LB4 Effects of glucuronic acid and *N*-acetyl-D-glucosamine on the in vitro fertilization of porcine oocytes. K. Schmidt*, K. Dalton, C. Durfey, K. Lemon, A. Mello, and B. D. Whitaker, *University of Findlay, Findlay, OH.*

Pig oocytes fertilized in vitro experience high polyspermic penetration rates due to inadequate cortical granule exocytosis. The objective was to minimize polyspermic penetration by increasing the perivitelline space (PVS) thickness through supplementation of its components, glucuronic acid (GA) and *N*-acetyl-D-glucosamine (GlcNAc) during maturation. Oocytes (n = 1,000) were supplemented during the last 24 h of maturation with either 0.01 m*M* GA, 0.01 m*M* GlcNAc, 0.01 m*M* GA and GlcNAc, or 0.005 m*M* GA and GlcNAc and then evaluated for zona pellucida and PVS thickness. Intracellular glutathione concentrations were determined after maturation in a portion of the oocytes (n = 300) and the remaining oocytes were fertilized. At 12 h post-fertilization oocytes (n = 300) were evaluated for fertilization and cortical granule characteristics and the remaining putative embryos were cultured and evaluated for cleavage and blastocyst formation at 48 h and 144 h postfertilization. There were no significant differences between the treatments for zona pellucida thickness, intracellular glutathione concentrations, penetration rates, or male pronuclear formation. The PVS thickness was significantly thicker ($P < 0.05$) in all treatments compared to the control (4.45 ± 0.71 μm). Oocytes supplemented with 0.01 m*M* GA (9.62 ± 0.87 μm) or 0.01 m*M* GA and GlcNAc (9.65 ± 0.91 μm) had significantly thicker PVS ($P < 0.05$) than 0.01 m*M* GlcNAc (7.57 ± 1.16 μm) or 0.005 m*M* GA and GlcNAc supplemented oocytes (5.99 ± 0.82 μm). Oocytes supplemented with 0.01 m*M* GA or 0.01 m*M* GA and GlcNAc had significantly more cortical granule exocytosis ($P < 0.05$) compared with the other treatments. Oocytes supplemented with GA had significantly lower incidences ($P < 0.05$) of polyspermic penetration compared with the control (32.00 ± 4.80%) or 0.01 m*M* GlcNAc (40.00 ± 7.93%) and significantly higher rates ($P < 0.05$) of cleavage and blastocyst formation by 48 and 144 h postfertilization. These observations indicate that supplementing GA during oocyte maturation decreases polyspermic penetration by increasing PVS thickness and cortical granule exocytosis in pigs.

Key Words: cortical granules, polyspermy, pig

LB5 Direct use of MACE EBV in the Walloon single-step Bayesian genomic evaluation system. J. Vandenplas[1,2], F. Colinet[1], P. Faux[1], S. Vanderick[1], and N. Gengler*[1] *[1]ULg-GxABT, Gembloux, Belgium, [2]FNRS, Brussels, Belgium.*

Single-step genomic evaluations (ssGBLUP) should reduce potential biases in the estimation of genomically enhanced breeding values (GEBV) by the simultaneous combination of genomic, pedigree and phenotypic information, also because fewer approximations are made than in multi-step methods. However, most current genomic evaluation systems are multi-step, relying heavily on the use of multiple across-country evaluation (MACE) results as the primary source of foreign phenotypic information. Recently a need was identified to develop direct use of MACE estimated breeding values (MACE EBV) in ssGBLUP. Therefore, the aim of this report is to show the development and practical use of an innovative method that considers simultaneously all available genotype, pedigree, local, and foreign information in a genomic evaluation system. The developed method is a Bayesian approach associated with ssGBLUP. The method allows a correct propagation of information and avoids multiple considerations of contributions. It also allows adding and subtracting contributions from different information sources; for example, to avoid double counting of local information already contributing to MACE EBV. Another advantage of this Bayesian approach is that it creates a model equivalent to a complete one directly combining all available information without any additional deregression steps. The approach was set up using 27,376 Holstein animals, 11,550 with a Walloon EBV and 1,345 bulls with MACE EBV. A total of 1,351 cows and bulls contributed to the genomic relationship matrix that was combined with the pedigree-based numerator relationship matrix. Phenotypic information was added through Walloon EBV and MACE EBV. Local information also included in MACE EBV was discounted for by subtracting in the Bayesian integration process the local EBV sent to Interbull. This genomic evaluation system passed the Interbull GEBV tests for milk, fat and protein yields and the majority of type traits in February 2013. This approach has the potential to improve current genomic prediction strategies also in beef and in other species (e.g., swine).

Key Words: Bayesian integration, MACE, genomic prediction

LB6 Genetic mechanisms that contribute to differences in beef tenderness following electrical stimulation. R. N. Vaughn*, A. K. Torres, K. J. Kochan, R. K. Miller, C. A. Gill, A. D. Herring, D. G. Riley, J. O. Sanders, J. W. Savell, T. H. Welsh, and P. K. Riggs, *Texas A&M University, College Station.*

Beef tenderness is valued by consumers and influenced by both environmental and genetic factors. Postmortem treatment by electrical stimulation (ES) increases tenderness and reduces, but does not eliminate, variation among carcasses. The purpose of this study was to examine genetic factors that influence tenderness, particularly in post-ES beef. Skeletal muscle samples were collected immediately after slaughter from crossbred F_2 Nellore-Angus steers. Warner-Bratzler shear force (WBSF) measurements following 14 d of aging were used as an objective measure of tenderness. Microarray analysis of samples from 48 steers, chosen for divergent response to ES, was used to identify networks of genes with significantly different gene expression between tenderness groups, and to identify significantly enriched signaling pathways. In addition, SNP haplotype blocks encompassing genes of interest were constructed to examine parent and breed of origin effects. The extracellular matrix (ECM) and focal adhesion pathways were enriched in the microarray assay. From this pathway, a total of 40 genes were assayed by qRT-PCR. Several genes in the integrin family were upregulated in the group that responded well to ES compared with the group that responded poorly. Through haplotype analysis, we found that breed and parent of origin had an effect on tenderness. Breed of origin of integrin alpha-6 (*ITGA6*) corresponded to a 0.15-kg difference in ES residual tenderness values when inherited maternally ($P = 0.03$). The gene fibronectin 1 (*FN1*) had a difference in ES residual tenderness of 0.23 kg for different paternally inherited haplotypes ($P < 0.01$). Also, *ITGA6* protein expression was closely related to mRNA expression in the subset analyzed by Western blot (gene and protein expression levels were both 1.8-fold higher in the tender group than the low; $P = 0.04$ and $P = 0.02$ respectively). This approach identified a network and biological mechanism associated with tenderness not previously established. These results also suggest that targeting components of the ECM represents a novel area of research for improving tenderness.

Key Words: tenderness, beef, electrical stimulation

LB7 A new inline device for predicting individual cow somatic cell count using ATP measurement technology. B. W. Woodward*[1], A. J. Seykora[2], and T. Koopman[3], *[1]NextGen, Lawrenceville, GA, [2]University of Minnesota, St. Paul, [3]Isogen Animal Care, De Meern, the Netherlands.*