Jersey Research References

Published April 2013 through April 2018

* Genome-wide association study for ketosis in US Jerseys using producer-recorded data K.L. Parker Gaddis, J.H. Megonigal Jr., J.S. Clay, C.W. Wolfe

Journal of Dairy Science, Vol. 101, Issue 1, p413–424

Ketosis is one of the most frequently reported metabolic health events in dairy herds. Several genetic analyses of ketosis in dairy cattle have been conducted; however, few have focused specifically on Jersey cattle. The objectives of this research included estimating variance components for susceptibility to ketosis and identification of genomic regions associated with ketosis in Jersey cattle. Voluntary producer-recorded health event data related to ketosis were available from Dairy Records Management Systems (Raleigh, NC).

Short communication: Two dominant paternal lineages for North American Jersey artificial insemination sires C.D. Dechow, W.S. Liu, J.S. Idun, B. Maness

Journal of Dairy Science, Vol. 101, Issue 3, p2281–2284

Jersey cattle are the second most prominent breed in the United States and represent a growing portion of the dairy cow population in the United States. The objectives of our study were to determine the male lineages of Jersey sires with official genetic evaluations and to determine whether there are differences in sire conception rate among lineages. Paternal lineages back to the 1950s were extracted from genetic evaluation files of the Council on Dairy Cattle Breeding (CDCB, Bowie, MD) for all sires with an official United States genetic evaluation and that were enrolled with the National Association of Animal Breeders (Madison, WI).

* Predicting hyperketonemia by logistic and linear regression using test-day milk and performance variables in early-lactation Holstein and Jersey cows T.L. Chandler, R.S. Pralle, J.R.R. Dórea, S.E. Poock, G.R. Oetzel, R.H. Fourdraine, H.M. White

Journal of Dairy Science, Vol. 101, Issue 3, p2476–2491

Although cowside testing strategies for diagnosing hyperketonemia (HYK) are available, many are labor intensive and costly, and some lack sufficient accuracy. Predicting milk ketone bodies by Fourier transform infrared spectrometry during routine milk sampling may offer a more practical monitoring strategy. The objectives of this study were to (1) develop linear and logistic regression models using all available test-day milk and performance variables for predicting HYK and (2) compare prediction methods (Fourier transform infrared milk ketone bodies, linear regression models, and logistic regression models) to determine which is the most predictive of HYK.

Jersey Research References

* *Technical note:* Evaluation of digital refractometers to estimate serum immunoglobulin G concentration and passive transfer in Jersey calves M.M. McCracken, K.M. Morrill, A.L. Fordyce, H.D. Tyler

Journal of Dairy Science, Vol. 100, Issue 10, p8438–8442

Housing and management characteristics of calf automated feeding systems in the Upper Midwest of the United States M.W. Jorgensen, K. Janni, A. Adams-Progar, H. Chester-Jones, J.A. Salfer, M.I. Endres

Journal of Dairy Science, Vol. 100, Issue 12, p9881–9891

Management, operational, animal health, and economic characteristics of large dairy herds in 4 states in the Upper Midwest of the United States T.L. Evink, M.I. Endres

Journal of Dairy Science, Vol. 100, Issue 11, p9466–9475

Genetic and nongenetic factors associated with milk color in dairy cows S. Scarso, S. McParland, G. Visentin, D.P. Berry, A. McDermott, M. De Marchi

Journal of Dairy Science, Vol. 100, Issue 9, p7345–7361

Effect of stocking rate and animal genotype on dry matter intake, milk production, body weight, and body condition score in spring-calving, grass-fed dairy cows E.L. Coffey, L. Delaby, S. Fitzgerald, N. Galvin, K.M. Pierce, B. Horan

Journal of Dairy Science, Vol. 100, Issue 9, p7556–7568

Short communication: Estimation of the financial benefit of using Jersey milk at different inclusion rates for Cheddar cheese production using partial budgeting J.H. Bland, A.P. Bailey, A.S. Grandison, C.C. Fagan

Journal of Dairy Science, Vol. 98, Issue 3, p1661–1665

Partial budgeting was used to estimate the net benefit of blending Jersey milk in Holstein-Friesian milk for Cheddar cheese production. Jersey milk increases Cheddar cheese yield. However, the cost of Jersey milk is also higher; thus, determining the balance of profitability is necessary, including consideration of seasonal effects. Input variables were based on a pilot plant experiment run from 2012 to 2013 and industry milk and cheese prices during this period. When Jersey milk was used at an increasing rate with Holstein-Friesian milk (25, 50, 75, and 100% Jersey milk), it resulted in an increase of average net profit of 3.41, 6.44, 8.57, and 11.18 pence per kilogram of milk, respectively, and this additional profit was constant throughout the year.

Jersey Research References

Effect of blending Jersey and Holstein-Friesian milk on Cheddar cheese processing, composition, and quality
J.H. Bland, A.S. Grandison, C.C. Fagan

Journal of Dairy Science, Vol. 98, Issue 1, p1–8

The effect of Jersey milk use solely or at different inclusion rates in Holstein-Friesian milk on Cheddar cheese production was investigated. Cheese was produced every month over a year using nonstandardized milk consisting of 0, 25, 50, 75, and 100% Jersey milk in Holstein-Friesian milk in a 100-L vat. Actual, theoretical, and moisture-adjusted yield increased linearly with percentage of Jersey milk. This was also associated with increased fat and protein recoveries and lower yield of whey. The composition of whey was also affected by the percentage of Jersey milk, with lower whey protein and higher whey lactose and solids.

* Validating a refractometer to evaluate immunoglobulin G concentration in Jersey colostrum and the effect of multiple freeze–thaw cycles on evaluating colostrum quality K.M. Morrill, K.E. Robertson, M.M. Spring, A.L. Robinson, H.D. Tyler

Journal of Dairy Science, Vol. 98, Issue 1, p595–601

The objectives of this study were to (1) validate a method using refractometry to rapidly and accurately determine immunoglobulin (IgG) concentration in Jersey colostrum, (2) determine whether there should be different refractive index (nD) and %Brix cut points for Jersey colostrum, and (3) evaluate the effect of multiple freeze–thaw (FT) cycles on radial immunodiffusion (RID) and a digital refractometer to determine IgG concentration in Jersey colostrum. Samples (n = 58; 3 L) of colostrum were collected from a dairy in northwestern Iowa.

Improving reliability of genomic predictions for Jersey sires using bootstrap aggregation sampling Ashley A. Mikshowsky, Daniel Gianola, Kent A. Weigel

Journal of Dairy Science, Vol. 99, Issue 5, p3632–3645

Genomic selection has revolutionized the dairy genetics industry and enhanced the rate of response to selection for most economically important traits. All young bulls are now genotyped using commercially available single nucleotide polymorphism arrays to compute genomic predicted transmitting ability (GPTA) and reliability (REL) values. Decisions regarding the purchasing, marketing, and culling of dairy bulls are based on GPTA until roughly 5 yr of age, when milk-recorded offspring become available.

* Dynamics of culling for Jersey, Holstein, and Jersey × Holstein crossbred cows in large multibreed dairy herds P.J. Pinedo, A. Daniels, J. Shumaker, A. De Vries

Journal of Dairy Science, Vol. 97, Issue 5, p2886–2895

The objective of this observational study was to describe and compare the dynamics of reason-specific culling risk for the genetic groups Jerseys (JE), Holsteins (HO), and Jersey × Holstein crossbreds (JH), considering parity, stage of lactation, and milk yield, among other variables, in large multibreed dairy herds in Texas. The secondary objective was to analyze the association between survival and management factors, such as breeding and replacement policies, type of facilities, and use of cooling systems.

The digestive system of 1-week-old Jersey calves is well suited to digest, absorb, and incorporate protein and energy into tissue growth even when calves are fed a high plane of milk replacer Yu Liang, Jeffery A. Carroll, Michael A. Ballou

Journal of Dairy Science, Vol. 99, Issue 3, p1929–1937

The objectives of the current study were to determine the apparent digestibilities of nitrogen, organic matter, ash, and energy as well as investigate the nitrogen retention of calves fed different planes of milk replacer nutrition during the first week of life. Twelve Jersey calves were blocked by body weight at birth and randomly assigned to either a high plane of nutrition (HPN) or low plane of nutrition (LPN) treatment. The HPN calves were offered 19.2 g of dry matter/kg of body weight of a 28% all-milk crude protein and 20% fat milk replacer.

Plane of nutrition influences the performance, innate leukocyte responses, and resistance to an oral *Salmonella enterica* serotype Typhimurium challenge in Jersey calves M.A. Ballou, D.L. Hanson, C.J. Cobb, B.S. Obeidat, M.D. Sellers, A.R. Pepper-Yowell, J.A. Carroll, T.J. Earleywine, and others

Journal of Dairy Science, Vol. 98, Issue 3, p1972–1982

Two experiments investigated how plane of nutrition influences performance, leukocyte responses, and resistance to an oral *Salmonella enterica* serotype Typhimurium challenge. In experiment 1, 46 (2 ± 1 d of age) calves were randomly assigned to 2 diets: a low (LPN; n = 23) and high plane of nutrition (HPN; n = 23). The LPN calves were fed 409 g/d of dry matter (DM) of a 20% crude protein and 20% fat milk replacer, whereas HPN calves were fed 610 and 735 g/d of DM of a 28% crude protein and 25% fat milk replacer during wk 1 and 2 to 6, respectively.

Across-country test-day model evaluations for Holstein, Nordic Red Cattle, and Jersey Martin H. Lidauer, Jukka Pösö, Jørn Pedersen, Jan Lassen, Per Madsen, Esa A. Mäntysaari, Ulrik S. Nielsen, Jan-Åke Eriksson, and others

Journal of Dairy Science, Vol. 98, Issue 2, p1296–1309

Three random regression models were developed for routine genetic evaluation of Danish, Finnish, and Swedish dairy cattle. Data included over 169 million test-day records with milk, protein, and fat yield observations from over 8.7 million dairy cows of all breeds. Variance component analyses showed significant differences in estimates between Holstein, Nordic Red Cattle, and Jersey, but only small to moderate differences within a breed across countries. The obtained variance component estimates were used to build, for each breed, their own set of covariance functions.

Jersey Research References

* Jersey calf performance in response to high-protein, high-fat liquid feeds with varied fatty acid profiles: Blood metabolites and liver gene expression V.A. Swank, W.S.Bowen Yoho, K.M. O'Diam, M.L. Eastridge, A.J. Niehaus, K.M. Daniels

Journal of Dairy Science, Vol. 96, Issue 6, p3845–3856

Most available Jersey calf milk replacers (CMR) use edible lard as the primary fat source, which lacks medium-chain fatty acids (MCFA). However, Jersey cow milk consists of over 10% MCFA. The objective of this trial was to determine whether altering the fatty acid profile of CMR by increasing the amount of MCFA would alter liver lipid infiltration, liver gene expression, and blood metabolites when fed to Jersey calves. Fifty Jersey calves were fed 1 of 4 diets: pasteurized saleable whole milk (pSWM) from Jersey cows [27.9% crude protein (CP), 33.5% fat, dry matter (DM) basis]; CMR containing 100% of fat as edible lard (100:00; 29.3% CP, 29.1% fat, DM basis); CMR containing 20% of fat as coconut oil (CO; 80:20; 28.2% CP, 28.0% fat); or CMR containing 40% of fat as CO (60:40; 28.2% CP, 28.3% fat).

* Housing system may affect behavior and growth performance of Jersey heifer calves J.A. Pempek, M.L. Eastridge, S.S. Swartzwelder, K.M. Daniels, T.T. Yohe

Journal of Dairy Science, Vol. 99, Issue 1, p569–578

Social pressure is increasing to adopt alternative housing and management practices that allow farm animals more opportunity to exercise and demonstrate social behavior. The present study investigated the effect of pair housing on the behavior and growth performance of Jersey heifer calves. Forty female Jersey calves were allocated to individual or pair housing at birth and monitored for 9 wk. Calves were provided with a single hutch, and those allocated to the pair housing treatment were provided a pen enclosure twice the size of individually housed calves and only one hutch was provided per pair.

Including different groups of genotyped females for genomic prediction in a Nordic Jersey population H. Gao, P. Madsen, U.S. Nielsen, G.P. Aamand, G. Su, K. Byskov, J. Jensen

Journal of Dairy Science, Vol. 98, Issue 12, p9051–9059

Including genotyped females in a reference population (RP) is an obvious way to increase the RP in genomic selection, especially for dairy breeds of limited population size. However, the incorporation of these females must be conducted cautiously because of the potential preferential treatment of the genotyped cows and lower reliabilities of phenotypes compared with the proven pseudo-phenotypes of bulls. Breeding organizations in Denmark, Finland, and Sweden have implemented a female-genotyping project with the possibility of genotyping entire herds using the low-density (LD) chip.

Jersey Research References

Single-step genomic model improved reliability and reduced the bias of genomic predictions in Danish Jersey
P. Ma, M.S. Lund, U.S. Nielsen, G.P. Aamand, G. Su

Journal of Dairy Science, Vol. 98, Issue 12, p9026–9034

A bias in the trend of genomic estimated breeding values (GEBV) was observed in the Danish Jersey population where the trend of GEBV was smaller than the deregressed proofs for individuals in the validation population. This study attempted to improve the prediction reliability and reduce the bias of predicted genetic trend in Danish Jersey. The data consisted of 1,238 Danish Jersey bulls and 611,695 cows. All bulls were genotyped with the 54K chip, and 1,744 cows were genotyped with either 7K chips (1,157 individuals) or 54K chips (587 individuals)

Short communication: A genetic study of mortality in Danish Jersey heifer calves E. Norberg, J.E. Pryce, J. Pedersen

Journal of Dairy Science, Vol. 96, Issue 6, p4026–4030

The aim of this study was to estimate genetic parameters for mortality of Jersey heifer calves during the first 6 mo after birth, calculate the genetic trend of the trait, and estimate breeding values of widely used Jersey sires. More than 260,000 heifer calves were included in the study. The mortality traits included in the analysis were defined as mortality in 8 different periods from 24 h after birth to age 180 d (d 1–14, d 15–30, d 31–60, d 61–90, d 91–120, d 121–150, and d 151–180) and mortality over the entire period.

Genetic analysis of leukosis incidence in United States Holstein and Jersey populations E.A. Abdalla, G.J.M. Rosa, K.A. Weigel, T. Byrem

Journal of Dairy Science, Vol. 96, Issue 9, p6022–6029

Bovine leukosis (BL) is a retroviral disease caused by the bovine leukosis virus that affects only cattle. It is associated with decreased milk production and increased cull rates due to development of lymphosarcoma. The virus also affects the immune system. Infected cows display a weak response to some vaccinations. It is important to determine if the heritability of BL susceptibility is greater than zero, or if the environment is the only factor that can be used to reduce the transmission and incidence of the disease.

* Jersey calf performance in response to high-protein, high-fat liquid feeds with varied fatty acid profiles: Intake and performance W.S. Bowen Yoho, V.A. Swank, M.L. Eastridge, K.M. O'Diam, K.M. Daniels

Journal of Dairy Science, Vol. 96, Issue 4, p2494–2506

The objective of this study was to determine whether altering the fatty acid (FA) profile of milk replacer (MR) with coconut oil, which contains a high concentration of medium-chain FA, to more closely match the FA profile typically found in whole milk from Jersey cows, would improve Jersey calf performance. Male (n = 18) and female (n = 32) Jersey calves were assigned at birth to 1 of 4 liquid diets: (1) pasteurized Jersey saleable whole milk [pSWM; 27.9% crude protein (CP) and 33.5% fat]; (2) 29.3% CP and 29.1% fat MR, containing 100% of fat as edible lard (100:00); (3) 28.2% CP and 28.0% fat MR, containing 80% of fat as lard and 20% as coconut oil (80:20); and (4) 28.2% CP and 28.3% fat MR, containing 60% of the fat as lard and 40% as coconut oil (60:40).

Short communication: Heterosis by environment and genotype by environment interactions for protein yield in Danish Jerseys E. Norberg, P. Madsen, G. Su, J.E. Pryce, J. Jensen, M. Kargo

Journal of Dairy Science, Vol. 97, Issue 7, p4557–4561

Crossing of lines or strains within and between breeds has been demonstrated to be beneficial for dairy cattle performance. However, even within breed, differences between strains may also give rise to heterosis. A key question is whether an interaction exists between heterosis and environment (H × E) that is independent of genotype by environment (G × E) interactions. In this study, H × E and G × E interactions were estimated in a population of approximately 300,000 Danish Jersey cows. The cows were a mixture of pure Danish Jerseys and crosses of US and Danish Jerseys.

Heat-treated (in single aliquot or batch) colostrum outperforms non-heat-treated colostrum in terms of quality and transfer of immunoglobulin G in neonatal Jersey calves A.A. Kryzer, S.M. Godden, R. Schell

Journal of Dairy Science, Vol. 98, Issue 3, p1870–1877

The objective of this randomized clinical trial was to describe the effect on colostrum characteristics and passive transfer of IgG in neonatal calves when using the Perfect Udder colostrum management system (single-aliquot treatment; Dairy Tech Inc., Greeley, CO) compared with a negative control (fresh refrigerated or fresh frozen colostrum) and a positive control (batch heat-treated colostrum). First-milking Jersey colostrum was pooled to achieve 31 unique batches with a minimum of 22.8 L per batch.

Milk production and fertility performance of Holstein, Friesian, and Jersey purebred cows and their respective crosses in seasonal-calving commercial farms E.L. Coffey, B. Horan, R.D. Evans, D.P. Berry

Journal of Dairy Science, Vol. 99, Issue 7, p5681–5689

There is renewed interest in dairy cow crossbreeding in Ireland as a means to further augment productivity and profitability. The objective of the present study was to compare milk production and fertility performance for Holstein, Friesian, and Jersey purebred cows, and their respective crosses in 40 Irish spring-calving commercial dairy herds from the years 2008 to 2012. Data on 24,279 lactations from 11,808 cows were available. The relationship between breed proportion, as well as heterosis and recombination coefficients with performance, was quantified within a mixed model framework that also contained the fixed effects of parity; cow and contemporary group of herd-year-season of calving were both included as random effects in the mixed model.

Jersey Research References

Including overseas performance information in genomic evaluations of Australian dairy cattle M. Haile-Mariam, J.E. Pryce, C. Schrooten, B.J. Hayes

Journal of Dairy Science, Vol. 98, Issue 5, p3443–3459

In dairy cattle, the rate of genetic gain from genomic selection depends on reliability of direct genomic values (DGV). One option to increase reliabilities could be to increase the size of the reference set used for prediction, by using genotyped bulls with daughter information in countries other than the evaluating country. The increase in reliabilities of DGV from using this information will depend on the extent of genotype by environment interaction between the evaluating country and countries contributing information, and whether this is correctly accounted for in the prediction method.

* Predicting hyperketonemia by logistic and linear regression using test-day milk and performance variables in early-lactation Holstein and Jersey cows T.L. Chandler, R.S. Pralle, J.R.R. Dórea, S.E. Poock, G.R. Oetzel, R.H. Fourdraine, H.M. Pralle

Journal of Dairy Science, Vol. 101, Issue 3, p2476–2491

Although cowside testing strategies for diagnosing hyperketonemia (HYK) are available, many are labor intensive and costly, and some lack sufficient accuracy. Predicting milk ketone bodies by Fourier transform infrared spectrometry during routine milk sampling may offer a more practical monitoring strategy. The objectives of this study were to (1) develop linear and logistic regression models using all available test-day milk and performance variables for predicting HYK and (2) compare prediction methods (Fourier transform infrared milk ketone bodies, linear regression models, and logistic regression models) to determine which is the most predictive of HYK.

Short communication: Use of young bulls in the United States J.L. Hutchison, J.B. Cole, D.M. Bickhart

Journal of Dairy Science, Vol. 97, Issue 5, p3213–3220

The availability of genomic evaluations since 2008 has resulted in many changes to dairy cattle breeding programs. One such change has been the increased contribution of young bulls (0.8 to 3.9 yr old) to those programs. The increased use of young bulls was investigated using pedigree data and breeding records obtained from the US national dairy database (Beltsville, MD). The adoption of genotyping was so rapid that by 2009, >90% of all Holstein artificial insemination (AI) service sires and 86% of Jersey AI service sires were genotyped, regardless of age.

Genomic selection for tolerance to heat stress in Australian dairy cattle Thuy T.T. Nguyen, Phil J. Bowman, Mekonnen Haile-Mariam, Jennie E. Pryce, Benjamin J. Hayes

Journal of Dairy Science, Vol. 99, Issue 4, p2849–2862

Temperature and humidity levels above a certain threshold decrease milk production in dairy cattle, and genetic variation is associated with the amount of lost production. To enable selection for improved heat tolerance, the aim of this study was to develop genomic estimated breeding values (GEBV) for heat tolerance in dairy cattle.

Heat tolerance was defined as the rate of decline in production under heat stress. We combined herd test-day recording data from 366,835 Holstein and 76,852 Jersey cows with daily temperature and humidity measurements from weather stations closest to the tested herds for test days between 2003 and 2013.

Genetic parameters for health traits using data collected from genomic information nucleus herds
M. Abdelsayed, M. Haile-Mariam, J.E. Pryce
Journal of Dairy Science, Vol. 100, Issue 12, p9643–9655

As with many other countries, data availability has been a limitation in Australia for developing breeding values for health traits. A genomic information nucleus of approximately 100 herds across the country, selected on the basis of their record keeping, has recently been established in Australia and is known as Ginfo. The objective of this study was to evaluate the feasibility of developing genomic breeding values for health traits using farmer-collected data from Ginfo herds. Having this genotyped population opens up opportunities to develop new genomic breeding values, such as dairy health traits.

Effect of feeding whole compared with cell-free colostrum on calf immune status: Vaccination response S.N. Langel, W.A. Wark, S.N. Garst, R.E. James, M.L. McGilliard, C.S. Petersson-Wolfe, I. Kanevsky-Mullarky

Journal of Dairy Science, Vol. 99, Issue 5, p3979–3994

Vaccination contributes to improved herd health and production. Boosting immune development at a young age may have long-term effects by enhancing vaccine immune response and efficacy. In the bovine, colostrum is the sole source of maternal immunity, having a substantial effect on health status in the neonate. To date, colostral antibody concentration is used to evaluate colostrum quality. However, colostrum also contains proteins and cells, which may affect immune development and future responses to vaccines.

Grain challenge affects systemic and hepatic molecular biomarkers of inflammation, stress, and metabolic responses to a greater extent in Holstein than Jersey cows T. Xu, F.C. Cardoso, A. Pineda, E. Trevisi, X. Shen, F. Rosa, J.S. Osorio, J.J. Loor

Journal of Dairy Science, Vol. 100, Issue 11, p9153–9162

Long-term feeding of high-grain diets to dairy cows often results in systemic inflammation characterized by alterations in acute-phase proteins and other biomarkers, both in plasma and immune-responsive tissues like the liver. The molecular and systemic changes that characterize an acute grain feeding challenge remain unclear. The current study involved 6 Holstein and 6 Jersey cows in a replicated 2 × 2 Latin square. Periods (10 d) were divided into 4 stages (S): S1, d 1 to 3, served as baseline with total mixed ration (TMR) ad libitum; S2, d 4, served as restricted feeding, with cows offered 50% of the average daily intake observed in S1; S3, d 5, a grain challenge was performed, in which cows were fed a TMR ad libitum without (CON) or with an additional pellet wheat-barley (1:1; HIG) at 20% of dry matter intake top-dressed onto the TMR; S4, d 6 to 10, served as recovery during which cows were allowed ad libitum access to the TMR.

Jersey Research References

Mating programs including genomic relationships and dominance effects C. Sun, P.M. VanRaden, J.R. O'Connell, K.A. Weigel, D. Gianola

Journal of Dairy Science, Vol. 96, Issue 12, p8014–8023

Computerized mating programs using genomic information are needed by breed associations, artificial-insemination organizations, and on-farm software providers, but such software is already challenged by the size of the relationship matrix. As of October 2012, over 230,000 Holsteins obtained genomic predictions in North America. Efficient methods of storing, computing, and transferring genomic relationships from a central database to customers via a web query were developed for approximately 165,000 genotyped cows and the subset of 1,518 bulls whose semen was available for purchase at that time.

* Influence of breed, milk yield, and temperature-humidity index on dairy cow lying time, neck activity, reticulorumen temperature, and rumination behavior A.E. Stone, B.W. Jones, C.A. Becker, J.M. Bewley

Journal of Dairy Science, Vol. 100, Issue 3, p2395–2403

The objective of this study was to compare weekly mean lying time (LT), neck activity (NA), reticulorumen temperature (RT), and rumination time (RU) among 3 breed groups, milk yield (MY), and temperature-humidity index (THI). Cows (n = 36; 12 Holstein, 12 crossbred, and 12 Jersey) were blocked by parity group (primiparous or multiparous), days in milk, and MY. Lying time, NA, RT, RU, and MY were recorded and averaged by day and then by week for each cow. For study inclusion, each cow was required to have 10 wk of LT, NA, RT, and RU data.

Factors associated with milk processing characteristics predicted by mid-infrared spectroscopy in a large database of dairy cows G. Visentin, M. De Marchi, D.P. Berry, A. McDermott, M.A. Fenelon, M. Penasa, S. McParland

Journal of Dairy Science, Vol. 100, Issue 4, p3293–3304

Despite milk processing characteristics being important quality traits, little is known about the factors underlying their variability, due primarily to the resources required to measure these characteristics in a sufficiently large population. Cow milk coagulation properties (rennet coagulation time, curd-firming time, curd firmness 30 and 60 min after rennet addition), heat coagulation time, casein micelle size, and pH were generated from available mid-infrared spectroscopy prediction models. The prediction models were applied to 136,807 spectra collected from 9,824 Irish dairy cows from research and commercial herds.

The impact of 3 strategies for incorporating polled genetics into a dairy cattle breeding program on the overall herd genetic merit D.M. Spurlock, M.L. Stock, J.F. Coetzee

Journal of Dairy Science, Vol. 97, Issue 8, p5265–5274

Dehorning in cattle has been associated with behavioral, physiological, and neuroendocrine responses indicative of pain. Unaddressed, the pain associated with a routine production procedure could contribute to a negative public perception of livestock production practices. Alternative considerations of dehorning include the selection of polled cattle within herds, thereby avoiding pain and production loss. As polledness results from an autosomal dominant pattern of inheritance, genetic selection for polled cattle could reduce the prevalence of the horned trait.

Genomic evaluation, breed identification, and population structure of Guernsey cattle in North America, Great Britain, and the Isle of Guernsey T.A. Cooper, S.A.E. Eaglen, G.R. Wiggans, J. Jenko, H.J. Huson, D.R. Morrice, M. Bichard, W. G. de L. Luff, and others

Journal of Dairy Science, Vol. 99, Issue 7, p5508–5515

As of December 2015, 2,376 Guernsey bulls and cows had genotypes from collaboration between the United States, Canada, the United Kingdom, and the Isle of Guernsey. Of those, 439 bulls and 504 cows had traditional US evaluations, which provided sufficient data to justify investigation of the possible benefits of genomic evaluation for the Guernsey breed. Evaluation accuracy was assessed using a traditional 4-yr cutoff study. Twenty-two traits were analyzed (5 yield traits, 3 functional traits, and 14 conformation traits).

The effect of changing cow production and fitness traits on net income and greenhouse gas emissions from Australian dairy systemsM.J. Bell, R.J. Eckard, M. Haile-Mariam, J.E. Pryce

Journal of Dairy Science, Vol. 96, Issue 12, p7918–7931

The aim of this study was to compare the effect of changing a range of biological traits on farm net income and greenhouse gas emissions (expressed in carbon dioxide equivalents, CO_2-eq.) in the Australian dairy cow population. An average cow was modeled, using breed-average information for Holsteins and Jerseys from the Australian Dairy Herd Improvement Scheme. A Markov chain approach was used to describe the steady-state herd structure, as well as estimate the CO_2-eq. emissions per cow and per kilogram of milk solids.

Customized recommendations for production management clusters of North American automatic milking systems Marlène Tremblay, Justin P. Hess, Brock M. Christenson, Kolby K. McIntyre, Ben Smink, Arjen J. van der Kamp, Lisanne G. de Jong, Dörte Döpfer

Journal of Dairy Science, Vol. 99, Issue 7, p5671–5680

Automatic milking systems (AMS) are implemented in a variety of situations and environments. Consequently, there is a need to characterize individual farming practices and regional challenges to streamline management advice and objectives for producers. Benchmarking is often used in the dairy industry to compare farms by computing percentile ranks of the production values of groups of farms. Grouping for conventional benchmarking is commonly limited to the use of a few factors such as farms' geographic region or breed of cattle.

Jersey Research References

Conceptus development and transcriptome at preimplantation stages in lactating dairy cows of distinct genetic groups and estrous cyclic statuses E.S. Ribeiro, A.P.A. Monteiro, R.S. Bisinotto, F.S. Lima, L.F. Greco, A.D. Ealy, W.W. Thatcher, J.E.P. Santos

Journal of Dairy Science, Vol. 99, Issue 6, p4761–4777

The objectives were to compare development and transcriptome of preimplantation conceptuses 15 d after synchronized ovulation and artificial insemination (AI) according to the genetic background of the cow and estrous cyclicity at the initiation of the synchronization program. On d 39 ± 3 postpartum, Holstein cows that were anovular (HA; n = 10), Holstein cows that were estrous cyclic (HC; n = 25), and Jersey/Holstein crossbred cows that were estrous cyclic (CC; n = 25) were randomly selected in a grazing herd and subjected to the Ovsynch protocol.

Genetic and nongenetic factors associated with milk color in dairy cows S. Scarso, S. McParland, G. Visentin, D.P. Berry, A. McDermott, M. De Marchi

Journal of Dairy Science, Vol. 100, Issue 9, p7345–7361

Milk color is one of the sensory properties that can influence consumer choice of one product over another and it influences the quality of processed dairy products. This study aims to quantify the cow-level genetic and nongenetic factors associated with bovine milk color traits. A total of 136,807 spectra from Irish commercial and research herds (with multiple breeds and crosses) were used. Milk lightness , red-green index and yellow-blue index were predicted for individual milk samples using only the mid-infrared spectrum of the milk sample.

* **Short communication: Heritability estimates for susceptibility to Mycobacterium avium subspecies paratuberculosis infection defined by ELISA and fecal culture test results in Jersey cattle** Y. Zare, G.E. Shook, M.T. Collins, B.W. Kirkpatrick

Journal of Dairy Science, Vol. 97, Issue 7, p4562–4567

Paratuberculosis (Johne's disease), an enteric disorder in ruminants caused by *Mycobacterium avium* ssp. *paratuberculosis*, causes economic losses in excess of $200 million annually to the US dairy industry. Costly diagnostic testing, cumbersome control programs, incurability, and ineffective vaccination all make *M. avium* ssp. *paratuberculosis* susceptibility a good candidate for genetic studies and genetic selection a potentially useful adjunct to management-based control programs. No report has been published for heritability of susceptibility to *M.*

Colostrum immunoglobulin G concentration of multiparous Jersey cows at first and second milking is associated with parity, colostrum yield, and time of first milking, and can be estimated with Brix refractometry N. Silva-del-Río, D. Rolle, A. García-Muñoz, S. Rodríguez-Jiménez, A. Valldecabres, A. Lago, P. Pandey

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The objective of this study was to evaluate colostrum IgG concentration harvested at first and second milking from multiparous Jersey cows, the dam's lactation number, colostrum yield, and time of first milking. In addition, we validated the use of a Brix refractometer to estimate IgG concentration in colostrum from multiparous Jersey cows using radial immunodiffusion as the reference method. Colostrum samples and total weight of colostrum harvested at first (n = 134) and second (n = 68) milking were collected from 134 multiparous Jersey cows housed in a California herd.

Estimating genomic **breed** composition of individual animals using selected SNPs]. He J, Qian CS, G Tait R Jr, Bauck S, Wu XL. Yi Chuan. 2018 Apr 20;40(4):305-314. doi: 10.16288/j.yczz.17-394. Chinese.

Abstract

Natural and artificial selection, geographical segregation and genetic drift can result in differentiation of allelic frequencies of single nucleotide polymorphism (SNP) at many loci in the animal genome. For individuals whose ancestors originated from different populations, their genetic compositions exhibit multiple components correlated with the genotypes or allele frequencies of these breeds or populations. Therefore, by using an appropriate statistical method, one can estimate the genomic contribution of each breed (ancestor) to the genome of each individualanimal, which is referred to as the genomic breed composition (GBC). This paper reviews the principles, statistical methods and steps for estimating GBC of individual animals using SNP genotype data. Based on a linear regression model and an admixture model respectively, the protocols were demonstrated by the breed characterization of 198 purported Akaushi cattle, which included selection of reference SNPsand reference individual animals, and computing GBC for animals to be evaluated. The reference populations consist of 36 574 cattle from five cattle breeds (Akaushi, Angus, Hereford, Holstein and Jersey), each genotyped on either a 40K or 50K SNP chip. Four common SNP panels scanned from commercial chips for estimating GBC of individual animals are optimally selected, thereby expanding the functionalities of the currently available commercial SNP chips. It remains to be explored in future studies as to how estimated GBC can be incorporated to improve the accuracies on genomic prediction in purebred animals and crossbreds as well.

Including gene networks to predict calving difficulty in Holstein, Brown Swiss and **Jersey** cattle. Tiezzi F, Arceo ME, Cole JB, Maltecca C.

BMC Genet. 2018 Apr 2;19(1):20. doi: 10.1186/s12863-018-0606-y.

BACKGROUND: Calving difficulty or dystocia has a great economic impact in the US dairy industry. Reported risk factors associated with calving difficulty are feto-pelvic disproportion, gestation length and conformation. Different dairy cattle breeds have different incidence of calving difficulty, with Holstein having the highest dystocia rates and Jersey the lowest. Genomic selection becomes important especially for complex traits with low heritability, where the accuracy of conventional selection is lower. However, for complex traits where a large number of genes influence the phenotype, genome-wide association studies showed limitations. Biological networks could overcome some of these limitations and better capture the genetic architecture of complex traits. In this paper, we characterize Holstein, Brown Swiss and Jersey breed-specific dystocia networks and employ them in genomic predictions.

RESULTS: Marker association analysis identified single nucleotide polymorphisms explaining the largest average proportion of genetic variance on BTA18 in Holstein, BTA25 in Brown Swiss, and BTA15 in Jersey. Gene networks derived from the genome-wide association included 1272 genes in Holstein, 1454 genes in Brown Swiss, and 1455 genes in Jersey. Furthermore, 256 genes in Holstein network, 275 genes in the Brown Swiss network, and 253 genes in the Jersey network were within previously reported dystocia quantitative trait loci. The across-breed network included 80 genes, with 9 genes being within previously reported dystocia quantitative trait loci. The gene-gene interactions in this network differed in the different breeds. Gene ontology enrichment analysis of genes in the networks showed Regulation of ARF GTPase was very significant ($FDR \leq 0.0098$) on Holstein. Neuron morphogenesis and differentiation was the term most enriched ($FDR \leq 0.0539$) on the across-breed network. Genomic prediction models enriched with network-derived relationship matrices did not outperform regular GBLUP models.

CONCLUSIONS: Regions identified in the genome were in the proximity of previously described quantitative trait loci that would most likely affect calving difficulty by altering the feto-pelvic proportion. Inclusion of identified networks did not increase prediction accuracy. The approach used in this paper could be extended to any instance with asymmetric distribution of phenotypes, for example, resistance to disease data.

Modeling homeorhetic trajectories of milk component yields, body composition and dry-matter intake in dairy cows: Influence of parity, milk production potential and **breed**. Daniel JB, Friggens NC, van Laar H, Ingvartsen KL, Sauvant D.

Animal. 2017 Nov 3:1-14. doi: 10.1017/S1751731117002828. [Epub ahead of print]

The control of nutrient partitioning is complex and affected by many factors, among them physiological state and production potential. Therefore, the current model aims to provide for dairy cows a dynamic framework to predict a consistent set of reference performance patterns (milk component yields, body composition change, dry-matter intake) sensitive to physiological status across a range of milk production potentials (within and between breeds). Flows and partition of net energy toward maintenance, growth, gestation, body reserves and milk components are described in the model. The structure of the model is characterized by two sub-models, a regulating sub-model of homeorhetic control which sets dynamic partitioning rules along the lactation, and an operating sub-model that translates this into animal performance. The regulating sub-model describes lactation as the result of three driving forces: (1) use of previously acquired resources through mobilization, (2) acquisition of new resources with a priority of partition towards milk and (3) subsequent use of resources towards body reserves gain. The dynamics of these three driving forces were adjusted separately for fat (milk and body), protein (milk and body) and lactose (milk). Milk yield is predicted from lactose and protein yields with an empirical equation developed from literature data. The model predicts desired dry-matter intake as an outcome of net energy requirements for a given dietary net energy content. The parameters controlling milk component yields and body composition changes were calibrated using two data sets in which the diet was the same for all animals. Weekly data from Holstein dairy cows was used to calibrate the model within-breed across milk production potentials. A second data set was used to evaluate the model and to calibrate it for breed differences (Holstein, Danish Red and Jersey) on the mobilization/reconstitution of body composition and on the yield of individual milk components. These calibrations showed that the model framework was able to adequately simulate milk yield, milk component yields, body composition changes and dry-matter intake throughout lactation for primiparous and multiparous cows differing in their production level.

KEYWORDS:

dairy cow; dynamic model; energy; milk composition

Animal. 2018 Feb;12(2):434-444. doi: 10.1017/S1751731117001471. Epub 2017 Jul 17.

Breed of cow and herd productivity affect milk nutrient recovery in curd, and cheese yield, efficiency and daily production.

Stocco G[1], Cipolat-Gotet C[1], Gasparotto V[1], Cecchinato A[1], Bittante G[1].

Little is known about cheese-making efficiency at the individual cow level, so our objective was to study the effects of herd productivity, individual herd within productivity class and breed of cow within herd by producing, then analyzing, 508 model cheeses from the milk of 508 cows of six different breeds reared in 41 multi-breed herds classified into two productivity classes (high v. low). For each cow we obtained six milk composition traits; four milk nutrient (fat, protein, solids and energy) recovery traits (REC) in curd; three actual % cheese yield traits (%CY); two theoretical %CYs (fresh cheese and cheese solids) calculated from milk composition; two overall cheese-making efficiencies (% ratio of actual to theoretical %CYs); daily milk yield (dMY); and three actual daily cheese yield traits (dCY). The aforementioned phenotypes were analyzed using a mixed model which included the fixed effects of herd productivity, parity, days in milk (DIM) and breed; the random effects were the water bath, vat, herd and residual. Cows reared in high-productivity herds yielded more milk with higher nutrient contents and more cheese per day, had greater theoretical %CY, and lower cheese-making efficiency than low-productivity herds, but there were no differences between them in terms of REC traits. Individual herd within productivity class was an intermediate source of total variation in REC, %CY and efficiency traits (10.0% to 17.2%), and a major source of variation in milk yield and dCY traits (43.1% to 46.3%). Parity of cows was an important source of variation for productivity traits, whereas DIM affected almost all traits. Breed within herd greatly affected all traits. Holsteins produced more milk, but Brown Swiss cows produced milk with higher actual and theoretical %CYs and cheese-making efficiency, so that the two large-framed breeds had the same dCY. Compared with the two large-framed breeds, the small Jersey cows produced much less milk, but with greater actual and theoretical %CYs, similar efficiencies and a slightly lower dCY. Compared with the average of the specialized dairy breeds, the three dual-purpose breeds (Simmental and

the local Rendena and Alpine Grey) had, on average, similar dMY, lower actual and theoretical %CY, similar fat and protein REC, and slightly greater cheese-making efficiency.

KEYWORDS:

cheese yield; cheese-making efficiency; fat recovery; herd effect; protein recovery

Robustness and sensitivity of a blueprint for on-farm estimation of dairy cow energy balance Vivi M. Thorup, Mizeck G.G. Chagunda, Amelie Fischer, Martin R. Weisbjerg, Nicolas C. Friggens

Journal of Dairy Science article in press

Low colostrum yield in Jersey cattle and potential risk factors K. Gavin, H. Neibergs, A. Hoffman, J.N. Kiser, M.A. Cornmesser, S. Amirpour Haredasht, B. Martínez-López, J.R. Wenz, and others

Journal of Dairy Science article in press

Multibreed genomic prediction using multitrait genomic residual maximum likelihood and multitask Bayesian variable selection M.P.L. Calus, M.E. Goddard, Y.C.J. Wientjes, P.J. Bowman, B.J. Hayes

Journal of Dairy Science, Vol. 101, Issue 5, p4279–4294

Effect of prophylactic oral calcium supplementation on postpartum mineral status and markers of energy balance of multiparous Jersey cows A. Valldecabres, J.A.A. Pires, N. Silva-del-Río

Journal of Dairy Science, Vol. 101, Issue 5, p4460–4472

Dairy cow breed interacts with stocking rate in temperate pasture-based dairy production systems O.K. Spaans, K.A. Macdonald, J.A.S. Lancaster, A.M. Bryant, J.R. Roche

Journal of Dairy Science, Vol. 101, Issue 5, p4690–4702

* Predicting blood β-hydroxybutyrate using milk Fourier transform infrared spectrum, milk composition, and producer-reported variables with multiple linear regression, partial least squares regression, and artificial neural network R.S. Pralle, K.W. Weigel, H.M. White

Journal of Dairy Science Volume 101, Issue 5, Pages 4378–4387

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Jersey Research References

Additional References from ARS-USDA

https://www.ars.usda.gov/research/publications/publications-at-this-location/?modeCode=80-42-05-30

Including gene networks to predict calving ease in Holstein, Brown Swiss and Jersey cattle
(Peer Reviewed Journal)

Multitrait modeling of first vs. later parities for US yield, somatic cell score, and fertility traits
(Abstract Only)

Validating genomic reliabilities and gains from phenotypic updates
(Proceedings)

Genomic evaluation of age at first calving (Peer Reviewed Journal)

Genomic predictions for crossbreds from all-breed data (Abstract Only)

Genomic selection in dairy cattle: the USDA experience (Other)

Genomic analysis of lactation persistency in four breeds of dairy cattle (Abstract Only)

Breed base representation in dairy animals of 5 breeds (Abstract Only)

Sharing reference data and including cows in the reference population improve genomic predictions in Danish Jersey (Peer Reviewed Journal)

The relationship between runs of homozygosity and inbreeding in Jersey cattle under selection
(Peer Reviewed Journal)

Recent artificial selection in U.S. Jersey cattle impacts autozygosity levels of specific genomic regions
(Peer Reviewed Journal)

Short communication: Improving accuracy of Jersey genomic evaluations in the United States and Denmark by sharing reference population bulls
(Peer Reviewed Journal)

A genetic investigation of isle of Jersey cattle, the foundation of the Jersey breed
(Abstract Only)