

**694 Characterization of pig genotypes.** PW Knap<sup>\*1</sup>, R Roehé<sup>2</sup>, K Kolstad<sup>3</sup>, C Pomar<sup>4</sup>, and P Luiting<sup>1</sup>, <sup>1</sup>PIC International Group, Schleswig, Germany, <sup>2</sup>Christian-Albrechts University, Kiel, Germany, <sup>3</sup>Akvaforsk and Agricultural University, Aas, Norway, <sup>4</sup>Agriculture and Agri-Food Canada, Lennoxville, Canada.

Simulation models for growing pigs are driven by descriptors of the pig's growth potential and of its environment, predicting growth from the interaction of both. Growth potential parameters relate to resource intake and its partitioning to maintenance, protein (P) deposition (PD) and lipid (L) deposition (LD), and quantify the pig's genotype (breed etc.). Simulation of a particular pig requires characterization of its genetic potential, in terms of the associated model parameters. This requires (i) a concise set of model parameters that fully describe the potential, (ii) real-life measurement of resource input and partitioning in a genotype, (iii) using those measurements to quantify those parameters for that genotype. (i) Resource partitioning is commonly covered with potential PD, required LD and maintenance requirement (ME<sub>m</sub>). The first two features often require three model parameters; ME<sub>m</sub> is here restricted to a neutral environment without additional coping functions (which would require extra parameters). Nutrient intake is most usefully modelled as resulting from nutrient requirements (for PD, LD, ME<sub>m</sub>) and constraints to physical uptake, either external (feed, climate, health, etc) or genetic (requiring an extra parameter). (ii) Resource intake/partitioning observations must reflect growth potential; hence environmental load must be minimized. Repeatedly measuring whole-body P and L and ad libitum ME intake over a wide enough maturity range (eg. 10-175 kg BW) requires serial slaughter trials with chemical analysis, or X-ray or isotope dilution techniques which allow for longitudinal studies and quantification of between-animal variation next to mean levels. (iii) Model parameters can be estimated by fitting observations to a body protein/lipid growth function. ME<sub>m</sub> comes out as the remainder of the ME budget, given valid assumptions about PD/LD efficiency. Alternatively, observed feed intake, growth rate and body composition can be fitted to their simulations by calibrating the model parameters. This "inverted modelling" avoids measurement of P and L but requires many observations per animal and an iterative routine to match resource requirements to resource allowance.

**Key Words:** Growth, Simulation, Genotype

**695 Modelling stochasticity: dealing with populations rather than individual pigs.** C. Pomar<sup>\*1</sup>, P. W. Knap<sup>2</sup>, I. Kyriazakis<sup>3</sup>, and G. C. Emmans<sup>3</sup>, <sup>1</sup>Agriculture and Agri-Food Canada, Lennoxville, Quebec, Canada, <sup>2</sup>PIC International Group, Schleswig, Germany, <sup>3</sup>Scottish Agricultural College, Edinburgh, UK.

Pig production efficiency results from the responses of individual animals. However, it is usual to interpret experimental results on the basis of mean animal responses with little emphasis given to the variation around the means. Animals with different performance potentials may respond differently to treatments, which makes it difficult to translate average population responses into either individual animal responses or across populations having different variation between animals. Nutritional theories that form the basis of current models are all at the level of the individual animal. The problem of how properly to integrate

across individuals to obtain population predictions is rarely addressed. To illustrate the impact of between-animal variation on population responses to dietary treatments, we use a comprehensive pig growth model that predicts voluntary feed intake from potential protein deposition and the desired lipid retention. The genetic growth potential of individual animals is defined in terms of the growth rate parameter, protein weight at maturity and the ratio of body lipid to protein at maturity. The model was made stochastic by simulating variation and covariation in these genetic parameters. The population responses to increasing levels of dietary protein and energy intake are interpreted based on the individual biological phenomena represented within the model. Variation originated from within the individual animal as growth potentials and nutrient requirements evolves over time and from their variable genetic potentials for growth. The effect of increasing the between-animal genetic variation of the simulated population on feed intake, ADG and protein and lipid deposition was also simulated. Finally, it is shown that the optimal levels of intake will differ between population with different degrees of genetic variation.

**Key Words:** Genetic variation, Growth, Simulation models

**696 Pig growth models: Future.** J. L. Black<sup>\*</sup>, John L. Black Consulting, Warrimoo, Australia.

Current pig growth models represent the biology controlling the utilization of energy, amino acids and major minerals with a high degree of accuracy when feed intake and the growth characteristics of the pig genotype are known. Many of the determinants of voluntary feed intake are also well understood and intake is often predicted with reasonable accuracy. Further research is needed to understand better the characteristics of cereal grains and other dietary ingredients that effect the site of feed digestion, passage through the digestive tract, physical limits to gut capacity and other factors causing the wide variation seen frequently between apparently similar diets in voluntary intake. Current pig models do not predict well the effects of stress and disease encountered by pigs reared in commercial environments. However, considerable advances have been made in recent years in understanding the physiological mechanisms associated with stress and disease and these concepts are now being incorporated into some pig growth models. Pig models that predict accurately animal performance and carcass characteristics are, by themselves, unlikely to be adopted widely by industry. The models need to be integrated with least-cost feed formulation packages and resource optimization software that will allow enterprise profitability to be predicted with high accuracy. Another limitation to the widespread use of models within the pig industry is the time and effort required to collect the information needed as inputs to the models and to record animal performance for verifying the predictions. A major effort is needed to enable the industry to adopt electronic methods of data capture and the automatic separation of stock to reduce the cost of applying the models on farms. Finally, the markets for decision support software within the pig industry are small relative to the costs of development and servicing the products. Consequently, ongoing industry funds appear necessary to enable the successful and widespread adoption of models across the pig industry.

**Key Words:** Model, Pig, Future

## Sheep Species

### Sheep Production in China

#### The Importance of Small Ruminants for Managing Vegetation

**697 Sheep genetic resources in northwest China.** M. A. Brown<sup>\*1</sup>, Jianping Wu<sup>2</sup>, Yuzhu Luo<sup>2</sup>, and S. Soderstrom<sup>3</sup>, <sup>1</sup>USDA-ARS, Grazinglands Research Laboratory, El Reno, OK, <sup>2</sup>Gansu Agricultural University, Lanzhou, Gansu, PRC, <sup>3</sup>World Bank, Washington, D.C..

In China's northwestern pastoral areas, challenges for rural development are especially daunting. Despite the political and strategic importance of the region and progress in agricultural development throughout China, there is a need for further economic growth in this area. This growth is impeded by lack of available production capital for the herders and by grassland degradation. However, animal husbandry will remain the major source of livelihoods and real economic growth in much of northwest China in the foreseeable future, since there are major limi-

tations on opportunities for non-farm enterprises. The government is placing a major emphasis on sheep breeding in the pastoral areas since the climate is particularly suited to fine wool and mutton production. Since the 1950's, extensive effort has gone into developing breeds of fine-wool sheep, based on the introduction of Merino breeds. However, despite this active breeding program, about 60 percent of the national flock of 127,350,000 sheep are still local coarse-wool sheep. Much of the fine-wool breed improvement was conducted on State Farms, where most of the better quality fine-wool sheep are now found. Still, average grease fleece production per sheep is about 2 kg, compared with more than 4 kg in the U.S., and the clean wool yield is 40-50 percent compared with nearly 63 percent in the U.S. Wool contamination is a major problem and the inherent environmental characteristics of the semi-arid pastoral areas contribute to the low yields. The fine wool that

is produced also suffers from a number of additional quality problems. Herders are moving from fine-wool production into more profitable meat production. This reflects not only a producer response to better markets for meat sheep but also to production risks associated with fine-wool sheep. This is creating concern over genetic regression in a significant proportion of the remaining fine-wool flocks in the pastoral areas and a need to evaluate breeding programs. Additionally, there is a need for programs to characterize and utilize breeds of mutton sheep in pastoral production systems. The objective of this presentation is to discuss genetic resources available in China for improvement of both fine-wool and mutton production and breeding programs to utilize these resources.

**Key Words:** China, Sheep, Genetic resources

**698 A new paradigm for small ruminant production.** J.W. Walker\*<sup>1</sup>, <sup>1</sup>*Texas Agricultural Experiment Station.*

In light of the decades long decline in the sheep industry it appears past time to reconsider the place of the industry in U.S. agriculture. Solutions to sheep industry problems have focused either at increasing the efficiency of production or increasing consumer demand for the products. It is doubtful that the potential for increasing productivity is great enough to offset the effect of currency exchange rates and high land prices. As for increasing demand, with lamb imports supplying 37% of domestic consumption and increasing at a rate of 6% annually, there is little evidence to support the need for increased product demand. The trend toward globalization of world economies suggest that foreign competition is here to stay and the only solution is to develop markets that foreign products can not compete for. The one market that imported lamb or wool cannot compete for is the potential positive effects of sheep on grazing land ecosystems. There are many examples of using sheep and goats to control noxious weeds and manage vegetation. Although the commodity can be imported the positive effects of sheep grazing cannot be imported. The American Sheep Industry Association is to be lauded for its sheep ecology program that promotes the use of sheep to improve grazing lands. Unfortunately few producers and even fewer academics give any consideration to the potential positive environmental benefits of sheep grazing. However, as shown by the latest issue of *The Futurist* magazine, which was subtitled *Eco-Economy*, the environment is the market of the future. Sheep producers need to accept the reality of the new economy while there is still infrastructure to process the by-products, i.e., lamb and wool, of their industry.

**Key Words:** Ecology, Grazing, Sheep

**699 Using sheep to graze noxious weeds in Montana.** B. Olson\*, *Montana State University.*

Noxious weeds are continuing to spread across Montana, despite extensive and expensive control efforts, primarily associated with herbicides. In 1991, we began a series of studies to assess the efficacy of using sheep to control noxious weeds. Animal related studies have included grazing behavior, grazing use patterns, nutritive value of weeds versus

native plants, and rumen microbial response to noxious weeds. Plant related studies have included response of plants, plant populations, and plant communities to sheep grazing, and noxious weed seed viability after passing through the digestive tract of sheep. A related study assessed the economic feasibility of using sheep to control leafy spurge. In Montana, over 2.2 million ha are infested with the Eurasian spotted knapweed, 0.2 million ha are infested with leafy spurge, also from Eurasia. In Montana, about 45,000 ha of noxious weeds are being grazed by sheep or goats with no or little exchange of money between sheep producer and landowner. In the long term, the declining number of sheep available to graze these weeds may limit the efficacy of this ecologically and economically viable tool to control weeds.

**Key Words:** Sheep, Grazing, Economics

**700 Using goats to control juniper.** C. A. Taylor, Jr., *Texas Agricultural Experiment Station, Sonora.*

Juniper infestation of Texas rangelands is an important dilemma because of its impact on forage and livestock production, water yield and quality, wildlife habitats, and rapidly increasing costs of conventional control methods. Ashe juniper (*Juniperus ashei*) is a serious problem on approximately 4.1 million hectares and redberry juniper (*Juniperus pinchotii*) on 4.9 million hectares of Texas rangelands. Junipers contain monoterpenoid oils, which are volatile. These phytochemicals are composed of terpene compounds, which are five-carbon rings with alcohol, ketone, and hydrogen side groups. The kind of side group makes a difference in the properties of each terpenoid. The terpenoids in juniper affect its taste and a number of the animal's metabolic processes. Since we know that juniper intake is limited by the presence of terpenoids, we can overcome this limitation through two different management schemes. We can manage juniper to reduce terpenoid concentration in the foliage and/or we can manage goats to increase their tolerance of the terpenoids. Terpenoid composition for immature juniper is lower than for mature juniper. There appears to be a threshold after which leaf material becomes significantly less palatable as the juniper foliage ages and terpenoid composition increases. This has important management implications. If juniper can be maintained below this threshold with control methods such as fire, consumption by goats can be increased. Our second approach to juniper management is to increase the tolerance of goats to the terpenoids. Terpenoids are thought to deter goat browsing of juniper plants by being toxic or by reducing nutrient assimilation, or by influencing forage selection at sub-toxic levels by imposing high detoxification costs post absorption. Because of the additional demand for nutrients, adequate nutrition is important to meet the demands of detoxification. Spanish or Spanish x Boer cross goats have a higher tolerance to terpenoids than Angora goats. Spanish goats crossed with the Ibex breed (wild goats) consume even larger quantities of juniper. There also appears to be large within-breed differences in regards to juniper intake. Habitability has ranged from near 0 to 26%.

**Key Words:** Goat, Juniper, Rangeland

## Milk Synthesis

**701 Production of DNA Arrays by Expression Profiling.** K.M.S. Smuga-Otto\*, W. Luo, J.L. Smith, E. Reinfried, and L.G. Sheffield, *University of Wisconsin, Madison.*

DNA arrays consisting of hundreds to thousands of DNA fragments arrayed on a solid support are widely available for humans and many model species. For less widely utilized species, the costs of obtaining DNA arrays can be prohibitive. Part of this cost is the redundancy involved in screening large numbers of clones to obtain complete coverage of the genome. Recently, we used display profiling to obtain a large library of low-redundancy bovine DNA sequences. mRNA was extracted from control and pokeweed mitogen-stimulated bovine leukocytes. Double stranded cDNA was synthesized and the resulting library digested with TaqI restriction endonuclease. Linkers were then ligated to the resulting sticky ends. These linkers were then used as primer sequences for PCR amplification of the library (to give a larger amount of starting material, not absolutely necessary for the procedure). Next, PCR primers containing the linker sequence, the TaqI recognition sequence and the first 3 bases of unknown sequence were synthesized. Each possible primer was synthesized independently, such that we had 64 possible primers.

These were then used in pairs to amplify the DNA fragments. A total of 2,016 non-redundant primer pairs are possible, each of which amplifies a small percentage of the possible DNA fragments in the sample. After PCR amplification with these primers, fragments were separated by PAGE electrophoresis, silver stained and bands excised manually. Each PCR reaction gave between 10 and 30 bands suitable for excision and reamplification. From 900 PCR reactions, we have isolated over 11,000 unique bands of sufficient quality for array production. Thus, this procedure provides a rapid and relatively inexpensive method of producing DNA arrays, well suited to species or projects for which a full-fledged functional genomics effort would be prohibitive.

**Key Words:** DNA Arrays, Expression Profiling, Array Methods