions

628 Source, amount and fate of nitrogen on US dairy farms. R. A. Kohn^{*1} and M. Wattiaux², ¹University of Maryland, College Park, ²University of Wisconsin, Madison.

The purpose of this review is to identify factors related to forage crop production that affect the efficiency of nitrogen (N) utilization on dairy farms, and may decrease N losses to the environment. Nitrogen enters most dairy farms in the form of fertilizer, N fixed by leguminous crops, atmospheric deposition, and imported feeds or manures. Typically less than half of the N entering the farm can be accounted for in milk, crop, cattle, or manure outputs, indicating considerable leakage of various chemical forms of N to the environment. Typically, less than 25% of the manure N produced by a dairy herd is recycled into home-grown feed N. Considering the entire agricultural system in support of milk production, all N in milk protein ultimately derives from atmospheric N. Atmospheric N becomes biologically active in one of two ways:

chemically by the Haber-Bosch process or biologically by the rhizobial bacteria associated with the roots of legumes. Total N inputs to agriculture for milk production are 3 to 10 times greater than the outputs as N in milk and meat. Most N is lost to ground and surface water through leaching and runoff, or lost to air via volatilization as ammonia, nitric oxide or nitrous oxide. These losses are harmful to the environment and human health in various ways. Some N is also denitrified back to the atmosphere as harmless N₂ gas. Whereas chemical fixation of N is highly dependent on non-renewable energy sources, legume crops fix N near crop roots for efficient utilization. However, high concentrations of legumes in rations oversupply ruminally-degraded protein, which increases N excretion, in particular in urinary N, which is highly vulnerable to volatilization. Although minimizing N losses to the environment requires that crops use N efficiently, it is equally important for animals to utilize feed N efficiently. Thus, the ideal cropping system would fix its own N,