

and sire into groups of 12, adapted to a corn silage-based diet (140g CP, 1.73 Mcal NEM and 1.22 Mcal Neg per kg DM), and trained to use calen gates. Feed offered was recorded on a daily basis and used to calculate average daily feed intake. Bulls were weighed every 14 d and growth (ADG) was determined by linear regression of weight against time. Mean ADG and DMI were  $1.52 \pm .23$  DM/day and  $7.25 \pm 1.12$  kg. Three measures of feed utilization were calculated and compared. Feed to gain ratio (FGR) was calculated by taking the average DMI of each bull divided by ADG. Residual feed intake (RFI) was calculated using two different methods. Method 1 was based on the NRC equations (NRFI) and for method 2 phenotypic regression using ADG and DMI adjusted to a common 42 day mid weight (RRFI) was used. Partial correlations with sire nested within year, year, and

pen as fixed effects were calculated. Correlations between NRFI with RRFI, FGR and ADG were 0.965, 0.794 and -0.217, respectively. Correlations between RRFI with FGR and ADG were 0.819 and -0.005. There were no relationships found to be significant between feed utilization calculations and ultrasonic measurements of intramuscular fat, rib eye area, rump fat and rib fat. As expected NRFI and RRFI were highly correlated indicating that they are the same trait. Both NRFI and RRFI were highly correlated with FGR. It was concluded that FGR is a good predictor of RFI. Alternative methods of calculating RFI were found to be nearly identical and independent of ultrasonic measures of body composition.

**Key Words:** Beef Cattle, Residual Beef Intake, Efficiency

## Breeding and Genetics - Livestock and Poultry: Dairy Cattle I

**223 Dry matter feed intakes for first lactation Holstein, Jersey and their reciprocal crosses in the Virginia Polytechnic Institute and State University crossbreeding project.** K. M. Olson\*, B. G. Cassell, and M. D. Hanigan, *Virginia Polytechnic Institute and State University, Blacksburg.*

The crossbreeding project at Virginia Polytechnic Institute and State University began in the fall of 2002. Holstein and Jersey foundation females were mated to four Holstein bulls and four Jersey bulls to create JJ, HH, JH and HJ breed groups (sire breed listed first). Collection of individual feed intakes on first lactation project cows began in September 2005 and continues through 2007. Individual feed intakes are measured in two week trials during every six week period (two weeks on, four weeks off) on first lactation cows less than 305 days in milk. All cows were fed the herd total mixed ration before and during the trial. Forages, grains and concentrates were submitted for nutrient analyses at least once during each trial period. An 'as-fed' intake and dry matter intake were calculated daily for the project cows during the feed intake cycle and averaged across week of production. A mixed model using repeated records was used to analyze dry matter intakes. Effects included trial, breed group [(HH (n=25), HJ (n=17), JH (n=15), JJ (n=11)], age at calving, week in milk and breed by week in milk interaction. Significant effects ( $P<0.05$ ) for dry matter intake included breed group and week in milk however, the interaction between week in milk and breed and differences between trials were not significant. LSM for dry matter intakes across all weeks were  $22.2 \pm 0.3$ ,  $21.2 \pm 0.3$ ,  $20.8 \pm 0.4$ , and  $17.5 \pm 0.4$  kg for HH, HJ, JH and JJ respectively. In general, dry matter intake reached a plateau at 13 weeks. All breed groups were significantly different from one another except the HJ and JH. Visual inspection of breed group means by week in milk suggests a positive heterosis for dry matter intake (untested).

**Key Words:** Crossbreeding, Dry Matter Intake, Feed Intake

**224 Comparison of Holstein–Friesian, Norwegian Red and Holstein–Friesian×Norwegian Red cows on Irish dairy farms: Milk production and udder health.** N. Begley\*<sup>1,2</sup>, M. Rath<sup>2</sup>, and F. Buckley<sup>1</sup>, <sup>1</sup>*Teagasc, Moorepark, Fermoy, Co. Cork, Ireland*, <sup>2</sup>*School of Life Sciences, UCD, Belfield, Dublin, Ireland.*

The objective of this study was to compare the milk production performance and udder health of Holstein–Friesian (HF), Norwegian

Red (NRF) and Holstein–Friesian×Norwegian Red (F1) cows in first lactation. This study forms part of a 3–year on–farm crossbreeding study comprising 46 dairy herds. Milk production data was available for 1327 first lactation cows: 710 HF, 325 NRF and 292 F1. Predicted 305 d yields were obtained from the Irish Cattle Breeding Federation. These were derived using the SLAC method which adjusts for calving month, age at calving, parity and season of calving. Production data were analyzed in SAS using proc GLM and udder health data were analyzed using proc LOGISTIC. Herd, breed and calving date (udder health only) were included in the model. The 305 d milk yields of the HF and F1 were similar at 5,353 kg and 5345 kg, respectively. The NRF produced slightly less milk at 5149 kg ( $P<0.001$ ). Fat content was highest for the HF at 4.00%, intermediate for the F1 at 3.96%, and lowest for the NRF at 3.94% ( $P<0.05$ ). Protein content was similar for all breeds; 3.46%, 3.45% and 3.45% for the HF, NRF and F1, respectively. The NRF and F1 showed superior udder health during lactation. Compared to the HF (2.04), the F1 and NRF cows had lower somatic cell score at 1.97 ( $P<0.01$ ) and 1.92 ( $P<0.001$ ), respectively. The proportion of NRF cows (5.8%) with somatic cell counts averaging greater than 400,000 during lactation was lower than the HF (9.9%;  $P<0.05$ ). That of the F1 (6.7%) tended to be lower ( $P=0.097$ ) than the HF. The incidence of mastitis was available for 42 of the 46 herds. Fourteen percent of the HF cows had mastitis at least once during lactation, compared to 9.5% for both the F1 ( $P=0.063$ ) and the NRF ( $P<0.05$ ). In conclusion, based on data from year one, the F1 cows produced similar levels of milk production to the HF. Both the NRF and F1 exhibited superior udder health compared to the HF.

**Key Words:** Norwegian Red, Udder Health, Milk Production

**225 Heritability of electronically recorded daily body weight across lactation using random regression models.** J. K. Toshniwal\*<sup>1</sup>, C. D. Dechow<sup>1</sup>, J. A. D. R. N. Appuhamy<sup>2</sup>, and B. G. Cassell<sup>2</sup>, <sup>1</sup>*The Pennsylvania State University, State College*, <sup>2</sup>*Virginia Polytechnic Institute and State University, Blacksburg.*

The objectives of this study were to estimate heritability for daily body weight (BW) and genetic correlations among BW at different days in milk (DIM). The Afiweigh cow body weighing system records BW of every cow exiting the milking parlor. The Afiweigh system was installed at the The Pennsylvania State University dairy herd in August of 2001 and in July of 2004 at the Virginia Polytechnic Institute and State University dairy herd. BW recorded after 365 DIM were

eliminated. Outliers were detected by generating a predicted BW curve for each cow and daily records more than four standard deviations from the curve were eliminated. The data included 202,143 observations from 575 The Pennsylvania State University and 120 Virginia Polytechnic Institute and State University Holstein cows, respectively. The random regression model in ASREML included fixed effects for age within parity, week of lactation and herd-date. Random effects included animal, permanent environment and error. The order of the polynomial was 4 for animal and 6 for permanent environment. Residual structures were grouped into the following months of lactation: 1, 2-3, 4-5, 6-8, and 9-12. Heritability estimates ranged from 0.48-0.56 and were highest between 200-230 days of lactation and lowest at 305 DIM. The genetic variance for BW declined for the first 30 DIM and climbed until the end of lactation. Genetic correlations between BW at different DIM ranged from 0.73 (DIM 0 and 100) to 1.0. The correlations among BW between early and later parts of lactation (0.83 between 0 and 305 DIM) were higher than correlations between early and mid lactation. Electronically recorded daily BW are heritable and they could be used for genetic evaluation of BW and BW change across the lactation.

**Key Words:** Body Weight, Heritability, Random Regression

**226 Evaluation of factors affecting changes in the ranking of sires over time.** A. D. Coburn<sup>\*1,2</sup>, K. A. Weigel<sup>1</sup>, S. A. Schnell<sup>2</sup>, and G. Abdel-Azim<sup>2</sup>, <sup>1</sup>University of Wisconsin, Madison, <sup>2</sup>Genex Cooperative, Inc., Shawano, WI.

Selection of sires for A.I. contract matings occurs primarily from the pool of active sires with initial progeny test results. Because high selection intensity is applied to small number of low reliability (REL) bulls, accuracy of sire evaluation significantly affects genetic progress in later generations. Our objective was to quantify mean change in rank of contract mating sires and their contemporary sires and to estimate how much of the change in rank can be attributed to redefinition of a trait or modification of the selection index. February 1999 active Holstein sires were used to determine contract mating sires and contemporary sires. Twenty-nine bulls were identified as influential mating sires with > 5 sons sampled in 2000 or later. Percentile rank of these sires was calculated annually through February 2006 for combined fat + protein (CFP), productive (PL), somatic cell score (SCS), udder composite (UDC) and Lifetime Net Merit (LNM). Mean change in rank of all active sires from 1999 to 2006 was zero for all traits. Mean absolute change in rank was 13-14% for CFP, SCS, and UDC and 20-22% for PL and LNM. The mean change in rank for contract mating sires was negative for all traits, as was mean absolute change of rank. Among subgroups based on REL of yield, bulls with high REL (>89%) tended to increase in rank for LNM, whereas bulls with intermediate (80-89%) or low (<80%) REL had negative mean change in rank with a negative skew. Multi-trait indices (MTI) were calculated weighting the aforementioned traits to mimic changes to the LNM formula in years 2000, 2003 and 2006. Mean absolute change in rank when using MTI for a given year was ≤ 8% for both sire groups. Although some change in rank can be attributed to changes in trait definition or revision of economic weights in the selection index, inaccuracy of sire evaluations for individual traits appears to contribute more significantly to the instability in rankings of A.I. contract mating sires.

**Key Words:** Dairy Cattle Breeding, AI Contract Mating Sires, Change in Rank

**227 SNP identification in genes involved in the SREBP1 pathway in dairy cattle.** J. F. Medrano\* and G. Rincon, *University of California, Davis.*

The objective of this analysis is to identify natural sequence variations in candidate genes that determine the quantities, compositions and structures of the lipids of milk in dairy cows. We developed a strategy to detect SNPs in 6 genes in the SREBP1 pathway, which closely regulates the Stearoyl-CoA-Desaturase (SCD). The analysis consisted in re-sequencing 1000bp of the 5'UTR, coding regions and 500bp of the 3'UTR in Sterol regulatory element-binding protein-1 (SREBP1), SREBP cleavage-activating protein (SCAP), Insulin induced protein 1 (INSIG1), Insulin induced protein 2 (INSIG2, Membrane-bound transcription factor protease, site 1 (MBTPS1) and Membrane-bound transcription factor protease, site 2 (MBTPS2) genes. Vista alignments were used to identify highly conserved regions for re-sequencing. The target gene regions were resequenced in 24 animals from three dairy breeds: Holstein, Jersey and Brown Swiss. All the sampled animals were unrelated with no common ancestors in a three generation pedigree. Haploview software was used to identify linkage disequilibrium regions within the breeds and to determine tag SNPs. A total of 49 SNPs were detected and 32 were identified as tag SNPs. The number of SNPs per gene was: 7 in SREBP1, 11 in SCAP, 17 in INSIG1, 11 in INSIG2, 2 in MBTPS1 and 1 in MBTPS2. Eleven SNPs were located in exons, 7 were synonymous and 4 were non-synonymous. SIFT and Polyphen analysis were performed in the non-synonymous SNPs and two of the SNPs were classified as 'not tolerated', the first one is an amino acid change Pro/Ser in SCAP and the second one is an amino acid change Leu/Pro in the SREBP1 protein. From this analysis we have detected haplotype blocks that identify the diversity between breeds and we were able to select SNP markers that will be the basis for genotyping cows to define possible associations with milk fatty acid composition.

**Key Words:** SNP, Candidate Genes, Fatty Acids

**228 First steps to model milk urea in a management perspective.** C. Bastin<sup>\*1</sup>, A. Gillon<sup>1</sup>, and N. Gengler<sup>1,2</sup>, <sup>1</sup>Gembloux Agricultural University, Gembloux, Belgium, <sup>2</sup>National Fund for Scientific Research, Brussels, Belgium.

Several studies have shown that milk urea concentration is an interesting tool for herd management because of its strong links with nutritional imbalance in dietary protein. It could also be a predictor for functional traits like fertility or longevity. The objectives of this study were to estimate variance components and heritabilities for milk urea concentration during the three first lactations using a multi-lactation single-trait random regression test day model. Potentialities of predicting milk urea concentration were also studied in order to bring nutritional management tools to breeders by comparing predicted and observed productions. Available data were 3,593,575 milk urea test day concentrations from the Walloon Region of Belgium collected from 2001 to 2006. Seven herd-based random sub data sets were created and (co)variances estimation was done by REML. In order to increase usefulness of the model to predict urea for each potential test-day the classical herd - test date fixed effect was replaced by the sum of a fixed herd - year effect, a fixed herd - season effect and a random herd - test date effect as recently proposed for yield traits. Mean heritabilities estimates for milk urea were 0.21, 0.24 and 0.25 for first, second and third parity, respectively. Variances components indicated also that high variance (approximately 50% of total variance)

was associated with the random herd test-day effect. Correlations across lactations for this effect showed very high values close to 1. These results could indicate the influence of local events (e.g., diet related) covering all lactations. Results have also large implications on the predictability of successive urea records. Additional research is required to check if adapted (co)variance structures linking successive test-day records could improve predictability of urea.

**Key Words:** Milk Urea, Modeling, Genetic Parameters

**229 Milk production, body condition score at breeding and reproductive efficiency of first lactation Holstein–Friesian, Jersey and Holstein–Friesian×Jersey cows under Irish grass–based production circumstances.** R. Prendiville<sup>\*1,2</sup>, F. Buckley<sup>1</sup>, N. Byrne<sup>1</sup>, and M. Rath<sup>2</sup>, <sup>1</sup>*Teagasc, Fermoy, Co. Cork., Ireland*, <sup>2</sup>*University College Dublin, Belfield, Dublin, Ireland*.

The objective of this study was to compare production, body condition score at breeding and reproductive performance of first lactation Holstein–Friesian (HF), Jersey (JE) and Jersey×Holstein–Friesian (JEX) cows across two seasonal grass–based milk production systems (low concentrate 750 kg or high concentrate 1,250 kg). The study included a total of 87 cows: 30 HF, 28 JE and 29 JEX. The mean calving date was February 19. Large differences in milk yield, fat content and protein content were observed ( $P < 0.001$ ). Milk yield ranged from 3836 kg for the JE to 4700 kg for the HF. The JEX produced 4294 kg. The JE had the highest milk fat content at 5.24%, compared to 3.95% for the HF and 4.67% for the JEX. Milk protein content was 3.42% for the HF, 3.71% for the JEX and 3.97% for the JE. Solids corrected milk yield (SCM) was similar for all breeds; 4387 kg, 4338 kg and 4509 kg for the HF, JE and JEX, respectively. BCS at breeding was 2.97, 3.04 and 3.13 for the HF, JE and JEX; significantly higher for the JEX compared to the HF and JE ( $P < 0.05$ ). Breeding started in late April and lasted 13 weeks. Mean submission rate in the first 3 weeks was 85%. Although not significantly different (due to data size), pregnancy rates observed did suggest differences in reproductive efficiency between the groups. The HF had the lowest reproductive performance (pregnancy rate to first service (PREG1) = 43%, incalf after 6 weeks breeding (PR42) = 57%, calving to conception interval (CCI) = 98 days, and number of services (NSERV) = 2.01). Comparable values for the JE and JEX were PREG1 = 64% and 65%, PR42 = 75 and 76%, CCI = 79 and 93 days, and NSERV = 1.57 and 1.55, respectively. In conclusion, first lactation results suggest that JE and JEX cows have a propensity to produce similar levels of SCM but have superior reproductive efficiency compared to the HF under Irish production circumstances.

**Key Words:** Milk Production, Reproductive Performance, Crossbreeding

**230 Effect of service sire and cow sire on gestation length.** H. D. Norman<sup>\*</sup>, J. R. Wright, P. M. VanRaden, and J. B. Cole, *Agricultural Research Service, USDA, Beltsville, MD*.

Variance components for effect of service sire and cow sire on gestation length (GL) indicate that bull differences exist and provide an opportunity to change GL. Bull predicted transmitting abilities (PTA) for GL as either a service sire or cow sire were derived using data from >8 million calvings from 1999 through 2005. Model effects

were calving year, calving herd-year, calving month, age-parity, calf birth code (gender and multiple-birth status), lactation length, milk yield, service sire, sire, and cow. All effects were fixed except service sire, sire, and cow. For bulls with  $\geq 100$  daughter records for GL, PTA were examined for all bulls (323 service sires and 397 sires with both heifer and cow records) and those in active artificial-insemination (AI) service (137 service sires and 67 sires). Standard deviations of service-sire PTA for all bulls were 1.43 d for heifer (parity 1) GL and 1.32 d for cow (parities 2 to 5) GL; corresponding standard deviations for sire PTA were 0.75 and 0.78 d. Among active-AI bulls, O-Bee Manfred Justice had the lowest PTA for daughter GL (–2.0 d) and an extremely low PTA for service-sire GL (–4.0 d); Silky Gibson had the highest PTA for daughter and service-sire GL (+2.3 d and +4.1 d, respectively). Correlation between heifer and cow service-sire PTA was 0.96 for all bulls and 0.97 for active-AI bulls; corresponding correlation for sire PTA was 0.83 for both all bulls and active-AI bulls. Correlation of sire with service-sire PTA for heifers was 0.63 for all bulls (192) and 0.49 for active-AI bulls (58); corresponding correlations for cows were 0.69 (2,441 bulls) and 0.70 (151 bulls). For bulls with  $\geq 500$  daughter records for GL, correlation of sire with service-sire PTA for cows was 0.74 for all bulls (588) and 0.69 for active-AI bulls (38). Although genetic information for GL would be useful for predicting expected calving date, substantially more research is needed to determine the potential consequences of selection for either shorter or longer GL.

**Key Words:** Gestation Length, Genetic Evaluation

**231 Inbreeding and relationship related to genetic estimates of calf survival in one Holstein sire family.** R. D. Shanks<sup>\*</sup>, *University of Illinois, Urbana*.

Calf survival was genetically estimated by PJ Berger of Iowa State University for 271 descendants of Carlin-M Ivanhoe Bell (Bell). This included 226 sons and 45 grandsons. The purpose of this study was to evaluate the contributions of relationship to Bell, inbreeding of descendants, and inbreeding of their daughters on these estimates of survival. The model explained almost 36% of the variability in calf survival. Relationship to Bell was the most significant factor in the model ( $p < 0.0001$ ). Genetic estimates of calf survival for sons averaged 0.0108 (standard error of 0.0004) and genetic estimates of calf survival of grandsons averaged 0.0018 (standard error of 0.0010). Genetic estimate of calf survival for Bell himself was 0.019. As expected, the genetic estimates of calf survival for descendants regressed back toward the mean of the population. Calf survival of sons was closer to estimate for Bell than that of the grandsons. Close relatives had greater resemblance for survival. The second significant factor ( $p < 0.01$ ) was regression of genetic estimate of calf survival on inbreeding of descendants. Genetic estimate of calf survival increased 0.065 (standard error of 0.024) per one percent increase of inbreeding of descendants. Inbreeding of active AI descendants of Bell was not detrimental to the survival of their offspring. Although in this sample, the regression of genetic estimate of calf survival on daughter inbreeding was not significant ( $p > 0.28$ ), the sign was negative, consistent with recommendation to minimize change in inbreeding in the female population. Genetic concept of resemblance between relatives is supported in this study. Consequences of inbreeding are shown to not always be detrimental. Inbreeding can be a useful genetic tool to improve calf survival.

**Key Words:** Genetic Estimates of Calf Survival, Inbreeding, Dairy Cattle

**232 Real-time PCR quantification of reproductive hormone receptor gene expression in superovulated MOET donor cows.** S. Wise\*<sup>1</sup>, M. A. Okomo-Adhiambo<sup>1</sup>, D. Joos<sup>1</sup>, W. Rauw<sup>1</sup>, A. Rink<sup>2</sup>, and L. Gomez-Raya<sup>1</sup>, <sup>1</sup>University of Nevada, Reno, <sup>2</sup>Animal Disease and Food Safety Laboratory, Reno, NV.

Multiple ovulation and embryo transfer (MOET) facilitates production of offspring from cattle of high genetic merit world-wide. Twelve multiparous non-lactating donor cows were synchronized to estrous by intravaginal insertion of 1.38g progesterone (Eazi-Breed™ CIDR®), in addition to intramuscular injection of 1ml combination of progesterone (150mg/ml) and 17-β-estradiol (10mg/ml). Evening of day 5, 5ml FSH (Folltropin® 20mg/ml) was given intramuscular, then every 12 hrs (AM and PM) over the next 4 days. Morning and evening of day 8, corresponding to day 4 of FSH treatment, 10ml prostaglandin (Lutalyse® 5mg/ml) was given intramuscular. Morning of day 9, the last FSH shots were given and CIDR® devices removed. Cows were monitored for heat and bred thrice by AI, and embryos collected 7 days after breeding. Superovulation and embryo flushing protocol was performed twice for all cows, yielding average 0-30 embryos. Blood and serum samples for nucleic acid and hormone biochemical analysis, respectively, were taken throughout the experimental period. Quantitative real-time PCR (QRT-PCR) was used to profile expression of 5 reproductive hormone receptor genes (ESR1, FSHR, LHR, OXTR and PGR), using total RNA isolated from blood sampled over 84 hrs of FSH treatment (0h, 12h, 24h, 36h, 48h, 60h, 72h, 84h), from two cows that yielded the highest number of embryos (30 and 24, respectively) and from the cow that yielded none. All five genes were significantly over-expressed (expression ratio ≥2.0 and t-test p-value ≤0.05) in the best performing cows (#119 and #128) compared to the least performing cow (#134), in at least five of the eight experimental time-points. In cow #119 compared to #134, ESR1 was up-regulated 2- to 4-fold (0-48h) and by 10-fold at 84h, while FSHR, LHR, OXTR and PGR were significantly up-regulated at all time-points. Similar results were observed in cow #128 compared to #134, suggesting that expression of hormone receptor genes is vital to a donor cow's physiological response to reproductive hormone treatments administered for superovulation.

**Key Words:** MOET, Reproductive Hormone Receptor Genes, Quantitative real-time PCR

## Companion Animals: Companion and Comparative Animal Nutrition

**234 Effect of gut-loading time on nutrient content of adult feeder crickets.** C. L. Dikeman\*, S. D. Plesuk, D. L. Klimek, and L. G. Simmons, *Omaha's Henry Doorly Zoo, Omaha, NE.*

Insectivorous amphibians and reptiles in captivity are typically limited to diets consisting primarily of feeder crickets. Without supplementation, farmed feeder crickets lack proper nutrient profiles to sustain the health of preying animals. While gut-loading of crickets is common practice among herpetologists, management of gut-loading crickets is poorly defined. The objective of this experiment was to determine optimal gut-loading time to best improve the nutrient profiles of feeder crickets for amphibians and reptiles in captive environments. Farmed crickets (*Acheta domesticus*) were purchased from a vendor (The Bug Company, Ham Lake, MN) and fed a commercial high-calcium cricket diet (PMI, St. Louis, MO) for 24, 48, 72, or 168 h, in a replicated block design. Dry matter (DM) concentrations of crickets gut-loaded for 24, 48, or 72 h (31.7, 31.5, and 31.8%, respectively) were higher (P<0.05) compared with 168 h (30.1%). No differences were

**233 Poisson versus logit models for genetic analysis of mastitis in Norwegian cattle.** A. I. Vázquez\*<sup>1</sup>, K. A. Weigel<sup>1</sup>, D. Gianola<sup>1</sup>, D. M. Bates<sup>1</sup>, and B. Heringstad<sup>2</sup>, <sup>1</sup>University of Wisconsin, Madison, <sup>2</sup>Norwegian University of Life Science, Ås, Norway.

Clinical mastitis incidence is typically coded as presence/absence during some period of exposure, and records are analyzed with linear or logit models. Since "presence" includes cows with multiple episodes, there is a loss of information when a count is treated as a binary response. Poisson (P) and logit (L) mixed models were fitted to clinical mastitis records on 36,178 first-lactation daughters of 245 Norwegian Red sires distributed over 5,286 herds. An R implementation (lme4 package) was modified to allow for correlations between random effects, such that pedigree information could be included. Since 26% of the cows had lactations shorter than 300 d, the log of days in milk (DIM) was included via the function  $\log(\lambda * \text{DIM}) = \text{fixed} + \text{herd} + \text{sire}$  effects, where  $\lambda$  is the per-day Poisson parameter peculiar to a record. Predictive ability of models was assessed via a two-fold cross-validation using mean squared error (MSE) as end-point. On average, there were 0.295 cases of mastitis per cow; 77% of the cows did not have the disease, and only about 1% of the cows had 3 or more episodes during lactation. Between-sire variance estimates were 0.065 in P and 0.093 in L. The ratio between herd and sire variances was 4.6 and 3.7 for P and L models, respectively. The correlation between predicted random effects from the two models was 0.95 and 0.94 for sires and herds, respectively. Predictive MSE for all data was smaller for the Poisson model: 0.346 vs. 0.351. Within healthy animals, MSE was 0.053 (L) and 0.085 (P). For animals with 1 case, MSE values were 0.583 (L) and 0.499 (P). For animals with 2 cases, and 3 or more cases, the P model also had a better predictive performance. The cross-validation suggested a better overall performance of the Poisson model over the logit model, primarily due to improved predictive ability within diseased animals. The P model may be even better in situations in which the disease is more prevalent.

**Key Words:** Mastitis, Poisson, Threshold

detected for organic matter (OM), crude protein (CP), acid-hydrolyzed fat (AHF), or crude fiber (CF) concentrations among gut-loading treatments. Calcium concentrations were higher (P<0.05) after crickets were gut-loaded for 24 h (1.39%) compared with 48, 72, or 168 h (0.42, 0.37, and 0.66%, respectively). Magnesium concentrations were higher (P<0.05) after gut-loading crickets for 24 or 168 h (0.20 and 0.18%, respectively), compared with 48 or 72 h (0.10 and 0.09%, respectively). Concentration of manganese in crickets was higher (P<0.05) after 24 h (59.5 ppm) compared with crickets gut-loaded for either 48 or 72 h (28.5 and 27.0 ppm, respectively). No differences were detected in concentrations of sulfur, phosphorus, potassium, sodium, iron, copper, or zinc. Overall, gut-loading crickets for 24 h appeared more effective in increasing mineral concentrations compared with other time treatments. Further research is needed to completely elucidate the most effective strategies to increase nutritive value of feeder crickets for captive amphibians and reptiles.

**Key Words:** Reptile, Amphibian, Minerals