SYMPOSIA AND ORAL SESSIONS

Animal Health: Emerging Foreign Animal and Zoonotic Diseases

272 Potential threat of foreign animal diseases to US agriculture. T. Beckham*, *Texas Veterinary Medical Diagnostic Laboratory, Texas A&M University System, College Station*.

Homeland Security Presidential Directive 9 designated agriculture as a US critical infrastructure. Protection of the agricultural industries is critical to protecting the nation's economy. Agriculture in the United States contributes approximately one-trillion/year towards the gross domestic product. Furthermore, fifteen percent of Americans are employed in food production and US agricultural industries export approximately 50 billion dollars worth of products annually. The US agricultural and livestock industries today face very real threats from foreign, emerging and/or zoonotic diseases. In particular, the past decade and more specifically the past year alone has demonstrated that the numbers of new and emerging diseases affecting our industries are on the rise. For example, new serotypes of Bluetongue virus continue to move through the European communities and Ebola virus was recently isolated from an atypical host (swine) in the Phillipines. While many of these examples do not originate in the United States, the disease threats that face our industries are still large. These threats stem in part from the globalization of commerce, the consolidation of our industries into larger commercial units and the interactions between humans, livestock and wildlife. Protection of our livestock industry will require state-of-the art diagnostic tools that enable us to conduct broad-level surveillance. This surveillance effort will be largely conducted in our state-veterinary diagnostic laboratories and will be a coordinated effort between veterinarians (our first line responders), state animal health authorities and the federal government.

Key Words: foreign animal disease, agricultural threats, national security

273 Preventing and detecting foreign animal diseases. T. McKenna*, *Wisconsin Veterinary Diagnostic Laboratory, Madison*.

The threat of a foreign animal disease introduction into the United States is very real. What can be done to prevent an introduction, and what is the role of detection in controlling an outbreak? We all have a part to play in the prevention of foreign animal disease introduction. Biosecurity on the farm and at the borders is paramount. Being able to identify an introduction early is crucial to limiting the impact of a foreign animal disease. Current diagnostic tools and surveillance approaches will be described.

Key Words: foreign animal disease, diagnosis, prevention

274 Responding to a foreign animal disease incident. M. Cochran*, *Texas Animal Health Commission, Austin*.

The devastating economic and animal health impacts of foreign animal diseases mandate an efficient response by animal health authorities, requiring the simultaneous coordination of local and national resources. The Incident Command System, well-tested in emergency responses of all types, allows for quick establishment of a chain of command and expansion as necessary for response to the foreign animal disease. Foreign animal disease investigations often start when a veterinarian or producer discovers a suspicious lesion or other symptoms in an animal or a herd. After this incident is reported to state or federal animal health authorities, a foreign animal disease diagnostician, a veterinarian trained in disease identification and specimen collection techniques, is dispatched to the premises in question. Careful laboratory analysis is required before confirmation is reported to the animal health authorities. Already on alert, animal health authorities quickly establish an incident command post in proximity to the first detected case. The incident commander and his or her team then work to determine the scope of the outbreak and establish quarantines and issue stop-movement orders as the situation requires. The approximate scope of the foreign animal disease outbreak will translate into establishment of an infected zone and a buffer surveillance zone around the infected zone. Coordination and control, coupled with cooperation at the local level, help minimize the spread of the disease. The end goal of a foreign animal disease response is disease eradication. With this goal in mind, laboratory diagnostics, strict biosecurity controls in both specimen collection and animal movement, analysis of the disease agent and environmental conditions, and selective culling of animals are required to eradicate a foreign animal disease with the least negative impact on animal health and production.

Key Words: animal health, incident command center, quarantine zones

Breeding and Genetics: Genomic Evaluation

275 Opportunities for genomic delection with redesign of breeding programs. J. C. M. Dekkers*[1], H. H. Zhao[2], D. Habier[3], and R. L. Fernando[1], [1]*Iowa State University, Ames*, [2]*Pioneer Hi-Bred Int., Johnston, IA*, [3]*Christian-Albrechts University of Kiel, Kiel, Germany*.

Genomic Selection (GS) using EBV from dense marker data is promising for genetic improvement but may require a complete redesign of breeding programs. Our objective was to develop and compare GS programs that capitalize on opportunities to reduce generation intervals and program sizes using layer chickens as an example. Assuming GS allows a reduction in generation intervals from 1 y to 6 mo, our goal was to develop a GS program that nearly doubles response but with a similar rate of inbreeding per y. Comparison was to a standard program with selection of the top 60 and 360 out of 1000 males and 3000 females based on BLUP EBV for a sex-limited trait with heritability 0.3. Using analytical predictions by selection index, a GS program with selection of the top 50 males and females out of 250 candidates per sex based on GS EBV was predicted to achieve this goal. These standard and GS programs were then evaluated by stochastic simula-

tion. A GS training population of 1000 individuals with phenotype for a trait with 200 segregating QTL and genotypes on 6000 SNPs on a 7.5 Morgan genome was used. Linkage disequilibrium was based on historical population sizes of 500 and 100 for 900 and 100 generations. GS EBV were predicted by Bayes-B, without or with retraining each generation after adding 250 females with phenotype from the previous generation. Assuming a generation interval of 6 mo versus 1 y, results showed that GS indeed achieved similar rates of inbreeding per year as the standard program. Responses for GS without and with retraining were 61 and 68% greater than for the standard program after 1 y of selection and 31 and 70% greater after 4 y. Variance of response was, however, greater for GS than for standard selection. These results demonstrate that with substantial redesign of breeding programs, GS can maintain or increase response to selection while controlling rates of inbreeding and achieve that with substantially reduced program sizes in terms of the number of individuals raised and phenotyped. *Financial support from Hy-Line Int., PIC-Genus and Monsanto Co.*

Key Words: genomic selection, breeding strategies

276 Computing procedures for genetic evaluation including phenotypic, full pedigree and genomic information. I. Aguilar*[1,2], I. Misztal[1], and A. Legarra[3], [1]*University of Georgia, Athens*, [2]*Instituto Nacional de Investigación Agropecuaria, Las Brujas, Uruguay*, [3]*INRA, SAGA, Castanet-Tolosan, France*.

The purpose of this study was to evaluate computing procedures to solve mixed models equations with additive relationship matrix H modified to account for genomic information. It is assumed that H=A+Δ, where A is a numerator relationship matrix based on pedigrees and Δ includes deviations due to the genomic information. To avoid computing H^{-1}, mixed model equations due to the additive effect, say $[Z'X\ Z'Z + kH^{-1}]$ can be expressed in an alternate Henderson form as [H Z'X H Z'Z + Ik]. The modified equations have a nonsymmetric left-hand side where H may be poorly conditioned numerically. Expressions involving A can be computed efficiently with conjugate gradient algorithms. Data included 4539 records of final score and 2697 pedigrees. Comparisons involved a repeatability animal model with simulated changes due to genomic relationships in a random sample of fifteen percent of the animals. Changes were simulated as Δ={UN(-b,b)} for different values of b (0, 0.01, 0.05). Solutions were Preconditioned Conjugate Gradient (PCG), which only works with symmetric matrices, and by Conjugate Gradient Squared (CGSQ) and Bi-Conjugate Gradient Stabilized (BiCGSTAB), which work with nonsymmetric matrices. With the original equations, PCG converged in 46 rounds, CGSQ in 33, and BiCGSTAB in 36 rounds. With the alternate equations and b=0, CGSQ converged in 36 rounds while BiCGSTAB converged in 29 rounds. With nonzero b, the change in convergence did not exceed two rounds despite some H being non positive definite. The cost of one round in CGSQ and BiCGSTAB was similar and approximately twice that cost in PCG. CGSQ and particularly BiCGSTAB are suitable for the alternative equations even if H is poorly conditioned. If computation of terms with Δ can be done efficiently, it may be possible to modify the existing evaluation to incorporate the genomic information at approximately double the cost of the original evaluation.

Key Words: BLUP, genomic selection, genetic evaluation

277 Genetic evaluation including phenotypic, full pedigree and genomic information. I. Misztal*[1], A. Legarra[2], and I. Aguilar[1], [1]*University of Georgia, Athens*, [2]*INRA SAGA, 32326 Castanet-Tolosan, France*.

Currently the genomic evaluations use multiple step procedures, which are complicated and prone to errors. For many traits, predictions involving estimation of SNP effects or BLUP using a genomic relationship matrix are equivalent. A single step procedure may be applicable by modifying the numerator relationship matrix A in a regular evaluation to H= A+Δ, where Δ includes deviations from original relationships. However, the traditional mixed model equations require H-1, which is difficult to obtain for large pedigrees. The computations with H are feasible when the mixed model equations are expressed in an alternate form given by Henderson that also applies for singular H, and when those equations are solved by the conjugate gradient techniques. Then the only computations involving H are in the form of Aq or Δq, where q is a vector; the product Ac can be calculated efficiently in linear time using Colleau's indirect algorithm. The alternative equations have a nonsymmetric left-hand side. Several alternative H are possible. A naïf possibility is to substitute the relationships of genotyped animals with the genomic relationship matrix. However, this results in incoherencies because the genomic relationship matrix includes information on relationships among ancestors and descendants. Another possibility is to condition the genetic value of ungenotyped animals on the genetic value of genotyped animals via the selection index (e.g., pedigree information), and then use the genomic relationship matrix for the latter. This results in a joint distribution of genotyped and ungenotyped genetic values, with a pedigree-genomic relationship matrix H. In this matrix genomic information is transmitted to the covariances among all ungenotyped individuals. Both possibilities allow for an efficient computing in the form of Δq. The proposed methodology may allow upgrading of an existing evaluation to incorporate the genomic information.

Key Words: genomic selection, genetic evaluation, SNP

278 Transition of genomic evaluation from a research project to a production system. G. R. Wiggans*[1], P. R. VanRaden[1], L. R Bacheller[1], F. A Ross[1], T. S Sonstegard[1], G. te Meerman[2], and C. P. Van Tassell[1], [1]*ARS, USDA, Beltsville, MD*, [2]*University Medical Center Groningen and University of Groningen, Groningen, the Netherlands*.

Genomic data began to be included in official USDA genetic evaluations of dairy cattle in January 2009. Numerous changes to the evaluation system were made to enable efficient management of genomic information, to incorporate it in official evaluations, and to distribute evaluations. Artificial-insemination and breed organizations can use an online query to designate animals to be genotyped, to determine if the animal has already been nominated, and to check for the reason if a genotype was rejected. Four commercial laboratories provide genotypes. A genomic sample scanner generates large files of intensity data, which are used to determine the genotype of each single-nucleotide polymorphism (SNP). A technique to adjust jointly for sample and SNP effects may improve call rate and allow automation of adjustment for differences among scanners and reagent batches. Genotypes for 58,336 SNP are stored in a database table with 1 row per animal genotype. Genotypes rejected from evaluation because of parentage conflicts are stored to allow easy recovery if the conflict is resolved. For evaluation, genotypes for new animals and those with pedigree changes are extracted, combined with verified genotypes from the previous evaluation, and searched for conflicts. Validated genotypes are shared with Canada. Data for all ancestors of genotyped animals are collected, and missing pedigrees and foreign cow evaluations prior to addition of genomic data are obtained. The most recent evaluations from the Interbull Centre

(Uppsala, Sweden) are combined with genomic data into a single evaluation that includes all available information. The US Jersey and Brown Swiss breed associations have sought additional animals to genotype, and the Brown Swiss association has arranged to share genotypes with European countries. The evaluation system is being streamlined to provide genomic evaluations that meet industry needs and can be produced with available resources.

Key Words: genomic evaluation, genotype, single-nucleotide polymorphism

279 Can you believe those genomic evaluations for young bulls? P. M. VanRaden, M. E. Tooker*, and J. B. Cole, *USDA Animal Improvement Programs Laboratory*, *Beltsville, MD*.

Breeders began selecting on official genomic tests for U.S. Holstein and Jersey bulls, cows, and heifers in January 2009. Statistical properties of genomic evaluations, traditional evaluations, and parent averages were validated using data from November 2004 to predict January 2009 daughter merit, weighted by reliability of 2009 data. The validation used 1,611 young and 4,422 proven Holstein bulls in 2004. The top 20 young and top 20 proven bulls were selected based on 2004 traditional or genomic net merit. To determine if selection was effective, means from 2004 and 2009 data were compared after subtracting $155 for the 2005 base change. Mean 2009 daughter merit was $395 for the young bulls selected on parent average, $516 for young bulls selected on genomic evaluation, $381 for proven bulls selected on traditional evaluation, and $463 for proven bulls selected on genomic evaluation. Thus, actual merit was highest for genomic tested young bulls and lowest for traditionally evaluated proven bulls. Evaluations in 2004 were higher than average daughter merit in 2009 for all 4 selected groups, with respective biases of $278, $130, $96, and $30. Regressions of 2009 daughter deviations on 2004 evaluations were expected to be 1.0 across all bulls but were 0.63, 0.74, 0.91, and 1.10 for the 4 groups. Thus, evaluations of young bulls are biased, but the bias is less with genomic tests than with parent average. Adjustments are needed such as further limits on phenotypic deviations or decreases in heritability to decrease bias, particularly for traditional parent average. Selection using traditional or genomic evaluations had only small effects on average relationships among selected animals. The correlation with expected future inbreeding was slightly higher for young bull parent average than for the genomic evaluation (0.21 vs. 0.13). Breeders should greatly increase use of the best young Holstein bulls because their merit already exceeds that of the best proven bulls, and advantages of young bulls over proven bulls will increase as more young animals are tested.

Key Words: genomic selection, net merit

280 Application of kernel partial least squares to estimate genomic breeding values of crossbred beef cattle. G. Vander Voort*[1], M. Kelly[1], T. Caldwell[1], D. Lu[1], Z. Wang[2], J. Mah[2], G. Platstow[2], S. Moore[2], and S. Miller[1], [1]*Centre for Genetic Improvement of Livestock, University of Guelph*, *Guelph, Ont., Canada*, [2]*Department of Agricultural, Food and Nutritional Science, University of Alberta*, *Edmonton, Alberta, Canada*.

A relatively small number of beef cattle are genotyped for a 50k SNP panel, leading to a data structure with a larger number of independent variables (SNP) relative to the number of dependent variables (phenotypes). Kernel partial least squares (KPLS) have been used in analysis of data with this structure to improve the accuracy of prediction. Data for a single trait analysis included adjusted phenotypes for a measure of beef tenderness, shear force in the longissimus dorsi 7 days post mortem (LM7D) of 783 crossbred cattle genotyped for a 50k SNP panel. Data was divided into a training data set of 632 records for estimation of SNP effects and a validation dataset of 151 records to test the predictive accuracy of SNP effects estimated with the training data. The training dataset included two University of Guelph research herds with alternate herds included in the validation data. Kernel matrices elements used in the analysis were a polynomial function of the dot product of 33800 SNP codes (0,1,2) included (low frequency SNP excluded) in the design matrix. KPLS predicted LM7D were correlated with observed LM7D at a high of 0.99 in the training data, but dropped to 0.45 in the validation dataset or 20% of the phenotype variation. This proportion of phenotypic variation translates to explaining most of the genetic variance, given LM7D heritability was estimated to be 0.23. By comparison, genomic selection using BLUP predicted LM7D in the validation data with a correlation of 0.08. Increase in accuracy of prediction of KPLS relative to BLUP estimates supports the utility of applying KPLS to estimate genomic breeding values. Current research focus is on expansion to a multivariate analysis and effect of kernel structure

Key Words: genomic selection, single nucleotide polymorphism, marker assisted selection

281 Visualization of results from genomic predictions. J. B. Cole*, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA*, *Beltsville, MD*.

Genomic predictions of estimated breeding values (EBV) include effects of tens-of-thousands of markers distributed over thirty chromosomes for many traits. There are so many numbers that data are difficult to compare, levels of detail are obscured, and data cannot easily be tabulated. Graphics can present data with higher density than text or tables and provide additional insight into the data. Estimates of marker effects are not currently exchanged between countries but plots of results can be shared without disclosing sensitive information. Genomic data can be visualized at several levels, such as the distribution of marker effects across the genome, proportions of additive genetic variance explained by markers on a chromosome, and relationships among markers on the same chromosome. Ratios of actual to expected genetic variance can be plotted as bar graphs, making it easy to identify chromosomes that deviate from expectations; stacked bar graphs allow for simultaneous comparisons of methods of estimating variance ratios. All markers affecting a trait can be plotted on the same ordinate to visualize the distribution of marker effects across the genome, colors or textures can be used to differentiate between chromosomes, and stacked graphs can be constructed to compare interesting groups of traits. Chromosomal EBV can be presented as sparklines, high-resolution graphics embedded in text, to provide an overview of individual animals for comparison to potential mates. Small multiples of chromosomal genetic correlation matrices can be used in conjunction with edge exclusion graphs to identify interesting patterns of association among traits, such as that on chromosome 18 associated with calving traits, conformation, and economic merit. Line plots of marker effects for autosomal recessives can be used to quickly locate chromosomal regions in which causative mutations are probably located, identifying areas of interest for further study. These graphics are easily produced automatically and add to online query systems, providing users with novel information at little cost.

Key Words: genomic prediction, quantitative trait loci, visualization

282 Comparison of Student's *t*, LASSO, and multiple shrinkage methods for the prediction of genomic breeding values. C. Maltecca* and J. P. Cassady, *North Carolina State University*, *Raleigh*.

The objective was to compare 4 different approaches for predicting genomic breeding values (GEBV). First an implementation of the Bayes-A (M1) was used. The second method was an extension of Bayes-A (M2) with scale and degrees of freedom of the mixing inverted Chi-square distribution treated as unknown and estimated from the data. Third (M3) a Laplace prior was employed to obtain LASSO estimates of SNPs effects. Finally a semi-parametric approach was investigated (M4) which allowed shrinkage of each coefficient toward multiple prior means with unknown location. A Dirichlet process prior was put on the mean and scale parameters in order to create few groups with different degree of shrinkage. Hierarchical modeling was employed for all the methods. We simulated 8000 SNPs and 12 QTL. Genotypes for 2000 individuals were generated in age order over 4 generations with the first 500 representing the training generation. All individuals were assigned a phenotypic value by adding a random residual to the true breeding value obtained as the sum of each marker effect. This was done in order to mimic estimated breeding values with different accuracies. Two different average levels of accuracy (0.95, 0.85) of the phenotypes were simulated. Five replicates of each scenario were performed. On average M2, M3, and M4 performed better that M1 in estimating markers effects and predicting GEBV in subsequent generations. The average increase in accuracy (measured as correlation between true and estimated GEBV in the next generation) was of .031(±0.004), .034(±.008) and .036(±.011) (M1 prediction accuracy 0.85 ±.011); .042(±.012), .048(±.009), .051(±.014) (M1 prediction accuracy 0.78 ±.013); .052(±0.015), .051(±0.018), .048(±0.017) (M1 prediction accuracy 0.71 ±.012) for M2, M3 and M4 over M1 for the first, second and third generation after training, respectively for phenotypes accuracy of 0.95. M3 and M4 performed on average better than M2 at higher phenotypic accuracy but failed to converge in some replicates at lower phenotypic accuracy. M2 was the least computationally demanding, and M4 was the most computationally demanding.

Key Words: GEBV, Bayesian methods, multiple shrinkage

283 Equivalent mixed model for joint genetic evaluation considering molecular and phenotypic information. N. Gengler*[1,2] and F. Colinet[1], [1]*Gembloux Agricultural University*, *B-5030 Gembloux, Belgium*, [2]*National Fund for Scientific Research*, *B-1000 Brussels, Belgium*.

Currently efforts are underway to introduce molecular information into genetic evaluation systems. A particular situation is genomic selection however simpler cases exists where major genes are known and used by breeders. A new alternative strategy for the prediction of gene effects and especially their smooth integration into genetic evaluations based on an equivalent method was developed from existing theory. Underlying hypothesis were based on the idea that knowledge of genotypes will not affect overall additive genetic variance but only change expected values of genetic effects for animals with known genotypes. The developed equations were modified to allow that not all animals were genotyped. As the underlying mixed model is open a very large range of models can be used in situations including random regression models, multiple-trait, maternal effects and multiple-across-country-evaluation models. Computations involved successive solving of two mixed models, with the use of an linear extrapolation to speed up convergence of gene effects. The method was tested for several known major genes and QTL, e.g. for the mh gene in the dual-purpose Belgian Blue population in Belgium. Modifications of the method could also be developed to be useful in the context of genomic selection.

Key Words: molecular Information, joint estimation, genomic selection

284 Effect of estimation approach and number of QTLs in accuracies of genomic breeding values for simulated data. G. Gaspa[1], E. L. Nicolazzi[2], R. Steri[1], C. Dimauro[1], and N. P. P. Macciotta*[1], [1]*Dipartimento di Scienze Zootecniche, Università di Sassari*, *Sassari, Italia*, [2]*Istituto di Zootecnica, Università Cattolica del Sacro Cuore*, *Piacenza, Italia*.

Accuracies of estimated genomic breeding values (GEBVs) in simulated data depends both on the relative efficiency of the methodology used but also on the assumptions made for the simulation. A key issue is represented by the number of QTLs related to the genome length and to the density of SNP markers. In this study two scenarios of number of QTLs, 10 or 20, for a genome size of 1 M length and with 1000 SNPs were tested. Initial allelic frequencies for both SNPs and QTLs were sampled from a uniform distribution. QTL effects were sampled from a gamma distribution (shape parameter 0.42). After 50 generations of random mating, two training (2,000 individuals) and three prediction (3,000 individuals) generations were created. Phenotypes of training individuals were generated by adding random noise to the true breeding value (TBV). Heritability was set at 0.5. The estimation step was performed by fitting phenotypes of training individuals with a mixed linear model that included the fixed effect of the mean and the random effect of: i) the genotype of all 1,000 SNP markers (ALL); or ii) the scores of the first 200 principal components extracted from the correlation matrix of the SNP genotypes (PCA). Estimates were then used to predict GEBVs in the prediction generations. Accuracy of prediction was evaluated as correlation between TBVs and GEBVs. Each scenario was replicated 10 times. Average accuracy of prediction for the training generations was 0.90 (standard deviation 0.04) and 0.86 (0.03) for BLUP or PCA calculations, respectively, when 10 QTLs were simulated. Values raise to 0.94 (0.02) and 0.87 (0.01) in the scenario with 20 QTLs. In the prediction generations, the PCA approach resulted in a higher accuracy of prediction in both scenarios: 0.66 (0.09) vs 0.53 (0.07) and 0.72 (0.06) vs 0.61 (0.07) for 10 and 20 QTLs respectively. Moreover, the decreasing trend of accuracy in the prediction generations was less pronounced reduced in the PCA approach. Both the number of QTLs considered and the mathematical approach used had an influence in the accuracy of GEBVs.

Key Words: genomic selection, number of QTLs, principal component analysis