

**2009 NATIONAL SWINE IMPROVEMENT FEDERATION**  
**ANNUAL CONFERENCE AND SYMPOSIUM**  
**DECEMBER 3 & 4, 2009**  
**EMBASSY SUITES, 10 CENTURY BOULEVARD**  
**NASHVILLE, TENNESSEE**  
Tennessee / Virginia Room

**THURSDAY, DECEMBER 3, 2009**

**SESSION I**

**Manipulating Input Costs Through Improvement of Feed Efficiency**

President, Dr. Doug Newcom, Moderator

8:30            A Geneticist's Perspective on Improving Feed Efficiency  
**Dr. Jack Dekkers**, Professor of Animal Science, Iowa State University

Dr. Dekkers is doing research on residual feed intake (RFI), which is defined as total feed intake less the estimated feed requirements for growth and maintenance. He talked about using a traditional animal breeding approach, growth models and RFI using indicator traits and genetic markers. Theoretically, it is better to use feed intake in the evaluation models rather than a ratio such as feed to gain. Total feed intake, however, is correlated with growth rate, so using RFI is a cleaner approach. In practice, using feed to gain gives similar results as RFI. Feed efficiency has improved because of the strong genetic correlation with lean growth. Adding feed intake data could increase progress in feed efficiency by 15 to 20%, depending on assumptions.

John Webb has done research showing that feed intake is limiting in the early growing period while growth rate is limiting later on. There is variation in the shape of the feed intake curve, which would allow improving intake in the early part relative to later in the growing period. Lean growth increases linearly until a pig reaches a plateau (maximum lean gain per day), after which further increase in intake will lead to increasing rate of fat deposition. Intake and growth curves vary by animal and line. The goal is to optimize intake capacity of the crossbreds, and not necessarily in the parent lines.

They have found that 30-35% of variation in feed intake is RFI. The goal is to reduce RFI. They have selected for a low RFI line and also have a control line for their research. They are currently farrowing their 7th generation. Most of the research is done on data from the first parity, but they typically also have data from a second parity. The RFI selected line is 1.6 standard deviations lower (-134 g/d or about 10%) for feed intake. Heritability of RFI is 25 to 30%. Loin eye has increased while backfat and IMF have decreased in the select line due to correlated responses. Despite the lower IMF, there have been no significant differences found in consumer preference, in contrast to similar French research which found negative effects on consumer preference. The shape of the feed intake curve has changed in the way that John Webb suggested i.e. higher in early growth and lower later. IGF-I concentrations in blood have decreased in the selected line. This is consistent with correlations found in other research. IGF-I in blood of young pigs could be an early indicator trait for RFI.

They have also looked at effect of selection for RFI on sow performance (Jennifer Young). Low RFI sows had slightly more piglets that were heavier at birth, opposite to what we might have expected. There was no difference in feed intake during lactation; however, low RFI sows mobilized more body reserves during lactation (lost more body weight). The select line lost more fat than the control line and some protein during lactation. However, the select line has higher protein mass to start because of faster growth.

They considered many possible reasons for RFI differences from a biological basis such as lower activity, less feed wastage, etc. They observed that the low RFI sows were more efficient with both restricted and ad lib feeding, required less feed (20% less) to maintain body weight, had lower internal organ mass, ate less often and larger meals and had less tissue turn-over.

They have looked at MC4R, which has been used extensively by PIC and is now available to the industry. They have also used the new 60K SNP panel for 740 pigs. The cost was \$150/pig. Animals were genotyped in the base generation and in the last two generations. MC4R is one region that stands out and there were several others related to ADG. Similarly, there were several regions associated with feed intake and there were even stronger associations with RFI. MC4R association was stronger with total feed intake than with RFI. There are some known genes in these regions that, from a biological understanding, we would expect to affect these traits.

He summarized with key findings: Selection for lean growth results in large correlated responses in feed efficiency. Opportunities exist to further increase response. We could have direct selection for reduced residual feed intake. We could better align feed intake capacity to growth curves. There may be a possibility to use IGF-I as an early indicator trait for RFI and good potential for use of molecular genetics markers.

9:15                    A Nutritionist Perspective on Improving Feed Efficiency  
**Dr. Dean Boyd**, the Hanor Company, Franklin, KY

Feed price and therefore composition has become volatile in recent times and is the most important cost factor in hog production. There is a need to get away from the classical definition of gross input over gross output (feed to gain). The most useful feed conversion efficiency (FCE) expression in nutrition practice is Mcal energy : gain. Energy in the US is expressed as ME, in Australia they use DE. Cost of feed is now about \$64 US per cwt. A change of 0.01 FCE is now worth \$0.306 (compared to \$0.151 from 1999-2006). In other words, improvements in FCE are worth twice as much as they were three years ago.

The goal is to capture the portion of genetic potential that is needed to deliver a financial optimum. Fat, lysine and other amino acid balance and particle size are important. Increasing fat levels results in lower feed intake and improved FCE with no change in carcass lean % (or even a slight increase). Increasing lysine from 0.35 to 1.25 showed FCR improving from 4.15 to 3.00 with a corresponding increase in lean deposition. Decreasing particle size in corn from 720 u in a meal to 450 u in pellets resulted in FCR improving from 4.72 to 2.50. Mortality + removal % increased from 2.70 to 3.20 (not significantly different). Pelleted feeds have been found to result in increased mortality in other studies. When fat is 3.6 times the price of corn, it is too expensive. Today fat:corn price is 4.65 : 1. Poorer feed conversion without the fat is therefore less expensive today. Similarly, we need to consider cost of amino acids when deciding on level. Optimum for net return will be lower as amino acid costs increase, even though ADG, FCE and lean yield will be poorer. He showed an example with lower lysine which saves \$1 per pig.

Manipulation through extraordinary means include use of ractopamine, somatotropin and immunocastration. These have greater value when feed costs are higher. Combining ractopamine and somatotropin gives an additive improvement in FCE. He noted that this does not eliminate differences among genetic lines.

He talked about how to go further, after doing the “easy” things we already know about. He mentioned: growth dilution of maintenance, regulating nutrient use by existing methods, mitochondrial operation efficiency improvement, fractional protein degradation reduction ( $150 \text{ g/d Pd} = 600 \text{ Ps} - 450 \text{ Pd}$ ), facilitating digestion improvement through intestinal length, and disease resistance (population FCE modifiers: death loss, inflammation). Immune stress is a robber of genetic capacity for FCE – soybean meal attenuates intermittent FCE disruption. Associations between FCE and mitochondrial function have been illustrated in poultry. Poorer FCE broilers exhibited apparent abnormalities in mitochondrial function. He noted that carbohydrates are by far the biggest component and cost, so concentrating on this offers greatest return (compared to protein and amino acids).

There is a balance between growth and response to illness in regards to protein degradation and synthesis. Care needs to be taken if we try to reduce degradation. We could do it and be fine until animal get sick.

10:00

Lauren Christian Memorial Graduate Student Award Presentation

Dr. Todd See introduced the award recipient, Justin Fix from North Carolina University. Justin's research was on impact of birth weight on pork production and its genetic relationship with performance traits. Traits included growth, efficiency, survival, composition and pig quality. A commercial farm trial with Smithfield Premium Genetics used a 2400 sow farrow-to-wean operation and test barn. All fully formed pigs over a 4-week period were tracked (July 6 to August 3, 2008). All pigs were tracked to weaning (n=4108), about a third were tracked in two finishing barns (n=3429) and half of these tracked through slaughter (n=1586). A pig quality assessment was done each time pigs were weighed: 3 = acceptable, 2 = somewhat poor quality and 1 = poor quality. Injuries and weight were considered.

Cross-fostering had negative effects on the fostered pigs. Birth weight up to about 3.5 lbs was linearly related to weights and growth later in life. Above 3.5 the effect levels off. Similarly, pig quality was poorer for lighter pigs up to 3.5 lbs and then leveled off. Pre-weaning and nursery survival (especially pre-weaning) increased linearly to 3.5 lbs and then leveled off. In the nursery the effect was smaller without a big change at 3.5 lbs. Full value at market increased linearly even beyond 3.5 lbs. It was noted that the data is censored in that many light birth weight pigs didn't make it to market. They are looking further at relationship between birth weight and efficiency.

Genetic analysis results: heritabilities estimated within two lines were approximately 6% for birth weight, 11% for weaning weight, 30% for off test weight, 50% for off test back fat, 33% for off test loin depth, and 30% for ADG. Fairly high genetic correlations were found between birth weight and weights at both weaning and end of test (~0.5) and smaller negative correlation with fat (lighter pigs at birth are fatter at market weight). Selection for heavier market weights should therefore increase birth weight. We could select directly for birth weight, but the heritability is quite low.

Economic analysis of the incremental impact of birth weight is in progress. The impact of birth weight is dramatic on many economically important traits and the impact is not linear.

10:30

Break

## SESSION II

### Animal Welfare and the Sow Herd

Dr. Ken Stalder: Iowa State University, Moderator

10:45

Insight on How Animal Welfare may be approached within the sow herd:

What are the target traits and how are they measured?

Dr. **Anna Johnson**, Assistant Professor, Animal Behavior and Well-Being Research, Iowa State University

There are three schools of welfare: mental – dependent on what the animal is feeling; naturalness – not just pain and suffering but also nurturing and fulfillment; and physical – state of an animal as it attempts to cope with its environment (body condition, ADG, lesions, health, physiology, behaviour). Dr. Johnson subscribes to the “physical” school.

Compared to wild pigs, most behaviours do not differ greatly. Differences include calmness and lower activity of domestic pigs. There haven't been many studies of genetics of behaviour in pigs, especially maternal behaviour. Specifically, in 2002, it was noted that essentially nothing was known about the biological basis for genetic differences in maternal traits and mothering ability.

During farrowing, increased sow mobility may be detrimental to welfare of her piglets. Sow behaviour during parturition is correlated to weaning traits. In a Dutch study 83% of time sows lay laterally (on their side) on average. They also monitored time lying ventrally, standing, sitting, kneeling, and changing positions. A change in percent of specific activities affected weaning traits.

During lactation: crushed piglets are important economically and also in regards to piglet welfare. 83% of sows stood up when hearing a piglet screaming. Several studies have looked at genetics of a sow's reaction to screaming. A Swedish study found 20% did nothing, 47% looked around, 12% sat up, and 21% stood up in reaction to a tape recorder of a piglet screaming. A second experiment looked at the sow's change in position in response to picking up a piglet and gently squeezing until it screamed. They recorded if the sow moved away or toward the handler and if it showed aggression or not. Around 40% of sows did nothing while 15 to 20% changed to one of the other 3 positions. Most sows didn't move, but of those that did, more moved away and fewer showed aggression. Strong response was related to lower mortality. No clear relationship was found between aggression and mortality. A German study using PIC lines and crosses found heritabilities from 2% to 7% for a variety of sow behaviour traits. Heritability for maternal ability was 5% and there was lots of variability.

Robustness, stress resistance, and temperament are societally important traits. How traits are recorded varies greatly in different studies and so far heritability estimates are low. There may be other traits, such as pawing behaviour, which could be useful indicator traits. Traits like "fear" (heritability = 28% to 38%) and scream test might be useful. Time and cost of collecting behaviour data is expensive, so indirect measures are still the best for now. Automation of collection of behaviour may help e.g. FIRE feeders or watering behaviour.

We need the drive for this, to identify a maternal care index for the sow, to agree upon a definition for each of the traits, to create / consider automation for collecting these maternal care indices, and to determine their accuracy / repeatability and heritability over time.

11:30                      Genetic Improvement of Sow Longevity  
**Dr. Linda Engblom**, Visiting Swedish Scientist, Iowa State University

Worldwide 50% of sows are removed annually and 30% of US sows are removed before parity 3. Reproductive disorders are about 1/3, old age is 1/5 and mortality next highest. It is worthy of more attention, but it is a tricky trait. There is a long time interval to collect data, selection is in breeding herds while interest is in commercial herds, and it is not normally distributed. Options are indirect selection (e.g. conformation), stayability to a certain parity and direct selection.

A Swedish study found longevity heritability ranged from 3% to 12%. Efficiency of indirect selection was generally low, except for stayability to 2nd parity based on age at first farrowing. Stayability, however, might select for sows that use up body resources early in life. Dr. Engblom has worked with commercial data (12,000 F1s) from Smithfield with 5 generations of pedigree. She has looked at indirect measures of lifetime born alive. She also has data on purebred herds (including some F1 data) from National Swine Registry. She analyzed many traits including age at first farrowing, number of born alive at parity 1, number of weaned piglets at parity 1, accumulated born alive at parity 2 (ABA2), 3 (ABA3) and 4 (ABA4), lifetime born alive (LPL), lifetime piglets weaned (LPW), using different software packages (DMU, GIBBS2CEN, THRGIBBS, Survival Kit 3.12).

Genetic correlations between pure and F1 levels are high for born alive in parity 1, but relatively low for lifetime indicator traits (0.5 to 0.25 range). This work is still in progress. Sire ranking for lifetime born alive (LBA) depends on software and data included, LBA analysis seems better if censoring is ignored, stayability heritability increases with a binomial model, accumulated born alive in medium parities appears to be a good indicator for lifetime production, and genetic correlations between purebreds and crossbreds are high in parity 1 but lower for other measures.

12:00                      Lunch

**SESSION III**  
**Factors That Limit Genetic Expression**  
Mr. Everett Forkner, TruLine Genetics, Moderator

1:00            Overview of Current and Future Health Concerns  
**Dr. Montserrat Torremorell**, The Allen D. Leman Chair in swine health and productivity, University of Minnesota College of Veterinary Medicine

Over time, some diseases are less of an issue or totally under control, while a few continue and numerous new ones have emerged. In the 1980s, App, atrophic rhinitis, dysentery, Aujeszky disease, mycoplasma, post-weaning scours were the main issues. PRRSV, SIV and PCV2 are current viral challenges. They effect grow-finish productivity, predispose to secondary bacterial infections and are difficult to control.

PRRS has been known for twenty years and has had a huge impact on how we do things e.g. co-mingling vs single flows, gilt acclimatization, changes in approach to disease control in general and biosecurity has been taken to a higher level. We do a better job in general because of this. Unfortunately, we have limited control tools for PRRS. Evolving nature of the virus – RNA, prone to mutate and evolve and new strains can be highly transmissible. Estimated cost in the US is \$5.15 per pig sold. Eradication is possible, using herd closure without introduction of gilts for many months, with a success rate higher than 90%. The failures are due to re-infections. Aerosol transmission is getting a lot of attention and can transmit 4.3 km or up to 9.1 km under severe disease conditions. Filtration appears to be very effective in research farms compared to non-filtered. Many AI centres have implemented filtration and it is starting in sow herds in the past 1.5 years. Regional elimination concepts are gaining momentum, and are developing in several states. Stevens County in MN has been at it for 5 years. It is a hog dense county. In 2004, about half the herds were known to have PRRS, many were unknown and a few were free. Today most are free. Momentum is building for a national eradication program. Minnesota is considering a state wide program, and looking at dividing the state in regions.

Swine influenza: 1918 Spanish Flu Pandemic, 1930 H1N1 evolves, cH1N1 (c = classical), 1997-98 double and triple reassortment, last 10 years many new strains. SIV is common. People can infect pigs and it is much less common for pigs to infect people. nH1N1 (novel) remains a human disease and not a pig disease. However, it has been found in pigs (and other species) and it is putting pressure on the swine industry to change how we deal with SIV. We may need to raise SIV negative pigs.

Circovirus (PCV2): It has been around for a long time, but only hit hard in the US in the last 5 years. Fortunately, it hit the US at the same time that vaccines were ready for commercialization, and the vaccines do work. Use of the vaccine coincided with an increase in national census to market by 2-3%. The vaccine controls disease and also increases ADG. However, there is starting to emerge indications of problems in some herds even with vaccination. It may be something to do with timing of the vaccination.

Top bacterial diseases (respiratory) are also important and exotic diseases are a threat to national security (CSF, ASF, FMD, PRV).

Most diseases are influenced by many genes and it is difficult to impact by disease specific selection for resistance. There are a few exceptions: E. coli F88, E. coli K88.

Diseases are a very expensive and moving target. Viral diseases are the main primary challenge. Bacterial diseases are very significant followers and are a challenge to control. Emerging diseases and re-emerging of old ones continue to be an issue. There will be increased scrutiny due to public safety concerns.

What's next: approach to SIV, regional/state PRRSV elimination programs, emerging and re-emerging diseases (dysentery, post weaning E. coli, ...).

In summary, yes, we can select for resistance to disease. There is lots of heritable variation. The challenge is how to implement practical breeding programs.

Many experiments demonstrate considerable phenotypic and genetic variance for response to disease. One of the first experiments was Wilkie & Mallard at the University of Guelph (1999). Blanco et al., 2008 looked at colostrum-deprived pigs inoculated with H. Parasuis – 10% of pigs were totally resistant, one sire had no resistant progeny. Dr. Johnson noted several other recent publications up to 2009 (Magnusson et al, 1998; Crawley et al, 2008; Vogelli et al, 1997; Gomez-Raya, 2009; Hotlig et al, 2009; Opriessing et al, 2006; Halbur et al 1998). Lewis, 2009 looked at genetic parameters before and after a PRRS outbreak. During a PRRSV phase heritability increased to 10% for mummified piglets, 46% for matings per conception (before PRRSV it was 3% and 4%, respectively). There are other studies looking at PCVAD and PRRSV showing that there are differences among breeds.

Nebraska experiments: PRRS and PCVAD - have collected phenotypes and plan to use 60K SNP to look for associations. One PRRS experiment infected one of a pair of littermates from 100 litters from two lines. One line is the experimental one and the other was a Duroc-Hampshire cross. The infected pigs grew slower and surprisingly, the select line did better after infection than the crossbreds. This was unexpected given the inbreeding level in the selected line. Response to the virus varied between populations, indicating underlying genetic differences. From the results they have identified high responders (susceptible) and low responders (resistant) and then used their uninfected littermates. They worked with Dr. Joan Lunney on this part. The high responder group maintained a high viral load through to day 14 and really didn't grow. The low responders had much lower viral load at day 14 and were growing well. They looked at gene expression and found that susceptible pigs were expressing more than the resistant pigs. There were no significant differences between lines. Unfortunately, they were not able to find anything that was expressed in the uninfected pigs that would be a good predictor of response to infection. He suggested that genomics may offer this tool. There were about 3500 genes differing in expression between infected and control pigs. Between high and low responders, there were about 100 genes differing in expression, and this is what was really of interest.

PCVAD was naturally occurring in the research herd. Pigs were given a PCVAD score (0=no, 1=light symptoms, 2=severe) on a weekly basis and were weighed and blood sampled. Necropsies were performed on a subsample of pigs. Serum viremia was measured on 900 pigs. They found no differences between lines on scores and other criteria. Heritability was 16% for PCVAD on the underlying scale. Viremia at day 90 had heritability of 38%. PCVAD was genetically correlated with birth weight, growth, viremia and antibodies. There are other genetic correlations. Using an index with correlated traits the expected response was -8% in first generation. Interestingly, including PCVAD itself didn't add any value. We need a way to select in uninfected pigs and MAS / genomic selection looks promising.

Disease resistance improvement:

- Incremental
- Multiple markers
- Complex breeding schemes
- Pig gene micro-arrays
- SNP panels
- Bioinformatics
- Need large DNA datasets from pedigreed populations with accurately measured health phenotypes

2:30 Genetic Improvement of Farrowing Rate  
**Dr. John Mabry**, Professor and Leader, Iowa Pork Industry Center, Iowa State University

Producers have often asked if there was a genetic solution to improve farrowing rate. So far, the answer has been no. We need to look at costs to maintain the sow herd and costs to get the sow pregnant, while not forgetting about revenue from output of viable pigs. Non-productive days are any time she is not pregnant or nursing a litter. Approximate costs are \$1.50 to \$2.00 / sow / day. Components include entry to first service, farrowing rate, wean to service and culling to removal. Entry to first service is generally a management decision, but gilts that have an earlier puberty will cycle quicker and be bred quicker. Heritability of puberty is 15 to 25%, but it is rarely measured. It is correlated to growth rate. Farrowing rate is a function of many environmental factors – timing, inseminator, semen, sow's fertility, and care of the sow to maintain pregnancy. Wean to service has heritability of 12 to 36% and can be selected for at the farm level. However, there isn't a lot of room for improvement since the interval is generally already quite low. Culling to removal is a management decision largely depending on marketing strategy for cull sows.

Improvement of farrowing rate offers the greatest potential for progress on sow productivity in piglets weaned per year. A repeat service means 21 non-productive days. Failure to pregnancy check an open sow is 121 days. If we can't do it directly, can we improve farrowing rate indirectly? PigChamp data was analyzed from 5 herds totaling 11,000 sows (1000 Landrace, 3000 York, 1000 York-X, 6000 Landrace-X – most of York-X and Landrace-X were F1s). The study looked at litters per sow per year (LSY). Data adjusted for parity was important, since calculation of LSY is higher for lower parities because entry to first service is amortized over the number of parities. LSY had a much more normal distribution than unadjusted. They will be expanding the dataset on commercial sows from genetic suppliers in Asia, Europe and North America. Increasing LSY by 0.1 will save 11 non-productive days.

Traits that influence returns (born alive, pre-weaning mortality) or costs (LSY, value per litter) are crucial but it is important to also think about sow productive life.

3:15 Break

**SESSION IV**  
**A New Look at Our Targets**  
Mr. Dale Miller, Editor, National Hog Farmer, Moderator

3:30 Economic Factors of Sow Herd Productivity: Do we focus on the correct traits?  
**Mark Rix**, Swine Management Services, Fremont, Nebraska

Swine Management Services (SMS) work with 650 farms. Financials are harder to standardize than production, particularly from small producers. Costs at a sow farm are largely fixed, so they need more pigs to lower the break-even point. Staff training, gilt development, farrowing rate, lactation feeding, and litter management are all important factors. Benchmarking percentiles from SMS are based on an overall ranking of the farm and not within each trait. It therefore shows what the top farms did to get in the top. Feed is the biggest cost. Labour is 4.05 to 6.28 \$ per weaned pig. Genetics cost is \$1.26 to \$3.95 per pig. Average parity doesn't vary much by percentile. Cull breeding stock income is \$1.77 to \$3.62 per weaned pig. Culling by parity: 13% before 1st parity, 13% in first parity, 8% in 2nd parity. Female death loss doesn't vary much by percentile. Death loss by parity: 13.5% of gilts before 1st parity, 18.7% in 1st parity, 15.3% in 2nd parity, 14% in 3rd parity, and continues to decrease with each parity after that. Breeding expense is \$1.61 to \$3.04 per weaned pig: the sow, the semen and the worker are all factors. Farrowing rate is higher (88.7%) in the top 10% of herds and much lower in the bottom 25% (78.1%). Average weaning age has increased in recent years and doesn't vary much by percentile. Wean to first service is lower for top producers. The number of litters per mated female per year is higher in top herds (2.47 vs 2.10). This statistic removes variation from how the producers enter their gilts. Born live is much higher in top herds (12.4 vs 10.6). The number is skewed because people don't know how to evaluate stillborns (some were alive at birth). Piglet survival (still born + pre-wean mortality) is higher in top herds

(82.8% vs 76.8%). Stillborn and pre-wean mortality are combined to remove variability in how stillborns are assessed. Weaned per female is much higher in top herds (11.13 vs 9.24). This one is affected by use of nurse sows. One more weaned pig per mated female per year lowers costs \$0.75 to \$1.50 per pig. Contact Dale Miller for information on financial benchmarking – information on how 17 different programs do the calculations. Starting Jan 1, 2010 some plants will require truckers to be TQA certified.

4:15                    Genome-Wide expression QTL (eQTL) analysis of loin muscle tissue to identify candidate genes in pigs  
**Dr. Ronald O. Bates**, Associate Professor, Michigan State University

Dr. Bates was unable to attend.

## FRIDAY, DECEMBER 4, 2009

### SESSION V

#### Perspectives on Research Needs and Emerging Technology

Dr. Max Rothschild, Iowa State University, Moderator

9:15                    Short and Long Term Genetic Research Needs within the Swine Industry  
**Dr. Mark Boggess**, USDA, ARS, Washington DC

We are seeing industry consolidation and expect 106M market hogs per year compared to 116M in 2008. Production costs are 20 to 25% higher (mostly due to feed costs increasing due to competition from ethanol plants). Pigs weaned per litter increased by 0.3 in the last year and are up a full pig from 10 years ago. We can expect this trend to continue. Hogs were 3lbs heavier than a year earlier.

Opportunities in genomics: production efficiencies and creating industry value; genomics is an umbrella over all pork industry traits; see the larger picture and program accordingly (political support, funding, collaboration); challenges and opportunities for production (PRRS), efficiency (feed, additional value creation, sow herd efficiency has not been explored adequately); reproductive efficiency (litter size, lifetime productivity, focus on pigs weaned - more than just litter size); other areas (adaptability, welfare and stress management; pork eating quality / nutritional value, pork safety, health concerns, nutritional efficiency); an emerging priority: human health/nutrition. All are complex challenges, require long term dedicated funds (3-5 years minimum) and will require multidisciplinary teams including all stakeholders. A looming critical issue is the lack of basic physiological research in the pork industry. This is the foundation for all applied research programs.

Administrative priorities for USDA don't mention pigs, and don't even mention primary agriculture. The current role of ARS within USDA hasn't changed, but they are now expected to find 50% external funding and collaborate much more extensively outside of ARS. The National Institute for Food and Agriculture (NIFA) replaces CSREES within USDA. They are specifically disconnected from industry, the cattle industry in particular and the focus is on the administrative priorities. There is also a focus on collaboration, including with industry, so some opportunities exist for industrial research. Historically there has been a disconnect between the pork industry and the USDA. It is important to connect the political dots.

Costs of research occur in the first 5 to 8 years while major benefits come from 10 to many years out. This doesn't fit with a short term return on investment focus to much of the current funding programs. Research at ARS: reproductive efficiency, nutritional efficiency, pork quality, welfare, food safety, PRRS resistance, H1N1 and others. Their main swine production unit is USMARC – Clay Center, Nebraska with new leadership of Dr. John Pollak. There will be a priority for genetics/genomics. Challenges are primarily funding. Cooperation will be a key to success.

10:00 Beef Cattle Viewpoint on DNA-Based Technology: Current Value and Outlook for the Future  
**Dr. Sally Northcutt**, Genetic Research Director, American Angus Association

The effort is to incorporate genomic information without adding more information to the large amount of information already available i.e. to make the current EPD information more accurate. Efforts started in 2006 to build an Angus specific panel at Angus Genetics Inc (AGI), a subsidiary of the American Angus Association. AGI has since initiated efforts for many other breed associations. The effort is done through cooperative research with many universities and an industry consortium. They have developed a lower density panel from a 50,000 SNP panel for use in genetic evaluation, in partnership with Merial (Igenity). The genomic information is combined with the traditional performance data. One trait of interest is marbling on the carcass which now is estimated through a combination of direct carcass measurements, live intramuscular fat (IMF) and genomic information. The genomic profile gives evaluations for a total of 14 carcass, performance and maternal traits. In September 2009 AGI started accepting DNA samples and Igenity provided profiles to breeders. In October they provided their first genomic-enhanced EPDs. AGI confirms identity of the animal for each sample, receive results from Igenity, genomic-enhanced EPDs are computed and they provide access to the results through a secure login on their web site. Samples are submitted on blot cards and a submission form is completed on-line at AGI. The accuracy from genomic information is similar to performance. Combining both increases accuracy by about 5% e.g. from 20% to 25%. Evaluations were done every 6 months in the past. Genomic information was coming in more frequently. They decided to do evaluations weekly – Thursday night and publish on the web Friday morning. This has been well-received by most. There was some concern from AI centres that print catalogues. They have been providing interim EPDs as animals are scanned and continue to do so, but these are not so much of interest any more since the full national EPDs including genomics information are available every Friday. They have developed a 400 SNP panel that is almost as accurate for marbling in Angus as the full 50,000 SNP panel. What's next: implement 384 SNP profiles into carcass evaluation, implement genomic-enhanced EPDs for new traits (feed intake, heifer pregnancy), continue breeder education and outreach efforts.

10:45 Break

11:00 Swine Viewpoint on DNA-Based Technology: Current Value and Outlook for the Future  
**Dr. Alan Mileham**, Head of Genomics, Genus/PIC USA, DeForest, Wisconsin

Genomics can contribute to selection and DNA-based identification (breed/line, parentage, and traceability) and veterinary diagnostics (what's causing an illness). The first DNA test for a major qualitative trait gene in pigs was Hal1843 and PSS in 1991. Since then, most research effort was QTL studies using divergent crosses and it was difficult to apply findings in commercial populations. An alternative was the candidate gene approach where you can look directly at commercial populations, but there was still a question if this would work. Collaboration between Max Rothschild and PIC found an RFLP in the ESR gene which had a major effect on litter size. This was the next commercial application with a large effect on an economic trait. Gene expression came in about 15 years ago allowing to look at expression from many genes simultaneously. Comparative mapping with the human genome allowed identification of potential candidate genes in regions of interest. Marker assisted selection (MAS) is most beneficial for traits that are low heritability, measured late in life, sex-limited, can't be measured on live animal, or expensive to measure. Genotyping technologies have evolved substantially from low volume RFLP done in-house to contracting out large volume of multiple markers.

With one SNP marker at frequency of 0.5 there will be 1 in 4 "best" genotypes. With 10 markers at 0.5 frequencies there will be 1 in a million with "best" for all markers. Chicken has 3M markers, bovine > 1M markers. The pig sequence draft will be completed in early 2010 (90% coverage) – a by-product is lots of polymorphisms. Marker testing costs have dropped dramatically (100 X cheaper in last 10 years). Genome-wide scanning era was approaching. In the past 5 years, PIC has tried to use the genome wide approach. First experiment on growth was 4 years, cost \$170 per SNP discovered and \$0.10 per genotype for 6.5 M genotypes. Second experiment on pig mortality was 2 years, \$135 per SNP, \$0.05 per genotype, 10.6M genotypes. Third on scrotal hernia was 6 months \$4 per SNP, 0.025 per genotype, 22.6M

genotypes. Latest on litter size was 3 months, no cost for SNP discovery, \$0.0025 per genotype, 125.8M genotypes.

Discovery marker panels are used to determine which markers are useful for which phenotypes. Use of markers increases accuracy of traditional EBVs. PIC currently uses 157 DNA markers in trait EBVs and another 59 in further validation before use in MA-BLUP.

Genomic selection uses a very large number of marker genotypes to predict total breeding value. The underlying assumption is markers are in linkage disequilibrium (LD) with QTLs that affect economic traits. Before applying this, we need a large training data set to determine the association between the markers and the total breeding value. This requires both historical phenotypes and corresponding tissue or DNA. PIC routinely uses docked tails as a source of DNA.

The 60K SNP chip costs about \$150 per animal. This is remarkably cheap, but still too expensive for use on every selection candidate. We could use a lower density panel of the most significant markers. PIC does this today. Need different panels for different lines and traits. A third way is to do 60K genotype on parents and a low density panel on progeny, and then computationally fill in the gaps from the parents based on assumed LD. Some research is needed on this approach including computationally feasible algorithms and how many SNPs are needed for the low density panel.

Future genomic focus: SNP discovery using trait specific pools of affected / non-affected animals; focus on specific regions, transcriptome / exome (affected versus non-affected pigs). The current 60K chip has room for > 1 M SNPs on each slide. Technology is evolving to be faster and cheaper. Use of information in traceability – could do this for about \$0.20 per slaughter pig. It will also be useful for disease diagnosis.

We need a large number of samples from pedigreed animals with accurate phenotypes, a large number of SNPs, the right genotyping technology, bioinformatics and lots of computing power.

12:00 Awards Luncheon