Breeding and Genetics: Genomic Selection in Dairy I

440 In vivo and in vitro heat shock proteins gene expression in cattle. A. C. A. P.M. Geraldo*[1], L. J. Oliveira[1], A. M. F. Pereira[2], F. Moreira da Silva[3], and E. A. L. Titto[1], *[1]Faculdade de Zootecnia e Engenharia de Alimentos-Universidade de Sao Paulo, Pirassununga, Sao Paulo, Brazil, [2]Universidade de Evora, Evora, Portugal, [3]Universidade dos Acores, Angra do Heroismo-Terceira, Acores, Portugal.*

The main purpose for this study was the quantification of the heat shock proteins HSPA1A and HSP90AA1, in cow lymphocytes, when subjected to heat stress directly - in vivo, or indirectly - in vitro. The aim was to identify differences between HSP expression in vitro and in vivo. The experiment was conducted in the Biometeorology and Ethology Laboratory of FZEA-USP. Were used 3 female Holstein Frisian, which were subjected to heat stress, by sun exposure. The blood samples were collected after sun exposure, with a temperature of 40 ± 2°C, during 3 d. For in vitro tests, blood of the same animals was collected and placed for a period of 4 h in a water bath at 40°C, thus simulating the thermal stress. Total RNA of lymphocytes was extracted, treated with DNase I and submitted to cDNA synthesis for gene expression quantification of HSPA1A and HSP90AA1, by real time PCR (qRT-PCR). The data were tested for normality by Kolmogorov-Smirnov test and for homocedasticity by Levene test. Data were analyzed according to a general linear model procedure with 2 fixed factors treatment and genes expression. Significantly different means were submitted to post-hoc comparisons of means (LSD test) and regarded as significantly different when $P \leq 0.05$. The results showed that there are no significant differences between the in vitro and the in vivo treatments, but there are significant differences in genes expression in the different treatments.

Key Words: cow, HSPA1A, HSP90AA1

441 Comparison of genomic inbreeding within a family-based structure in Holstein cattle. D. W. Bjelland*[1], K. A. Weigel[1], A. Coburn[2], R. D. Wilson[2], and A. Lasecki[2], *[1]University of Wisconsin-Madison, Madison, [2]Genex Cooperative Inc./CRI, Shawano, WI.*

Pedigree inbreeding estimates the percentage of alleles of individual which are identical by descent. With the use of genomic information, more accurate measures of inbreeding have been developed. These methods are utilized in this study to compare the expected genomic inbreeding derived from sire-dam mating pairs to the actual genomic inbreeding of their progeny as well as compare genomic inbreeding measures between full siblings. Genomic information consisting of 54,001 SNP markers for 3,601 Holstein cattle were available for this study. A total of 638 sire-dam-progeny trios and 3,906 full sibling pairs were available for analysis. The percent homozygosity of SNPs remaining after editing for minor allele frequency, call rate, and Hardy-Weinberg equilibrium (32,114 remaining SNPs) and the percentage of the genome contained within a run of homozygosity were utilized as the 2 measures of genomic inbreeding calculated for each animal. The expected percent homozygosity for progeny resulting from each sire-dam mating pair was also calculated. Average percent homozygosity for all animals was 62.6 ± 1.1% while average inbreeding calculated from runs of homozygosity was 6.2 ± 2.4%. The expected percent homozygosity between sire-dam mating pairs was 65.1 ± 0.9%, which was on average 2.4 ± 0.9% greater than the percent homozygosity of the actual progeny. When comparing one full sibling to another, measures of percent homozygosity had a correlation of 0.48 while genomic inbreeding derived from runs of homozygosity had a correlation of 0.52. The largest difference in percent homozygosity shown between 2 siblings was 4.8%, while the largest difference in inbreeding derived from runs of homozygosity was 10.7%. Results of this study indicate that the progeny produced have less overall homozygosity than what would be expected from their parents. This may indicate that the progeny which would have been more homozygous, were not viable and were lost early in development. Furthermore, while pedigree information has provided reasonable estimates of the alleles which are identical by descent, differences between full siblings reconfirm that the actual measure can vary greatly.

Key Words: inbreeding, genomics

442 Genomic selection of Sahiwal cattle: A developing country perspective. M. Moaeen ud Din*, G. Bilal, and H. M. Waheed, *Animal Breeding and Genetics Lab, Faculty of Veterinary and Animal Sciences PMAS-Arid Agriculture University, Rawalpindi, Pakistan.*

The objective of present study was to explore the potential application of genomic selection in a typical developing country situation using Sahiwal cattle of Pakistan as an example. Sahiwal breed of cattle is one of the top milk producers under harsh climatic conditions of tropics and sub-tropics owing to its characteristic of disease and parasitic resistance. A selection program to enhance the genetic potential for milk production of Sahiwal cattle using progeny testing program is going on in Pakistan. Traditional progeny testing program has made a remarkable improvement in the genetic potential of dairy animals in the developed world. However, progeny testing program faces severe implementation issues in the developing countries due to limitation of resources and lack of basic infrastructure. Simulated studies in developed countries have shown the potential of genomic selection in shortening generation interval and increasing the accuracy of selection (especially young bulls) that can bring a relatively rapid genetic improvement as compared traditional progeny testing approach. Based on the available genetic and phenotypic parameters of Sahiwal dairy cattle; a comparison was made between typical progeny testing program and genomic selection. The assumed size of the training population for genomic selection was 6962 cows registered with Research Centre for Conservation of Sahiwal Cattle. The results revealed that genomic selection can reduce the generation interval in the male to male selection pathway from 10.5 years down to 2.75 years along with a substantial reduction in generation interval of other selection pathways. Genomic selection resulted in a 2.5 times increase in response to selection compared with that in a progeny testing program. Furthermore, it reduced the costs of proving bulls up to 96%. The present study may encourage the researchers and policy makers to initiate the program of genomic selection for Sahiwal cattle in Pakistan and it may also serve as an example for other developing countries.

Key Words: developing country, genomic selection, Sahiwal cattle

443 Implementation of a routine genetic and genomic evaluation for mastitis resistance using producer-recorded health data and indicator traits in Canadian dairy cattle. J. Jamrozik[1], A. Koeck[1], G. J. Kistemaker[2], and F. Miglior*[2,3], *[1]CGIL, Dept. of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, [2]Canadian Dairy Network, Guelph, ON, Canada, [3]Guelph Food Research Centre, Agriculture and Agri-Food Canada, Guelph, ON, Canada.*

Genetic evaluation model for mastitis resistance has been developed for Canadian dairy breeds. Traits were mastitis (MAST), mean SCS,

SD of SCS and excessive test-day SCC (>500,000 cells/mL) in the first 150 DIM of lactation, and 3 first-lactation conformation traits: udder depth (UD), fore udder attachment (FUA), and body condition score (BCS). Binary mastitis trait (0 = no case, 1 = at least one case) and 4 SCS related indicators were considered as different traits in first and later (up to the 5th) lactations, giving in total 11 traits in the multiple-trait animal linear model. Models for specific traits included fixed effects of herd-parity, year-season-parity and age-season-parity (MAST and SCS traits), and herd-round-classifier and age-season-time of classification (conformation traits). Random effects were animal additive genetic, permanent environmental and herd-year (MAST and SCS traits only). Genetic parameters for the Holstein breed were estimated using a sample data on 59,819 cows with 113,123 lactations and Bayesian methods via Gibbs sampling. Estimates of heritability for MAST were 0.03 and 0.05 for first and later lactations, respectively. Heritability for SCS traits ranged from 0.02 (SD of SCS) to 0.17 (average SCS). Conformation traits were moderately heritable, from 0.26 (BCS) to 0.50 (UD). Mastitis in 1st lactation was a different trait that mastitis in older cows (genetic correlation = 0.59) and it was relatively highly genetically correlated with SCS traits (from 0.51 to 0.71, and from 0.60 to 0.78 for first and later lactations, respectively). Genetic correlations between MAST and conformation based indicator traits were moderate and stronger for the 1st lactation (from −0.34 for BSC to −0.52 for UD) compared with later parities (from −0.09 for FUA to −0.27 for UD). The new model for mastitis resistance in Canadian dairy breeds will allow complementing currently used indicator traits with direct information on clinical mastitis and it is expected to generate more accurate genetic and genomic evaluations for this trait.

Key Words: mastitis resistance, genetic evaluation

444 Genetic analysis of leukosis incidence in a US Holstein population including phenotypes from relatives without genotypes. E. A. Abdalla*[1], G. J. M. Rosa[1], K. A. Weigel[2], T. Byrem[3], and Francisco Penagaricano[1], *[1]Department of Animal Sciences, University of Wisconsin-Madison, Madison, [2]Department of Dairy Science, University of Wisconsin-Madison, Madison, [3]Antel BioSystems Inc., Lansing, MI.*

Bovine leukosis virus (BLV), a retrovirus closely related to the human T cell leukemia virus type 1 (HTLV-1), is an oncogenic virus that infects bovine B cells causing bovine leukosis (BL) disease. Up to this point, no vaccine is available for the virus and BL has spread widely in dairy herds in the US and in several other countries. The economic impact of BL on the US dairy cattle industry has been reported in many studies and in official reports released by the US Department of Agriculture. In addition, BLV is suspected to be one possible cause of HTLV-1 and it has been found to be responsible for a significant worldwide proportion of breast cancer cases. The objectives of the study were to identify genomic regions and biologically relevant pathways potentially associated with BL incidence in dairy cattle. Milk ELISA test results were available for 11,554 Holsteins from 112 herds in 16 US states, which were daughters of 3,002 sires. The genomic information for 961 of those bulls as well as for 3,000 additional bulls was available. A single-step analysis combining phenotypic, pedigree and genomic information was performed using BLUPf90 family programs. Gene set enrichment analysis was conducted to find possible Gene Ontology (GO) and KEGG pathways related to this trait. Estimated SNP effects indicated some genomic regions that might be associated with BL incidence, such as in chromosomes 1, 14 and 17. Additionally, we found in total 12 GO terms and 2 KEGG pathways significantly enriched with genes associated with BL. Interestingly, several of these functional categories such as cytoskeleton, calcium ion homeostasis, intracellular signaling cascade and regulation of small GTPase mediated signal transduction are involved in biological process that could be associated with BL. Results of this study are in agreement with our previous findings and indicate a potential for selection improvement to decrease BL incidence in dairy cattle. In addition, these results could provide insight into the genetic architecture of this complex trait in cattle.

Key Words: bovine leukosis, ssGBLUP, GWAS

445 Identification of loci associated with fertility traits via genome-wide association studies in the Holstein breed. M. K. Abo-Ismail*[1], S. P. Miller[1,2], M. Sargolzaei[1,3], D. A. Grossi[1], S. S. Moore[3], G. Plastow[3], P. Stothard[3], S. Nayeri[3], and F. Schenkel[1], *[1]Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, [2]Livestock Gentec, University of Alberta, Edmonton, AB, Canada, [3]L'Alliance Boviteq, Saint-Hyacinthe, QC, Canada.*

Improving the accuracy of genomic selection for fertility traits could help reduce fertility problems in the Holstein breed. The objectives of this study were to identify significant genomic regions for 11 fertility traits, fine map these regions, and run an in-silico functional analysis for the corresponding genes. Genome-wide association studies (GWAS) were performed using a generalized quasi-likelihood score test, using genotypes from the BovineSNP50 Bead-Chip and imputed genotypes of the Illumina Bovine HD BeadChip (300,339 SNPs) with accuracy of about 99% from 9015 Holstein bulls with progeny proofs. The GWAS identified 1203, 835, 808, 553, 162, 214, 1410, 1008, 373, 380 and 36 SNPs associated with calving ability (CA), daughter calving ability (DCA), calving ease for heifer and cow (CEh and CEc), calf survival for heifer and cow (CSh and CSc), sire calving ease for heifer and cow (SCEh and SCEc), sire calf survival for heifer and cow (SCSh and SCSc) and sire conception rate (SCR) at 5% chromosome-wise significance level by Bonferroni correction. A total of 5425 genes were found to overlap with or to be nearby significant SNPs (within 5kbp) for the 11 fertility traits using UMD3.1 bovine genome assembly. Most of the genes were on chromosome 5 (13%), 18 (9%), 3 (6%), 19 (6%) and 23 (6%). The in-silico functional analysis for the genes holding significant SNPs using annotations from human orthologs suggested enrichment of 356 biological processes ($P < 0.05$) and 192 pathways, which included GnRH signaling, oocyte meiosis, and steroid hormone biosynthesis. Further research is underway to validate significant SNPs and assess their predictive ability for the genetic merit of fertility traits in dairy cattle.

Key Words: genome-wide association study, candidate gene, fertility trait

446 Analysis of health trait data from on-farm computer systems in the United States. I: Pedigree and genomic variance components estimation. K. L. Parker Gaddis*[1], J. B. Cole[2], J. S. Clay[3], and C. Maltecca[1], *[1]North Carolina State University, Raleigh, [2]Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD, [3]Dairy Records Management Systems, Raleigh, NC.*

With an emphasis on increasing profit through increased dairy cow production, a negative relationship with fitness traits such as health has become apparent. Decreased cow health can affect herd profitability through increased rates of involuntary culling and decreased or lost milk sales. Improvement of health traits through genetic selection is an appealing tool; however, there is no mandated or consistent recording system for health data in the US. Producer-recorded health information may provide a wealth of information for improvement of dairy

cow health, thus improving the profitability of a farm. The principal objective of this study was to use health data collected from on-farm computer systems to estimate variance components and heritability for health traits commonly experienced by dairy cows. The single-step method was then used to incorporate genomic data in a multiple trait analysis. Single-trait binomial analyses were performed for 9 health traits using a sire model. Health traits included cystic ovaries, digestive disorders, displaced abomasum, ketosis, lameness, mastitis, metritis, reproductive disorders, and retained placenta. Parity and year-season were included as fixed effects and herd-year and sire were included as random effects. Heritability estimates ranged from 0.03 (SE = 0.06) for cystic ovaries to 0.20 (SE = 0.02) for displaced abomasum. Variance component estimates were used in a multiple trait analysis including the aforementioned health traits. Heritability estimates calculated from the multiple trait model ranged from 0.02 [95% highest posterior density (HPD) = 0.01, 0.03] for lameness to 0.13 (95% HPD = 0.11, 0.16) for displaced abomasum. A strong genetic correlation was found between displaced abomasum and ketosis (0.81). The single-step genomic analysis calculated heritability estimates that ranged from 0.01 (95% HPD = 0.004, 0.014) for lameness to 0.09 (95% HPD = 0.073, 0.107) for mastitis as well as comparable genetic correlations. From the results of these analyses, it was concluded that genetic selection for health traits using producer-recorded data are feasible.

Key Words: dairy, health, variance component

447 Analysis of health trait data from on-farm computer systems in the United States. II: Comparison of genomic analyses including two-stage and single-step methods. K. L. Parker Gaddis*[1], J. B. Cole[2], J. S. Clay[3], and C. Maltecca[1], *[1]North Carolina State University, Raleigh, [2]Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD, [3]Dairy Records Management Systems, Raleigh, NC.*

The development of genomic selection methodology, with accompanying substantial gains in reliability for low-heritability traits, may dramatically improve the feasibility of genetic improvement of dairy cow health. Many methods for genomic analysis have now been developed, including the "Bayesian Alphabet" and single-step methods. However, little research has been conducted to analyze the performance of these methods when applied to lowly heritable traits, such as health events. This may be due in part to a lack of documented phenotypes for health events. Producer-recorded health information may be able to fill this gap and provide health-related phenotypes, allowing substantial improvements to be made in these traits. The principal objective of this study was to investigate various genomic methods applied to health data collected from on-farm computer systems in the US. A single-step analysis was conducted to estimate variance components and heritabilities of health traits commonly experienced by dairy cows including displaced abomasum, ketosis, lameness, mastitis, metritis, and retained placenta. A blended H-matrix was constructed for a one-step threshold model with fixed effects of parity and year-season and random effects of herd-year and sire. Two-stage Bayesian methods were also implemented including single-trait and multiple-trait Bayes A analyses using deregressed sire breeding values as pseudo-phenotypes. The deregressed breeding values were obtained from prior analyses using threshold sire models. The data were split into 4 groups for cross-validation using K-means clustering. Mean reliabilities of genomic estimated breeding values calculated with the single-step method ranged from 0.35 to 0.41. Mean reliability of genomic estimated breeding values, calculated using single-step methods, increased 33% from previous estimates calculated from pedigree information for all traits. Comparable increases in reliability were obtained using 2-stage methods. It was concluded that the addition of genomic information can improve the estimates of lowly heritable health traits.

Key Words: dairy health, genomic, single-step