Breeding and Genetics: Dairy Cattle Breeding I: Genetic Improvement of Animal Health

226 Genomics of functional traits in dairy cattle. N. Vukasinovic*[1], Y. Li[2], J. D. Nkrumah[1], P. Boddhireddy[1], J. Osterstock[1], F. A. Di Croce[1], M. Kelly[2], M. Hvinden[1], D. J. Weigel[3], and S. K. DeNise[1], *[1]Pfizer Animal Genetics, Kalamazoo, MI, [2]Pfizer Animal Genetics, Brisbane, Australia, [3]Pfizer Animal Health, Kalamazoo, MI.*

Functional traits in dairy cows include fertility, health, longevity, and other traits that affect efficiency of dairy operations by decreasing input rather than increasing output. Genetic improvement of functional traits is challenging because of low heritabilities and difficulties related to phenotype recording. Application of genomics-assisted selection seems to be promising for functional traits. In the scope of this study, genomic predictions for several traits describing various aspects of mastitis, reproduction, and postpartum metabolic disorders were developed using a 50K SNP panel. The reference population included over 4,500 Holstein cows sampled from 9 large commercial herds located in 5 different states in the US. The animals had complete pedigree and extensive phenotype information for the traits of interest. The validation population included about 1,200 Holstein cows from an independent herd. The phenotypes of all animals, along with the pedigree consisting of 14,685 individuals, were used to obtain estimated breeding values (EBVs) for the traits of interest. The EBVs of the reference animals, weighted by their accuracies, were used in the genomic analyses to derive marker effects. The estimated marker effects were then used to obtain direct genomic values (DGVs) for the validation animals. The accuracy of DGVs was assessed by calculating correlations between originally estimated EBVs and DGVs. Preliminary results show that genomic information can be used to predict genetic potential of animals for functional traits.

Key Words: dairy cows, functional traits, genomics

227 Genomic selection for enhanced immune response to improve dairy health. K. Thompson-Crispi*[1], R. Ventura[2,3], F. Schenkel[2], F. Miglior[4,5], and B. Mallard[1], *[1]Department of Pathobiology, Ontario Veterinary College, Guelph, ON, Canada, [2]Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, [3]Beef Improvement Opportunities, Guelph, ON, Canada, [4]Guelph Food Research Center, Agriculture and Agri-Food Canada, Guelph, ON, Canada, [5]Canadian Dairy Network, Guelph, ON, Canada.*

Infectious diseases contribute to substantial economic loss in the dairy industry with human and animal health implications. The immune system is a tightly genetically regulated system that largely controls response to infectious disease. Including immune response (IR) traits in a selection index has the potential to improve inherent animal health. Previously, cows classified as High Immune Responders in dairy herds across Canada and one herd in the US were found to have improved response to commercial vaccination, increased milk and colostrum quality and decreased incidence of diseases including mastitis, metritis, ketosis and retained placenta. The objective of this research was to perform a genome-wide association study to determine genetic profiles associated with antibody-mediated immune responses (AMIR). In collaboration with the Canadian Bovine Mastitis Research Network, 680 Holstein cows from 58 herds across Canada were immunized to measure serum antibody to a putative type 2 test antigen. Cows were classified as High, Average and Low immune responders based on EBV for AMIR. A total of 163 cows (81 High IR and 82 Low IR) were genotyped using the Illumina Bovine SNP50 BeadChip. A generalized quasi-likelihood score method was used to determine SNPs significantly associated with AMIR. Preliminary results show 484 SNPs significantly (comparison-wise $P < 0.001$) associated with AMIR. The majority of the SNPs are on chromosome 23 (98/484) followed by chromosome 9 (32/484), 1 (31/484) and 11 (30/484). Determining potential genes and biological pathways associated with these SNPs is currently underway. Results of this study will help to determine if AMIR could potentially be included in genomic selection indices to decrease the incidence and severity of disease in the dairy industry.

Key Words: dairy cattle, genomic selection, immune response

228 Telomere length assessment of Holstein cows in 10 Pennsylvania dairy herds. D. E. Brown,* C. D. Dechow, W. S. Liu, and K. J. Harvatine, *The Pennsylvania State University, University Park.*

Telomeres are known to shorten in humans with increasing age due to the inability of cells to completely replicate chromosomal DNA. Additionally, stress factors in humans are generally associated with a decrease in telomere length. The objective of this study was to assess telomere length variation in dairy cattle using a quantitative PCR (QPCR) procedure and determine if telomere length varied among herds and with age. DNA samples were obtained from purebred Holstein dairy cows from 10 dairy herds. A monochrome multiplex QPCR method was used to quantify relative telomere length for each cow. Primers were designed to create a 79 base pair telomere product and a 144 base pair standard reference gene product with each amplicon having different melting temperatures. Both primer sets were used in the same QPCR reaction well. This allowed independent measurement of amplification, while decreasing variation due to pipetting error and minimized experimental costs. QPCR results for 201 cows, which were run in triplicate, were analyzed using ASREML. Fixed effects of the model included gene, plate, cow, age, herd, the interaction of gene and plate, the interaction of age and gene, and the interaction of gene and herd. Random effects included the interaction of cow and gene, interaction of cow and plate, and the 3-way interaction of cow, plate, and gene. The effect of herd was significant for telomere length ($P < 0.001$). The effect of cow age was significant ($P < 0.05$), with telomere length decreasing as age increased. Least squares means for herd telomere length were positively correlated with rolling herd average milk production ($P < 0.05$). Herd environment appeared to be associated with a physiological response in the telomere length of dairy cattle. However, higher milk production did not appear to elicit a negative effect on telomere length. Telomere assessment may provide a quantifiable measure for future cattle welfare studies.

Key Words: telomere, telomere length, stress

229 Incidence validation and causal relationship analysis of producer-recorded health event data from on-farm computer systems in the United States. K. L. Parker Gaddis*[1], J. P. Cassady[1], J. B. Cole[2], and C. Maltecca[1], *[1]North Carolina State University, Raleigh, [2]Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

Substantial progress has been made in the genetic improvement of production traits in dairy cattle. Due to a negative correlation between production and fitness traits, the health and fitness of dairy cattle have

declined as yields have increased. Health and fitness traits are generally difficult and/or expensive to measure, but health event data collected from on-farm computer management systems may provide an effective and low-cost source of health event information. The principle objective of this study was to analyze the reliability of health event data recorded with on-farm recording systems throughout the United States. To validate editing methods, incidence rates of on-farm recorded health event data were compared with incidence rates reported in the literature. A second aim of this study was to examine putative causal relationships among common health events using data recorded in on-farm computer systems. Calculated incidence rates ranged from 1.4% for respiratory problems to 8% for clinical mastitis. Most health events reported had incidence rates lower than the average incidence rate found in literature. This may represent under-reporting by dairy farmers who record disease events only when a treatment or other intervention is required. Logistic regression was used to examine putative causal relationships among health events within a lactation for 3 timeframes: 0 to 60 d in milk (DIM), 61 to 90 DIM, and 91 to 150 DIM. Herd, season, parity, breed, and year were included in each model as fixed effects. Health events occurring on average before the health event of interest were included in the model as predictors when significant ($P < 0.05$). Path diagrams developed using odds ratios calculated from logistic regression models for each of 13 common health events allowed putative relationships to be examined. The greatest odds ratios were estimated to be the influence of ketosis on displaced abomasum (15.5) and the influence of retained placenta on metritis (8.37), and were consistent with earlier reports. The results of this analysis provide evidence for the usefulness of on-farm recorded health information.

Key Words: dairy, health, path analysis

230 Genetic relationships of mastitis, cystic ovaries and lameness with milk yield and somatic cell score in first-lactation Canadian Holstein cows.

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The objective of this study was to investigate the genetic relationships of the 3 most frequent dairy cattle diseases (mastitis, cystic ovaries and lameness) with test-day milk yield (MY) and somatic cell score (SCS) in first lactation Canadian Holstein cows using random regression models. Health data recorded by producers were available from the National Dairy Cattle Health System in Canada. Disease traits were defined as binary traits (1 = affected, 0 = unaffected) based on whether or not the cow had at least one disease case recorded within 305 d after calving. Random regressions on second order Legendre polynomials were used to model the daily genetic and permanent environmental variances of test-day MY and SCS, while only the intercept term was fitted for disease traits. Genetic correlations between MY and diseases were unfavorable with estimates ranging from 0.21 to 0.42 between MY and mastitis, from −0.05 to 0.29 between MY and cystic ovaries, and from 0.23 to 0.36 between MY and lameness. In contrast, favorable associations were found between SCS and diseases. Genetic correlations varied from 0.64 to 0.71 between SCS and mastitis, from 0.10 to 0.22 between SCS and cystic ovaries, and from 0.19 to 0.29 between SCS and lameness. Unfavorable associations between MY and diseases imply that production and health traits should be considered simultaneously in genetic selection.

Key Words: genetic correlation, disease, milk yield and somatic cell score

231 Genetic relationships among health related fatty acids in milk of Canadian Holsteins.

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The objective of the present study was to estimate heritabilities of and genetic correlations among fatty acids in milk of Canadian Holsteins. The fatty acids studied were chosen because they are important in human health. One morning milk sample was collected from 3185 dairy cows between February and June 2010 from 52 commercial herds enrolled in Dairy Production Centre of Expertise, Valacta. Individual fatty acid percentages (g/100g of total fatty acids) were determined for each sample by gas chromatography. Edits were applied to the databased on registration status of the cow, breed, country, cow and sire and dam identifications, age at calving and stage of lactation. Cows were sampled between 3 to 450 d in milk and were in either parity 1, 2 or 3. Herd-year-season of calving classes were formed considering 2 season effects in a year; that is, March 1 to August 31 and September 1 to February 28/29. Each herd-year-season of calving class was required to have 5 or more observations. Editing reduced the data set to 2573 cows representing 46 herds. Ten fatty acids were studied and included 3 omega-3 fatty acids (C18–3n3ALA, C20:5n3, C22:5n3), 2 conjugated linoleic acids (CLA-9c11t, CLA-10t12c), 2 omega-6 fatty acids (C20:3n6, C20:4n6), C22:0, C23:0 and C24:0. Genetic parameters were estimated using a 10-trait animal model fitted under REML using Wombat software. The model included fixed effects of age at calving and stage of lactation nested within parity; random effects of herd-year-season of calving, animal and residual. The pedigree of animals with data was traced back 5 generations on both the male and female side to account for relationships among animals. The estimates of heritability ranged from 0.01 to 0.21 with standard errors ranging from 0.01 to 0.04. Genetic correlations among fatty acids ranged from 0.74 to −0.72 with standard errors ranging from 0.1 to 0.5. Improvement of the fatty acid proportions in milk through genetic selection is possible as individual fatty acids can respond differently.

Key Words: cow milk fatty acids, health, genetic parameters

232 Crossbreds of Holstein with Jersey and Montbéliarde compared to pure Holsteins for 305-d production and mastitis in a pasture production system.

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Montbéliarde × Holstein crossbred cows (MH, n = 30); Montbéliarde × Jersey × Holstein crossbred cows (MJH, n = 49); Jersey × Montbéliarde × Holstein crossbred cows (JMH, n = 32); Holstein × Montbéliarde × Jersey × Holstein cows (HMJH, n = 47); and Holstein × Jersey × Montbéliarde × Holstein crossbred cows (HJMH, n = 10) were compared with pure Holstein cows (HO; n = 114) for 305-d milk, fat, and protein production; SCS; and mastitis incidence during their first 3 lactations. Cows were housed at the University of Minnesota West Central Research and Outreach Center, Morris, Minnesota, a grazing herd, and calved from March 2006 to June 2011. Best Prediction was used to calculate actual production (milk, fat, protein, and SCS) for 305-d lactations with adjustment for age at calving, and records less than 305 d were projected to 305 d. Incidence of clinical mastitis was recorded in a binary manner as treated (1) or not treated (0) during a lactation. Independent variables for statistical analysis were the fixed effects of year-season of calving (6-mo seasons), crossbred group (2-breed, 3-breed, or 4th generation crossbred), breed group nested within crossbred group, parity nested within breed group and crossbred group, and random cow within breed group. Across the first 3 lactations, pure HO cows had significantly ($P < 0.01$) higher milk (7,766 kg) production than JMH (6,790 kg) cows, but were not significantly ($P > 0.05$) different than MH (8,054 kg), MJH (7,562 kg), HMJH (8,041 kg) and HJMH (7,230 kg) cows for milk production. The MH (520 kg), MJH (511 kg), JMH (476 kg), and HJMH (499 kg) cows were not significantly ($P > 0.05$) different from pure HO (499 kg) cows for fat plus protein production during the first 3 lactations; however, the HMJH (526) cows had significantly ($P < 0.05$) greater fat plus protein production than pure HO cows. The crossbred cows were not significantly ($P > 0.05$) different from pure HO cows for SCS during the first 3 lactations. The MH (37.9%), MJH (26.3%), and HJMH (23.7%) cows had significantly ($P < 0.05$) less clinical mastitis than pure HO (56.4%) cows during the first 3 lactations.

Key Words: crossbreeding, mastitis, pasture

233 An update: Responses of production and mastitis to selection for milk yield with a control population in a pasture production system.

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The University of Minnesota initiated a designed study of yield selection in 1964 that included an unselected control group of cows. The study continues at the West Central Research and Outreach Center (WCROC), Morris, Minnesota, and is currently part of the low-input sustainable and organic grazing dairy project. At time of dispersal from the Southern Research and Outreach Center, Waseca, in 2003, rolling herd averages were control line (5,964 kg milk, 221 kg fat, 179 kg protein, 3.3 SCS) and selection line (10,099 kg milk, 384 kg fat, 303 kg protein, 2.0 SCS). The control line of cows has not been evaluated in a pasture-based dairy production system. Therefore, control Holstein cows (n = 118) were compared with contemporary Holstein cows (n = 267) for 305-d milk, fat, and protein production; SCS; and mastitis incidence during their first 5 lactations. Cows were housed at the WCROC, a grazing herd, and calved from January 2003 to May 2011. Best Prediction was used to calculate actual production (milk, fat, protein, and SCS) for 305-d lactations with adjustment for age at calving, and records less than 305 d were projected to 305 d. Incidence of clinical mastitis was recorded in a binary manner as treated (1) or not treated (0) during a lactation. Independent variables for statistical analysis were the fixed effects of year-season of calving (6-mo seasons), genetic line, parity nested within genetic line, and random cow within genetic line. Across the 5 lactations, control Holstein cows had significantly ($P < 0.01$) less milk (6,034 versus 8,234 kg), fat (205 versus 271 kg), protein (188 versus 254 kg), and fat plus protein (393 versus 525 kg) production compared with contemporary Holstein cows. The control Holstein cows were not significantly ($P > 0.05$) different from contemporary Holstein cows (3.49 versus 3.42, respectively) for SCS during the first 5 lactations. However, the control line cows (31.9%) had significantly ($P < 0.01$) less clinical mastitis than contemporary Holstein cows (47.1%) during the first 5 lactations.

Key Words: genetic selection, mastitis, pasture

234 Genetic analysis of leukosis incidence in a US Holstein cattle population.

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Bovine leukosis (BL) is a retroviral disease caused by the bovine leukosis virus (BLV) that affects only cattle. It is associated with decreased milk production in addition to death losses. On average, a BLV negative cow has a longer life span, produces 3.5% more milk per lactation, and has 48 fewer days open than does a BLV positive cow. The virus also affects the immune system. Infected cows display a muted response to immunization with J5 bacterin. The aim of this study was to estimate the heritability for BL incidence and the genetic merit of sires for leukosis resistance in the US Holstein population. Continuous and binary data of milk ELISA score for 14,120 cows from 114 dairy herds across 16 US states were considered. Data were obtained from commercial testing records at Antel BioSystems located in Lansing, Michigan. Data used for analysis were limited to animals with a minimum of 3 test results. Out of the 14,120 animals tested, 38% were infected with the disease. Linear and threshold animal models were used to analyze the continuous and binary data, respectively. Variance components and breeding values for animals were estimated using the 2 models and the agreement between the estimated breeding values from each model was assessed. Estimates of heritability obtained with the 2 approaches were very similar and around 7%, indicating that there is a considerable genetic component underlying BL disease incidence. The correlation between the estimated breeding values from the 2 methods was 0.797, and the lists of top 10% bulls selected from each model had a 65.3% overlap. In summary, results indicate that the simple linear model approach using the continuous ELISA scores as response variable is a reasonable approach for the genetic analysis of BL incidence in cattle. In addition, the levels of heritability found indicate that selection could also be used to improve resistance to BL in Holstein populations.

Key Words: bovine leukosis, heritability, threshold model

235 Production traits, somatic cell score, and days open of crossbred cows versus pure Holsteins during their first lactation in Italian commercial dairy herds.

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The objective of this study was to compare Swedish Red (SR) × Holstein (HO) crossbred cows (n = 385), Montbéliarde (MO) × HO crossbred cows (n = 71), and Brown Swiss (BS) × HO crossbred cows (n = 52) with pure HO cows (n = 1,583) for production traits. A total of 563,158 test-day information for milk yield and 15,348 for fat and protein, and somatic cell score were recorded on first parity cows milked in 4 herds of northern Italy. Production traits were analyzed through a mixed linear model that included effects of herd-test-day, days in milk based on the Wilmink function, breed group, days open, and the random effects of cow nested within breed group and residual. Days open were grouped into classes of 60 d each, except for the first, which was a class of non-pregnant cows and the last, which was an open class (>240 d). The Wilmink model was used to investigate differences in the shape of lactation curves of milk yield among breed groups. Parameters were estimated for each cow and then used as response variables in linear models including the effects of breed group, herd, and classes of days open. HO produced more milk than SR × HO and MO × HO crossbreds (+2.86 and +2.34 kg/d, respectively) and protein (+0.04 and +0.03 kg/d, respectively), but lower protein percentage (−0.14 and −0.08%, respectively). SR × HO and MO × HO cows became pregnant about 20 d earlier than HO cows. BS × HO produced less milk (−1.47 kg/d) than pure HO cows, but higher (+0.11%) protein percentage. BS × HO and SR × HO had also significantly lower SCS (−0.42 and −0.37, respectively) than HO cows. According to previous results, the Wilmink function showed that milk production was lower for crossbreds compared with pure HO cows, which highlighted stronger increase toward the peak then SR × HO and MO × HO. Breed groups did not differ for the parameter describing the decreasing part of the lactation curve, which was affected by days open. Results indicate that SR and MO are candidate breeds for crossbreeding with HO to maintain good levels of production and improve fertility of dairy herds.

Key Words: crossbreeding, milk traits, days open

236 Birth weight, gestation length, calving-ease and mortality in Holstein, Jersey, and crossbred cows in a pasture-based dairy herd. K. Dhakal,* J. Cassady, C. Maltecca, and S. Washburn, *North Carolina State University, Raleigh.*

Holstein (H) and Jersey (J) cows were mated to H or J bulls to form purebreds, reciprocal crosses, and backcrosses in a criss-cross mating system in the herd located at the Center for Environmental Farming Systems in Goldsboro, North Carolina. Data for birth weight (BW = 31.1 ± 5.9 kg), calving ease (CE = 0 for unassisted, n = 1106, and 1 for assisted, n = 74), and mortality (0 for alive, n = 1150, and 1 for abortions recorded after mid-gestation, stillborn, and dead within 48 h, n = 30) of calves (n = 1231) were recorded over 9 calving seasons from 2003 through 2011. Gestation lengths (GL = 276.7 ± 5.9 d) were determined from insemination and subsequent calving dates. Linear mixed models for BW and GL included fixed effects of sex, parity (first vs. later parities), twin status, and genetic groups [purebred Holsteins (HH), purebred Jerseys (JJ), reciprocal F1 crosses (HJ, JH), crosses > 50% Holsteins (HX) and crosses > 50% Jerseys (JX)]. The BW model also included GL as covariate. Logistic regression for CE and mortality included fixed effects of sex, parity, and genetic groups. Genetic groups were replaced by linear regression using percentage H genes as coefficients on above models and included as covariates to determine the type of genetic control. Heifer calves, twins and calves born at first parity had lower BW. Differences in genetic groups were observed for BW ($P < 0.01$). Percentage H genes in the calf (direct genetic effects) and percentage H genes in the dams (maternal genetic effects) increased BW ($P < 0.01$). Shorter GL were observed for twin births and for first parity. Direct genetic effects shortened GL ($P < 0.01$), whereas maternal genetic effects increased GL ($P < 0.01$). First parity cows had more assisted births than older cows ($P < 0.01$). Female calves had lower odds ratio (0.27, CI = 0.11, 0.67) for mortality than male calves. Higher percentages of heterosis in the dams (maternal heterosis) reduced calf mortality ($P = 0.015$).

Key Words: crossbreeding, genetic groups, percentage Holsteins

237 Genetic parameters associated with feedlot bovine respiratory disease complex morbidity and mortality. B. W. Brigham*[1], C. M. McAllister[1], R. K. Peel[1], R. L. Weaber[2], H. VanCampin[1], G. H. Loneragan[3], J. L. Salak-Johnson[4], C. C. L. Chase[5], J. J. Wagner[1], and R. M. Enns[1], *[1]Colorado State University, Fort Collins, [2]Kansas State University, Manhattan, [3]Texas Tech University, Lubbock, [4]University of Illinois, Urbana, [5]South Dakota State University, Brookings.*

Bovine respiratory disease complex (BRDC) is a broad term associated with host of infectious agents that occur in cattle. Morbidity and mortality caused by BRDC in the feedlot is associated with annual costs estimated in excess of a billion dollars. Indirect effects of BRDC include depressed performance and carcass quality. Therefore, the objective of this study was to quantify the genetic control of feedlot morbidity and mortality associated with BRDC. Crossbred steers from a single source were shipped from western Nebraska to southeast Colorado over a 2 year period (year 1 n = 1,551, year 2 n = 1,319). Steers were processed the day following arrival and placed in feedlot pens where they remained unless identified as sick and in need of health treatment by feedlot staff. If an animal was pulled as sick it was treated according to defined protocols and housed separately with other sick animals until recovered. Processing and treatment protocols were nearly identical across the 2 years of the study. In the event of mortality, field necropsies were conducted and biological samples were taken to ascertain the cause of death. Treatment and mortality rates attributed to BRDC varied greatly of the 2 years of the study, in year one morbidity and mortality rates were 45% and 6% compared with year 2 8% and 2% respectively. A probit threshold link function in ASReml was used to convert binary observations for both morbidity and mortality to the underlying scale. Variance components were estimated through univariate sire models using the 2,870 total observations and 3,255 pedigree relationships. Fixed effects included contemporary group (ranch unit and feedlot pen) and year. Heritability and standard errors for feedlot morbidity or feedlot mortality were, 0.17 (0.06) and 0.08 (0.16) respectively. These results suggest some amount of genetic control in the susceptibility to BRDC and the inability to recover from an infection. The ability to select for animals with greater disease tolerance or immune function could result in increased performance and decreased input requirements in the feedlot.

Key Words: feedlot, morbidity, mortality

238 Performance of a German Holstein cattle population under stressful conditions near Benghazi, Libya. R. S. Gargoum*[1], S. A. M. Bozrayda[1], and E. Abdalla[2], *[1]Department of Animal Production, University of Benghazi, Benghazi, Libya, [2]Department of Animal Sciences, University of Wisconsin-Madison, Madison.*

The aim of this study was to evaluate productive and reproductive performance of German Holstein Friesian dairy cows and subsequent generations that were born in Libya. Animals were managed by a Dutch company from 1986 to 1990, and Libyan managers were used after 1990. The number of cows that had the first lactation record included in the study was 2094. Data were analyzed using REML to estimate factors affecting milk yield and reproductive traits. The model included month, year of calving, management, generation, origin of sire as fixed effects. In addition, age at first calving and lactation period included for milk yield traits as covariates. Total milk yield was generally high (8409 Liters) and achieved with reproductive efficiency (110 d open) during Dutch management, and at the expense of the reproductive traits (161 d open) during Libyan management. Management, calving year, calving month, age at first calving and lactation period had a significant effect on both milk yield and reproductive traits. In addition, milk yield and days open were affected by the temperature-humidity index (THI). Different trends of milk yield and days open were found during cold and hot seasons. However, Days open were more affected by the increasing in THI than does milk yield. Reasons of culling were mainly due to low fertility (37%), mastitis and udder injuries (15%) and accidental defects (16%). Management plays important role to maintain high productivity with reproductive efficiency under heat stress conditions.

Key Words: milk yield, reproductive traits, THI