Breeding and Genetics
Factors Affecting Fertility and Longevity

349   Assessment of trends in involuntary culling in expanding herds using survival analysis methodology. K. A. Weigel*, R. W. Palmer, and D. Z. Caraviello, *University of Wisconsin - Madison*.

Trends in voluntary and involuntary culling were examined in 141 Wisconsin dairy herds that expanded significantly between 1994 and 1998. Data included 59,280 Holstein cows that calved from January 1987 through December 1999. Mean failure time (from first calving until culling) for uncensored observations was 767 days. Data were analyzed using a Weibull proportional hazards model that included a random, time-independent effect of herd, as well as fixed, time-dependent effects of year-season, parity by stage of lactation, and milk yield by expansion time. Cows were grouped into deciles according to within herd-year ranking for milk yield (after adjustment for age and parity), and the effect of milk yield on culling was considered before, during (same year and following year), and after the most recent major expansion. Prior to expansion, the lowest producing cows in each herd were 6.82 times as likely to be culled, as compared with average cows, but this risk ratio decreased to 4.29 during the expansion period and 1.51 after the expansion. Meanwhile, the highest producing cows were 0.61 times as likely to be culled as average cows prior to expansion, and this risk ratio increased to 0.71 during the expansion period and 0.84 after the expansion. This indicates a trend over time toward less voluntary culling of unprofitable cows and more involuntary culling of sick, injured, or infertile cows, at least in expanding herds. This trend could reflect greater stress of production, reduced individual cow care, poorer health among (inferior quality) purchased animals, or problems with biosecurity. This trend is undesirable, in terms of genetic progress, because it reflects a reduction in the intensity of selection of dams of replacement heifers. In addition, this trend likely contributes to the shortage of replacement heifers on many modern dairy farms.

Key Words: Expansion, Survival, Holsteins

350   Analysis of the relationship between linear type traits, inbreeding, and survival in US Jersey cows using a Weibull model. D. Z. Caraviello*, K. A. Weigel, and D. Gianola, *University of Wisconsin Madison WI USA*.

The ability of a dairy cow to resist involuntary culling is of high economic importance to the dairy farmer. Genetic improvement of survival can lead to lower replacement costs, decreased veterinary costs, more opportunities for voluntary culling, and a higher proportion of cows producing at a mature level. The objective of this study was to evaluate the relationship between linear type traits, inbreeding and survival in Jersey cattle using a Weibull model. Data were obtained from USDA Animal Improvement Programs Laboratory, and these included 284,943 Jersey cows with first calving between January 1, 1981 and August 17, 2000 from 2,913 herds. Average failure time was 880 days after first calving. Our model included the effects of herd-year-season of calving, inbreeding, age at first calving, parity-stage of lactation and within-herd quartiles for mature equivalent milk. Linear type traits were analyzed one at a time. All udder traits jointly, all locomotion traits jointly and final score were evaluated in three additional models. Each one of the type traits was divided in ten classes and class number five was chosen as reference. The 5 traits with the highest impact on survival were Udder Depth, Suspensory Ligament, Fore Udder, Front Teat Placement, and Rear Udder Height. Animals in class number one for these traits had between 1.50 and 1.87 times higher risk of being culled than animals in class number five.

Key Words: survival, type traits, inbreeding

351   Correlations among measures of dairy cattle fertility and longevity. P. M. VanRaden*, H. D. Norman, and R. H. Miller, *USDA Animal Improvement Programs Lab, Beltsville, MD USA*.

Genetic correlations among fertility, longevity, and other traits were estimated by multitrait REML from three data sets. Five reproductive traits were compared using individual breeding data from 2,195,643 lactations of Holstein cows from 3447 sires and 3440 mating bulls. Lactations were initiated in 1998 through 2000. Heritabilities for cow fertility traits were 6.6% for days to first breeding, 4.0% for days to last breeding, 1.8% for number of inseminations, 1.0% for 70-d nonreturn rate, and 10% for gestation length. Days to last breeding were more correlated with days to first breeding (0.85) than with number of inseminations (0.61) or nonreturn rate (-.21). Mating bull fertility contributed 0.5% of phenotypic variance for nonreturn rate. Very similar estimates were obtained using 145,976 lactations of Jersey cows except that days to first breeding had a lower heritability (4.0%). Two longevity traits were compared using data from 1,062,791 Holstein cows born during 1992 through 1994 from 3080 sires. Productive life, which is limited to 10 mo of credit per lactation, was compared with lifespan, which included credit for all months between lactations. Heritabilities were 7.6% for productive life and 6.7% for lifespan; genetic correlation of the two traits was 0.986. Calving interval from first to second lactation was the measure of cow fertility. Cows culled after first lactation were assigned a mean calving interval of 415 d except those culled for reproductive failure, which were assigned the trait limit of 530 d. High protein and fat yields were correlated genetically (0.32) with long calving intervals. Many of the genes that affect fertility also affect longevity. Fertility was more correlated with productive life (-0.59) than with lifespan (-0.46); somatic cell score also was more correlated with productive life (-0.31) than with lifespan (-0.28). Thus, productive life was preferred to lifespan as a measure of longevity. Selection for productive life has reduced the decline in cow fertility, but direct selection on fertility evaluations could be more profitable.

Key Words: Fertility, Longevity, Genetic correlation

352   Modeling length of productive life in beef cows. N. Vukasinovic*[1], M. Berweger Baschnagel[2], and N. Kuenzi[3], [1]*Utah State University*, [2]*SVAMH, Switzerland*, [3]*Swiss Federal Institute of Technology*.

This study investigated factors influencing the length of productive life (LPL) in the population of registered Angus beef cows in Switzerland using survival analysis techniques. The data included 7,090 records on cows calving between 1975 and 1998. LPL was defined as the number of days from the first calving to the weaning of the last calf. Cows that were still alive at the end of the data collection period, as well as those cows with no further records up to 250 days after the weaning of the last calf, were defined as censored. Cows with missing first calving date were defined as left truncated. The data included 45% censored and 16% left truncated records. The mean LPL was 1,683 days for uncensored records and 1,815 days for censored records, reflecting the fact that more records on cows with longer LPL were from the recent years. LPL was modeled using a mixed Weibull survival model. The following fixed effects were included in the model: age at first calving, proportion of Angus genes, housing system, and a cow's scores for type, feet and legs, and udder. Time dependent covariates included in the model were stage of lactation, calving year and season, and birth and weaning weight of the calf. A random effect of herd-year-season, assumed to follow a loggamma distribution with the parameter $\gamma = 5.00$, was also included in the model, but it was integrated out in the analysis. The estimated shape and scale parameters of the baseline (Weibull) hazard function were 2.36 and 0.02, respectively. The model explained about 83% of the variability in LPL. All effects in the model except the housing effect were significant (p-value < 0.05). The relative culling risk was estimated for each level of each effect. The greatest increase in relative culling risk was observed in first calving cows immediately after the weaning of the calf. These cows had up to five times higher risk of being culled than an average cow, suggesting that most selection decisions were made after a cow completed her first production cycle. Also, cows with very low or very high weaning weights of the calf were at a higher than average culling risk, indicating that low production and fertility problems appear to be major reasons for culling of beef cows.

Key Words: Beef cattle, Length of productive life, Survival analysis

353 **Genetic relationships among fertility traits of Holsteins and Jerseys.** H. D. Norman*[1], R. H. Miller[1], P. M. VanRaden[1], J. R. Wright[1], and J. S. Clay[2], [1]*Animal Improvement Programs Laboratory, Agricultural Research Service, Beltsville, MD,* [2]*North Carolina State University, Raleigh.*

Dairy Herd Improvement data with service dates from 2,195,643 Holstein and 171,981 Jersey sire-identified lactations from 1995 through 2000 were used to assess genetic variation in and relationships among fertility traits: days to first service (**D1**), days to last reported service (**DL**), nonreturn rate to first service before 70 d (**NR**), and number of services (**NS**). Mean NR was calculated by herd-year, and herd-years with NR of <10% or >90% were excluded; NR was not examined for cows that left the herd before 70 d after first insemination or if first service was after September 15, 2000. Phenotypic means for D1, DL, NR, and NS, respectively, were 90 d, 141 d, 55%, and 2.10 services for Holsteins and 83 d, 125 d, 57%, and 1.99 services for Jerseys. Data were adjusted for fixed effects of parity for all fertility traits and also for lactation stage at first service for NR and NS. Adjustment was also made for partial regression of fertility trait on mean of two highest test-day yields of milk, fat, and protein and for deviation of calving age from mean for corresponding parity. In the table below, heritabilities (diagonals) and genetic correlations (above diagonals) were estimated by multitrait REML with an adjustment for herd-year-season of first service; phenotypic correlations are below diagonals. Standard errors for heritability estimates for Holsteins and Jerseys, respectively, were 0.003 and 0.009 for D1, 0.002 and 0.008 for DL, 0.001 and 0.006 for NR, and 0.001 and 0.006 for NS. Genetic variation for NR is low, but progeny groups can be large. Because DL has a higher heritability than NR and a moderate to high genetic correlation with D1 and NS, it may be the best single criterion of cow fertility of the four traits.

	Holstein				Jersey			
Trait	D1	DL	NR	NS	D1	DL	NR	NS
D1	**0.066**	0.85	0.24	0.15	**0.040**	0.73	0.09	0.05
DL	0.41	**0.040**	-0.21	0.61	0.41	**0.029**	-0.55	0.70
NR	0.00	-0.32	**0.010**	-0.88	0.00	-0.36	**0.011**	-0.97
NS	0.00	0.76	-0.57	**0.018**	0.00	0.76	-0.62	**0.022**

Key Words: Fertility, Nonreturn rate, Reproduction

354 **Results of 25 years of selection for functional traits.** A. Karlsen*, T. Steine, E. Sehested, M. Svendsen, and I.M.A. Ranberg, *GENO Breeding and A.I. Association.*

Norwegian Dairy Cattle (NRF) have been selected for functional traits and yield for more than 25 years. Major emphasis has been put on fertility and mastitis in the breeding goal as well as on production traits, calving ease, and stillbirths. Information on production, calvings, fertility, and health status is stored in the Norwegian Dairy Herd Recording (NDHR). In total 92% of the farms, representing approximately 290,000 cows, are members of the NDHR, where recording is compulsory. Only veterinarians can perform medical treatments, and veterinary treatments are included in the NDHR. Progeny testing for functional traits is based on 250-350 daughters to obtain breeding values with high accuracy. Sires with a high total merit index based on production and functional traits are used in the breeding scheme. Genetic trends are estimated for all traits. The genetic trend for fertility shows a significant increase in 60 days non-return rate for heifers for the last 25 years. The phenotypic average 56 days non-return rate of heifers is currently more than 77%, with a calving interval of approximately 1 year. Increased resistance to mastitis has a weight of 22% in the breeding goal. The genetic trend shows a very significant increase for resistance to mastitis; in 2000 the phenotypic average shows that approximately 11% of the heifers were treated for mastitis. Only veterinarians can prescribe antibiotics, and routine use of antibiotics to prevent mastitis is not allowed. Calving ease as well as stillbirths have been included in the breeding goal since 1978, and are now not considered a problem in the NRF-population. More than 93% of the calvings are reported as having no problems at calving. Only 2% of the calvings are reported as having major problems. The percentage of abortions is less than 1, and less than 3% of the calves are stillborn.

Key Words: Functional Traits, Cattle, Genetic Trends

355 **Correlations between Estimated Breeding Values (EBVs) of juvenile growth traits and cows' stayability in an Angus herd.** D.P. Rasali*[1], G.H. Crow[1], J.N.B. Shrestha[2], and A. Brule-Babel[3], [1]*Dept. of Animal Science, University of Manitoba, Winnipeg, MB R3T 2N2,* [2]*Agriculture and Agri-Food Canada, Lennoxville, QC J1M 1Z3,* [3]*Dept. of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2.*

Records of 3,284 animals for juvenile growth traits and 581 cows for stayability to 3 years of age (Stay3) from an Angus herd in Manitoba were analysed to estimate the correlations between their EBVs. Univariate animal models (ASREML) were used to analyse body weights at birth (BW), at 205-d weaning (WW) and at one year of age (YW), pre-weaning daily gain (WG) and post-weaning gain to one year of age (PWG). The models included fixed effects due to birth year, birth type, calf's sex and age of dam (a covariate), and random direct and maternal genetic effects. The study also utilized an ASREML univariate logit animal model that included fixed effects due to cow's birth herd and year, and a random direct genetic effect for Stay3 as a binary scored trait. Survival analysis revealed that the risk of a cow being culled from the herd rose sharply after 3 years of age given the maximum calving opportunity up to 10 years. The direct h^2 estimates for BW, WW, YW, WG and PWG were .54, .22, .24, .18 and .21, respectively. Corresponding maternal h^2 estimates were .14, .18, .10, .19 and .01, respectively. The direct h^2 estimate for Stay3 was .17. All estimates were within the range of those published previously. Product-moment and rank correlations of direct and maternal EBVs for growth traits with direct EBV for Stay3 were all significant, except that there was no relationship of direct EBVs for WG and PWG with that for Stay3. The correlations of direct EBV for BW and maternal EBVs for BW, WW and WG with EBV for Stay3 ranged from .11 to .23, while the product-moment and rank correlations between maternal EBV for PWG with direct EBV for Stay3 were -.14 and -.12, respectively. The results suggest that the genetic merit of cows' stayability to 3 year of age has a favorable relationship with the maternal genetic merits of pre-weaning growth traits, but there appears to be an antagonism with that of post-weaning gain.

Key Words: Beef cattle, Growth and stayability, Correlations of EBVs

356 **A genetic study of longevity in swine.** F. Fortin* and R. I. Cue, *Department of Animal Science, McGill University (Macdonald Campus), Montreal, Quebec, Canada.*

Data from the Quebec swine breeding program (1996 to 2001) were used to estimate genetic parameters for longevity and to evaluate the contribution of non-genetic factors. After data verifications there were 10039 Yorkshire sows and 8856 Landrace with records of herd life. The program 'The Survival Kit V3.12' (Ducrocq and Slkner, 2001) was used to estimate heritability separately within each breed, using a Cox proportional hazard model. Time-independent fixed effects of year of birth, estimated breeding values (EBV) backfat, EBV age to 100 kilos, EBV litter size and their interactions with herd, and age at first service were included. The effect of litter size within parity and the effect of event (farrowing, weaning or heat) were treated as fixed time-dependent variables. The random effect of sire using sire relationships back 2 generations was considered as the source of genetic variation. Length of productive life (longevity) was defined as the number of days from first service until culling. In the survival analyses of the Yorkshire sows, all explanatory factors had a significant effect (P<0.05) on longevity of sows while only age at first service was not significant (P<0.05) for the Landrace breed. The effects of litter size within parity and event had the largest influence among the factors included. There is an increasing culling risk for the period after weaning compared to the period after farrowing or heat. Also, the risk of being culled is higher at lower parity and with lower litter size. The significant interaction factors of herd and EBV's show that EBV's can have divergent effects on the culling risk for different herds. For the Yorkshire sows, the effect of age at first service shows a tendency of higher culling risk for a higher age. The sire variances were 0.042 and 0.032 for the Yorkshire and Landrace, respectively, which correspond to heritabilities of 0.16 and 0.13. It can be concluded that there is genetic variation that can be used for increasing longevity by selection.

Key Words: Longevity, Swine, Heritability

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