

Genetic parameters of cyclicity and other fertility indicators in dairy cattle

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Resumption of ovarian cyclicity after calving is crucial to achieving reproductive efficiency in cattle. Early onset of ovulation after calving decreases veterinary costs, reduce calving intervals, augments milk production and length of lactation, and accelerates the genetic improvement of the herd. Four fertility indicators are frequently used: probability of cycling at 45d post-calving (Pr_Cyc), probability of disease diagnosis at 45d post-calving (Pr_Sck), probability of pregnancy after 2 AIs (Pr_Prg), and days open (DO). The goal of this study was to identify significant covariables that affect these fertility indicators and to estimate their genetic parameters in dairy cattle. Measurements from 4,996 cows from three regions in 9 herds across two calving years were analyzed and relevant covariables were identified by stepwise selection. The three indicator probabilities were described using a logistic model including the explanatory variables: dystocia, retained placenta, stillbirth, body condition score at 7d and 35d post-calving (BCS7 and BCS35, respectively), score of vaginal mucous (0 = no mucus to 5 = brownish fetid discharge) at 7d, 12d, and 35d post-calving, and blood β -hydroxybutyrate (BHBA) indicator of subclinical ketosis. A univariate sire model including the effects of contemporary group and lactation number was used to estimate the genetic parameters of Pr_Cyc, Pr_Sck, Pr_Prg, and DO. The percentage of cows cycling, diagnosed with a disease, and pregnant after 2 AIs were 75.5%, 16.6%, and 62.5%, respectively. The marginal probabilities of the significant (P-value < 0.05) covariables indicated that Pr_Cyc was 4.8%, 1.5%, and 1.2% lower per unit increase in BHBA, and mucus score at 7d and 35d post-calving, respectively. Also, Pr_Cyc was 7.0% higher per unit increase in BCS35. Similarly, the Pr_Prg was 3.2% and 3.0% lower per unit increase in BHBA and mucus score at 35d post-calving, respectively. The Pr_Sck increased 33.8% per unit increase in BHBA and 2.3% with stillbirth. The heritability estimates (and standard errors) for Pr_Cyc, Pr_Sck, Pr_Prg, and DO were 0.12 (0.04), 0.03(0.02), 0.07(0.03), and 0.06(0.03), respectively. Our findings corroborate that early resumption of cyclicity postpartum is an important indicator of cow reproduction performance and has substantial genetic variability that can be exploited in selection practices. Improved accuracy of pregnancy predictions is maybe one of the potential benefits of including this indicator in fertility indices. These findings contribute to a long-term multistate project database (USDA-NIFA-AFRI-003542) for direct measures of fertility.

Genetic parameters and impact of post-partum diseases on lactation curves in dairy cattle.
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Keywords: lactation curves, metritis, non-linear mixed models

Genetic improvement in milk production has impacted the shape of the lactation curve, in addition to the total production. Likewise, diseases incidence early in the lactation can affect the lactation curve. The objective of this study simultaneously considers both health and genetic factors influencing the lactation curve. Test-day milk records on 6,283 Holstein cows across four U.S. states and nine herds were evaluated. The trajectory of the lactation curve was modeled using non-linear mixed effects models including Wood's and Wilmink's functions. The effects of environmental and health indicators on the level of milk yield; increase in milk production early in lactation (Wood's) or milk yield at peak (Wilmink's); and persistency thereafter were evaluated. These effects included: season (summer or winter), state, parity, vaginal mucus score at 7d postpartum, metritis at 7d postpartum, mastitis cases within the first 60d postpartum, blood β -hydroxybutyrate (BHBA) indicating subclinical ketosis, body condition score at 35d (BCS35), displaced abomasum by 60d postpartum (DA), respiratory illness by 60d postpartum (Resp), and lameness at 35d. The sire of the cow was included as random effect. Estimates from the Wood's model indicated that multiparous cows have significantly higher levels of milk yield at calving and lower persistency than primiparous cows. Lactation curves in winter had higher yield at calving and lower persistency than in summer. Metritis had a negative effect on milk yield level at calving and lower persistency. Mucus score and abomasum displacement had a negative impact on milk yield level at calving that may be correlated with the positive and significant effect on the rise in milk yield thereafter. Consistent with Wood's estimates, the estimates from the Wilmink's model indicated that multiparous cows have higher milk production and lower persistency than primiparous cows. Number of mastitis cases and displacement of abomasum were associated with lower overall milk production and higher persistency. BHBA was associated with higher level of milk yield and lower persistency. The ratio of sire to residual variance estimates from Wood's and Wilmink's functions were consistent and approximately 0.4. Wood's model offered a better fit for the lactation curves considered. Our findings demonstrate the need to incorporate disease indicators on the assessment of the genetic component influencing the trajectory of the lactation curve. These findings contribute to a long-term multistate project database (USDA-NIFA-AFRI-003542) for direct measures of fertility.

Influence of reproductive indicators and genetic parameters on lactation curves

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Keywords: lactation curves, reproductive efficiency, non-linear mixed models

Weak reproduction indicators in dairy farms are linked to low net returns associated with low milk production and replacement levels and high breeding and veterinary costs. The objectives of this study were to assess the association between both reproductive efficiency and genetic variation on the lactation curve. A novel reproductive metric that integrates information on conception and pregnancy loss after first and second artificial insemination was developed. Wilmink's and Wood's functions were used to describe the lactation curve and nonlinear mixed effects models including the effect of sire, contemporary group, lactation number, the novel reproductive metric, months open, and cyclicity status at day 35 after calving. Data on more than 50,000 test-day milk records from more than 6,000 U.S. Holstein cows were considered. Cyclicity status was not associated with any lactation curve parameter. Higher months open was associated with higher persistency in milk yield. Estimates from the Wilmink function indicated that cows that conceived and maintain pregnancy after first artificial insemination or failed to conceive at first artificial insemination but conceived and maintained pregnancy after the second artificial insemination had significantly higher levels of milk yield during lactation, higher milk yield at peak production, and lower persistency than cows that failed to conceive at both artificial insemination events. The Wood's parameter estimates confirmed the higher milk yield at the start of lactation, higher incline in milk yield after calving, and higher persistency of the former relative to the latter reproductive groups. The ratio of sire to residual variance estimates was 0.4 and was consistent across models. The novel reproductive metric that combines information on conception and pregnancy loss at the first two artificial insemination events together with genetic parameter estimates offered insights into the factors influencing the lactation curve. These findings contribute to a long-term multistate project database (USDA-NIFA-AFRI-003542) for direct measures of fertility.

Genetic parameters of early lactation diseases in dairy cattle

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Key-words: resistance, metritis,

Early lactation diseases impact herd profitability, compromise animal welfare, and affect consumer preferences. Therefore, genetic improvement of disease resistance is becoming an increasingly important goal. The objectives of this study were to estimate the genetic parameters of major disease indicators and to identify variables that affect the incidence of these diseases. Disease indicators evaluated included the probability of a cow to develop: metritis (Pr_Met), clinical endometritis (Pr_End), ketosis (Pr_Sck), and clinical mastitis (Pr_Mas) to support management decisions and. Disease records from approximately 4,900 cows across U.S. regions and two calving years were analyzed. Univariate logistic sire models including the effects of contemporary group and lactation number and additional covariates were used to estimate genetic parameters. Additional explanatory variables included: dystocia, retained placenta, stillbirth, body condition score at 7d and 35d post-calving (BCS7 and BCS35, respectively), vaginal mucous score at 7d, 12d, and 35d post-calving (on scale of 0 = no mucus to 5 = brownish fetid discharge), and blood beta-hydroxybutyrate (BHBA) indicator of subclinical ketosis. Stepwise selection enabled the identification of the explanatory variables significantly associated with the probability of each disease. The percentage of cows with metritis, endometritis, ketosis, and mastitis were 28.8%, 22.4%, 16.6%, and 7.6%, respectively. Among the significant explanatory variables, Pr_Met increased 17.0%, 3.4%, and 2.1% per unit increase in mucous score at 7d and 35d, and BHBA, respectively. Also, Pr_Met increased 11.0% and 4.2% in cows diagnosed with retained placenta and dystocia, respectively. On the other hand, Pr_Met decreased 6.1% per unit increase of BCS7. The heritability estimates (and standard errors) for Pr_Met, Pr_End, Pr_Sck, and Pr_Mas were 0.01 (0.001), 0.01(0.001), 0.03(0.02), and 0.02(0.007), respectively. The association between explanatory variables and early postpartum disease probabilities and low heritability estimates identified in this study confirm that reliable prediction of disease incidence in dairy herds requires comprehensive accounting for health and management information. These findings contribute to a long-term multistate project database (USDA-NIFA-AFRI-003542) for direct measures of fertility.

Genetic and environmental components of disease traits in dairy cattle

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Key-words: metritis, postpartum, production.

Diseases in U.S. Holstein are responsible for approximately \$ 1 billion annually in dairy production due to reduced milk production and increased costs. The objective was to assess the impact of environmental factors and scale of genetic parameters on the incidence of prevalent diseases in dairy cows early (< 10d) and late (35 to 60d) postpartum. Binary and multinomial disease records on 6,283 Holstein cows across 4 U.S. regions were evaluated using mixed effects logistic and Poisson models. Early postpartum binary diseases included: dystocia, retained placenta, subclinical ketosis (blood β -hydroxybutyrate BHBA > 1), and metritis. Late postpartum binary diseases included: displacement of abomasum, mastitis, respiratory problems and clinical endometritis. Mucus score at 7d, number of mastitis cases up to 60d, and lameness at 35d (5 levels) were analyzed assuming a Poisson model. Fixed effects in all models included: lactation number (3 levels), season (summer and winter), and U.S. region. Other fixed effects evaluated depending on the disease included: twins, body condition score, BHBA level, calf gender, stillbirth, first test-day milk production record and other diseases. The cow's sire was included as random effect. Overall lactation, region, and season had a significant effect on the incidence of all diseases, except for lactation on respiratory problems and season on mastitis. First lactation cows exhibited the highest incidence of dystocia, metritis, and clinical endometritis and lowest incidence of mastitis, retained placenta, lameness, and displacement of abomasum. Clinical endometritis, metritis, lameness and respiratory problems were lower in summer than winter. Dystocia, retained placenta, and subclinical ketosis were positively and significantly associated with clinical endometritis and metritis. Subclinical ketosis and dystocia were positively and significantly associated with displacement of abomasum. Mastitis was negatively and significantly associated with milk yield at first test-day. Heritability estimates for the diseases were on average 0.27. The differences in genetic parameter estimates among alternative disease indicators offer insights into most effective approaches to lower the incidence of disease through selection. These findings contribute to a long-term multistate project database (USDA-NIFA-AFRI-003542) for direct measures of fertility.

Management and genetic components of fertility indicators in dairy cattle

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Key-words: reproduction, pregnancy, dairy cattle.

Management and genetic strategies are employed to attain high fertility rates in dairy farms. These high rates in turn enable higher profits from higher milk production, higher replacement rates, higher genetic progress, and lower expenses compared to those in systems with lower fertility efficiency. The goal of this study was to characterize the joint effect of management and genetic variation on fertility indicators that are linked to the cost-effectiveness of dairy production systems. Fertility, disease, production, environment, and pedigree records from over 6,200 Holstein cows across 9 farms in the U.S.A. were analyzed. Binary fertility variables included pregnancy at first and second artificial insemination (AI), pregnancy loss after first and second AI, ovarian cyclicity status, and open status 60 days after calving. Explanatory variables included AI method, farm, lactation number, season, body condition score at day 35 post-calving, milk yield during the first three test days, retained placenta, twin calving, and dystocia. First lactation cows had significantly higher odds of conception at first and second AI, longer open rates, lower odds of cyclicity than older cows and lower odds of pregnancy loss after first and second AI. Milk yield during the first test day was significant and negatively associated with pregnancy loss at second AI. Retained placenta lowered the odds of cyclicity status. Likewise, calving of twins significantly deteriorated the odds of cyclicity. Timed AI had significantly shorter open period, followed by estrus-guided AI, and natural AI. Higher body condition score was positively and significantly associated with odds of cyclicity. The odds of pregnancy after first and second AI were lower among cows calving during summer relative to winter meanwhile the odds of pregnancy loss after first and second AI were higher during the summer. Heritability estimates were approximately 0.08. These results highlight availability of genetic variation and the major relevance of non-genetic component on fertility indicators.

Genomic selection for improved fertility of dairy cows with emphasis on cyclicity and pregnancy

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The objective was to develop a fertility database with genotypes and phenotypes based on objective and direct measures of fertility in Holstein dairy cows and subsequently identify SNPs and haplotypes significantly associated with fertility traits by use of genome-wide analyses and use this information to obtain genomic-estimated breeding values that can be applied in selection of dairy cattle for improved fertility. A total of 12,000 Holsteins cows from 7 states (NY, MN, WI, TX, CA, FL, OH), comprising 2 to 3 farms per state, were enrolled at calving and weekly monitored until pregnancy. Main events were uterine health, metabolic disorders, cyclicity, estrus, pregnancy per A.I., and pregnancy loss, together with milk yield until 305 DIM. Overall, 71% of the population resumed ovarian cyclicity by 50 DIM. Conception at first and second A.I. were 32.8% and 33.7% and pregnancy loss between 32 and 60 d after A.I. were 10% and 8.7%, respectively. 19.7% and 4% of the population was sold or died before 305 DIM. A reproductive index (**RI**), calculating the predicted probability of pregnancy at first A.I. (PP1) after calving, was generated using a logistic regression model that included cow-level variables that were thought to have a genetic component (diseases, anovulation, BCS, milk yield, etc.). Within each farm cows were stratified as pregnant on d 60 after the first AI (high-fertility population) and as non-pregnant on d 60 after 2 A.I. (low-fertility population). Within farm, season (cool and hot), and each of the two populations, the RI was be used to rank cows in a high-fertility pregnant (850 cows) and a low-fertility non-pregnant population (1,750 cows). The PP1 for the highest RI quartile was 0.43 while 42% of this population was pregnant at first A.I. The PP1 for the lowest RI quartile was 0.21 while 20.8% of this population was pregnant.

Keywords: Genomics, fertility, dairy