

20th Brian Kennedy Memorial Colloquium

May 10-11, 2004, Guelph

The 20th Brian Kennedy Colloquium was held in University of Guelph on May 10-11, 2004. Over 40 people from University of Guelph, University of Cornell, University of Michigan, Canadian Centre for Swine Improvement, Canadian Dairy Network and Argentina participated in this event. Laurence Maignel and Yuefu Liu from CCSI attended the Colloquium. The Colloquium of this year was also simultaneously presented to University of Buenos Aires in Argentina via video conferencing system. Around 10 people presented in the video conference room in Argentina.

Larry Schaeffer from University of Guelph chaired the colloquium and delivered a short opening remark.

Swine researches

There were four presentations on swine researches. Three of them were on genomics (or molecular genetics) research and one on transgenic research.

- Andy Robinson from University of Guelph talked about “**Swine Genomics Research at Guelph**”, and gave a summarized report on swine genomics programs in CGIL at University of Guelph during the past years. (1) He began with the Candidate gene mapping studies carried out by joint effort of the CGIL of University of Guelph and Roslin Institute of UK. A group of candidate genes related to female reproduction was studied based on the resource populations developed by Roslin Institute. This includes candidate genes, FGG, STE, FSHB, AREG, GNRHR, IBSP, FSHIR, ESR, SPP1 etc. He referred to a C-T SNP in a coding region that is associated significantly with birth weight of piglets, but not with litter size. (2) Then, he talked about the candidate gene study based on the (H×D)×Y resource population in Ridgetown, including 429 full/half sibs. A huge number of traits measured were available for this resource population. Two candidate gene families, FABP and HDAC, were studied using this resource population. Some gene-trait associations were unveiled, such as the associations of FABP4 with loin fat and back fat, FABP5 with body weight, HDAC3 with weight of trimming belly, and HDAC5 with loin fat and PH. (3) Comparative mapping is an ongoing study in CGIL. Chromosome 3 has been mapped,

chromosome 6 is under study, and mapping chromosome 9 is a research of next step.

- Valencia Rilington from Michigan State University presented her functional genomics study: “**Identification and mapping of differentially expressed genes in fetal and postnatal pig skeletal muscle**”. She studied the changes of gene expression levels from 60 days of gestation to 7 weeks of age using cDNA array techniques. She checked 740 cDNA clones. Significant expression differences of myotilin gene ($p < 0.0005$) were found among 60th day and 105th day of gestation and 7th week of age. The expression differences of paxillin and myoglobin were also detected in her study. Right now, she is trying to associate the expressed genes with genome DNA locations.
- David Edwards from Michigan State University introduced the **Duroc × Piétrain swine resource population in Michigan State University for genomic studies**. The resource population started with crossing 4 Duroc boars and 16 Piétrain sows. Six males and 52 females were selected from F1 population and crossed each other to produce F2 generation. F2 generation includes 142 litters and 1259 piglets. 959 of them were slaughtered, and carcass and meat quality data were collected in 2004. The study will include QTL analysis, microarray analysis for gene expression differences and association of markers with gene expression signals as phenotypes.
- Serguei P. Golovan from University of Guelph (from Forsberg’s research group), talked about their **EnviroPig study**. Using transgenic technology, the research group developed a type of transgenic pigs that can produce more salivary phytase, which can break down the phosphate in stomach and reduce the phosphate in fecal. The fecal phosphate from transgenic pigs is one third as much as that from non-transgenic pigs. When questioned the comparison with adding phytase in feed, Golovan recognized that transgenic pig program is a research (at current stage), instead of a practical solution.

Other researches:

In addition to the four presentations on swine researches, there were thirteen presentations on other species:

Beef cattle:

- Bob Weaver, from Cornell University, presented a study on the **comparison of alternative herd size testing and selection schemes for large commercial ranches**, based on schemes with commercial testing and progeny testing. The

- study also included a sensitivity analysis of models to changes of heritability, exposure rate and progeny test cost per calf. His conclusions were that progeny test selection schemes have profit potential in a number of scenarios, and that simulation provides effective means of optimizing selection schemes at various levels.
- Dave Kirschten from Cornell University talked about **genetic evaluation of feed efficiency for beef**. He used the Cornell Value Discovery System (CVDS) to predict individual feed consumption from the group feed consumption. His conclusion is that there is no need to measure individual feed intake.
 - Reynold Bergen from University of Guelph delivered two presentations on beef carcass study. He investigated the **relationship between age-constant measurements on yearling beef bulls with commercial carcass measurements**, and studied the methods of **using ultrasound measurements to predict the lean meat yields of carcasses**.
 - Rodolfo Cantet, from University of Buenos Aires, Argentina, presented a study on **Bayesian estimation of variance components in animal models with skewed normal errors**. Some continuous traits, such as calving interval, may exhibit skewness in their distributions. The objective of the study was to develop a statistical model for repeated measurements, based on the methodology proposed by Sahu et al. (2000).
 - Vanerlai Roso from University of Guelph presented a study on **comparisons of different statistical methods handling multicollinearity problem in beef genetic evaluation**. In beef genetic evaluation, origins of breeds is an important factor that causes the colinearity. He introduced a random ridge regression model to solve the colinearity problem.
 - Dick Quaas from Cornell University presented a review on the **assessment of DNA tests for quantitative traits**. The objective was to develop a protocol for validation of genes and markers based on independent field data. He mentioned a number of genes and markers for which tests are now available, through Bovigen, Frontier Beef Systems, MMI Genomics, Merial, etc. There is a need to provide information based on field test, and to publish it in some form, and use it to assess DNA tests.
 - Kwan-Suk Kim, from Michigan State University, talked about the **evaluation of microsatellite markers on bovine chromosomes 1 and 5 for potential allelic associations with meat characteristics and growth traits in beef**. The objective was to detect specific Quantitative Trait Haplotype Blocks (QTHB) associated with interesting phenotypes. A statistical analysis was carried out between haplotypes and phenotypes.

- Renate Van Dorp from Michigan State University presented **Analysis of gene expression of parturition induced changes in bovine peripheral blood mononuclear cells**. In her large scale analysis of microarray data for gene expression, she detected 243 significant genes ($p < 0.05$) that were expressed differently during parturition. She grouped these genes according to their functions based on searching the data bases of gene sequences and is attempting to associate these genes with phenotypes. She also handled the multiple test problems in data analysis to control false discovery rates.

Dairy cattle :

- Asheber Sewalem, from the Canadian Dairy Network, presented results of a study on **functional herd life in Canadian dairy breeds**. The objectives were to determine the parameters influencing culling process, to estimate genetic parameters for functional traits, and to compare genetic trends using different approaches.
- Rob Tempelman, from Michigan State University, gave a talk on **multiple breed genetic inference: hierarchical approaches to robust genetic evaluations**. Tempelman and his colleagues compared different distributions assumed for model residuals under hierarchical Bayesian approach, including homogenous and heteroscedastic Gaussian, student t and slash distributions. The student t heteroscedastic model had the best fit to the data analysed.
- Larry Schaeffer, from University of Guelph, gave a talk on the **Female Fertility Project**, carried out at CGIL. Four traits were evaluated as a first shot, even if a lot more were recorded: age at first service, non-return rate for heifers, non-return rate for cows, interval from calving to first service. A synthetic index was developed using Bethany Muir's work, looking at different weights and response to selection.

Sheep

- Rachel Rupp, from INRA (France), talked about a research program on the **genetics of mastitis resistance in French dairy sheep**. The French dairy sheep population is quite large: 1.4 million females, including 20% in the selection nucleus. The breeding program has been carried out since 1970's. Genetic evaluations for somatic cell counts (SCC) were developed at INRA. This trait was shown to be a good indicator for resistance to mastitis. A granddaughter design (10 families and 316 sons) and a backcross design (967 daughters originated from 10 F1 families) were devised in order to detect QTL associated with SCC of the first three lactations. Two QTLs were detected for somatic cell counts. A fine-

scale mapping is going on in France by adding more markers in QTL mapping and recording clinical mastitis in addition to SSC.

- Rachel also presented results on **polygenic variation involved in the resistance/susceptibility to scrapie in a Romanov flock**. The objective was to detect and quantify polygenic variation in resistance to scrapie in Romanov sheep, using information recorded in a herd infected by scrapie during several years. Major genes associated with resistance/susceptibility to scrapie were already identified such as PrP gene. It was shown that polygenic variance may explain 20% of the total genetic variation involved in the resistance.