changes in the number of common bulls, probably because few bulls can potentially provide a significant amount of genetic links. Subsets selected based on different measures of connectedness resulted in higher average genetic correlations and larger number of correlations that are biologically sensible (>0.75). Time edit resulted in increased estimates among countries that share young bulls and decreased estimates among countries that rely heavily on the importation of old proven bulls.

Key Words: Connectedness, data subset, time edit

895   Alternative strategies for estimation of country sire variance in international evaluations of dairy bulls. F. Miglior*[1], P. G. Sullivan[2], and B. J. VanDoormaal[1], [1]*Canadian Dairy Network*, [2]*CGIL, University of Guelph, Guelph, ON, Canada.*

Three alternatives were compared to estimate sire variances in Interbull evaluations. Sire variance estimates are used in international evaluations of dairy bulls to account for different scales of proof expression in each country. Currently these variances are estimated in MACE using all bulls that have daughters in at least 10 herds by country. This group includes locally sampled bulls and imported bulls first sampled abroad. Sire variances are estimated using approximate Mendelian sampling terms (MS), which have an assumed expected value of 0 for all bulls. While average MS of bulls sampled locally may be close to zero, MS of imported bulls tends to be positive, as only top proven bulls are imported in any country. A total of 59,657 Holstein bulls from ten major dairy countries were evaluated with MACE, based on genetic evaluation files and genetic correlation estimates used by Interbull in the November 2000 routine run. Sire variances were estimated for each country using MS of either: a) all bulls (the current Interbull procedure); b) only bulls sampled locally; or c) only bulls born in the last five years (1992-96). The last group included mostly first crop locally sampled bulls. Variances were estimated by birth year and across all years for each of the three data sets for milk, fat and protein yield. For protein yield, sire variances estimated using only locally sampled bulls ranged from -1% to -12% lower than variance estimated using all bulls. Sire variances estimated using bulls born in the last 5 years ranged from -8% to +9% of the variance estimated using all bulls. In order to quantify the impact of different estimates of sire variability on international evaluations, changes in bull rankings and bull proofs were also compared. A simulation study is required to identify the most accurate strategy to estimate sire variance in a MACE evaluation.

Key Words: International evaluations, sire variance estimation

896   Variance of effects of lactation stage within herd by herd yield. N. Gengler*[1,2] and G.R. Wiggans[3], [1]*Gembloux Agricultural University, Belgium*, [2]*National Fund for Scientific Research, Brussels, Belgium*, [3]*Agricultural Research Service, USDA, Beltsville, MD.*

First-lactation test-day yields from New York, Wisconsin, and California herds with low (<7257 kg), medium (9072 to 9525 kg), and high (>11,340 kg) annual milk yields were adjusted additively for age and lactation stage. Two random regression models with third-order Legendre polynomials for permanent environmental and genetic effects were used. The second model also included a random effect with the same polynomial regressions for 2-yr intervals within herd (herd-stage effect). Mean adjusted test-day milk yields were 35.4 kg (75,838 test days in 9108 lactations) for high-yield herds, 28.8 kg (74,845 test days in 8887 lactations) for medium-yield herds, and 25.6 kg (71,996 test days in 8490 lactations) for low-yield herds. Although estimated phenotypic variances also declined with herd yield, those variances were surprisingly similar for medium- and low-yield herds. Herd-stage effect on phenotypic variance was negligible. Heritabilities for high- and medium-yield herds initially decreased and then gradually increased across lactation stages. Maximum heritability (0.33, high-yield herds; 0.30, medium-yield herds) was reached from 200 to 300 d in milk. Heritabilities were lower for low-yield herds but increased rapidly (maximum of 0.22 at lactation end). Introduction of a herd-stage effect eliminated the heritability decrease in early lactation for high- and medium-yield herds and reduced the increase in late lactation for low-yield herds. Heritabilities generally were lower with inclusion of a herd-stage effect, which indicated that variances for this effect were partly considered genetic in the less complete model. Herd-stage variances relative to phenotypic variance were highest at the beginning (12%) and end of lactation (7%) for medium-yield herds. Herd yield and stage had a large effect on variance size and change across lactation stages during first lactation and should be considered when accounting for heterogeneous variances in genetic evaluations.

Key Words: Heterogeneous variance, Test-day model

897   Lactation curves of milk production traits of Italian Water Buffaloes estimated by a mixed linear model. N.P.P. Macciotta*[1], G. Catillo[2], G. Pulina[1], A. Carretta[2], and A. Cappio-Borlino[1], [1]*Dipartimento di Scienze Zootecniche, universit di Sassari, Italia*, [2]*Istituto Sperimentale per la Zootecnia, Roma.*

Aim of the work is the estimation of lactation curves of milk production traits of Italian water Buffaloes pertaining to different age classes and seasons of calving. Data were 4064 Test Day records of milk production traits (milk yield, fat and protein percentages) recorded on 534 Italian buffalo cows during the years 1986-1999 in a farm of the Istituto Sperimentale per la Zootecnia. Animals were grouped according to 6 level of age at calving and to 4 levels of season of calving. Data were analysed with a mixed linear model that included test date, age at calving, season of calving and stage of lactation as fixed effects plus a random animal effect associated with each lactation. Average lactation curves were estimated by solving for the effects of stage of lactation nested within age at calving and season of calving. Milk yield lactation curves of animals of different ages resulted clearly separated till 20 weeks from parturition, with buffaloes of 4-5 years having the highest curve. Peak yield occurred at around the 6th week of lactation in all age classes; buffalo cows of 2-3 years of age showed the highest persistency which, however, is markedly lower than in dairy cattle. No effect of age at calving could be observed for fat and protein percentages. Season of calving affected milk yield only in the first phase of lactation, with the lowest production levels for summer calvings; no effect could be observed on fat and protein contents. Actually, the inclusion of a TD effect accounted for much of the seasonal variation normally observed among buffalo cows calving in different seasons, in agreement with previous results obtained in dairy cattle. Average correlations among TD measures within animal or repeatabilities, calculated on the basis of the variance component associated to the random animal effect and of the residual variance, were 0.59, 0.31 and 0.36 for milk yield, fat and protein percentages respectively.

Key Words: Buffalo, Milk Production Traits, Lactation Curves

898   Heritability estimates for birth weight of exotic dairy breeds in Nigeria. O.T.F. Abanikannda*[1], O. Olutogun[2], A.O. Leigh[1], M. Orunmuyi[3], and O.Y. Apena[1], [1]*Department of Zoology, Lagos State University, Nigeria*, [2]*Department of Animal Science, University of Ibadan, Nigeria*, [3]*Department of Animal Science, Ahmadu Bello University, Zaria, Nigeria.*

Genetic parameter estimates for traits are specific for a particular breed in a specified environment. Weight of calves at birth has been established to be the first and quickest index of some of the performance traits of cattle. The correlation of birth weight to other performance traits as weaning weight, milk yield and survivability has been well documented. This research aim at computing the heritability of birth weight of Holstein and Jersey breeds, calved and bred in the medium to high trypanosomiasis-risk zone of Southern Nigeria. The 475 Holstein calves used in this analysis are from 13 sires and the 39 Jersey calves are from 4 sires. Factors studied included year of birth, season of birth, sex of calf, parity of calf as fixed effects and the sire effect was used as random effect. The SPSS (1996) software was used for both the analysis of variance and the variance component estimation. The General Linear Model (GLM) for variance component estimation using the ANOVA method was used to estimate the variance components. The paternal half sib method of Henderson ($h^2 = 4\sigma_s^2 / \sigma_s^2 + \sigma_w^2$) was used to compute heritability for both breeds. In the Holstein calves, all factors except the parity were highly significant (P<0.01), while only the sire effect was significant (P<0.05) in the Jersey calves. The mean birth weight for the Holstein and Jersey calves are 32.59 ± 0.24kg and 21.15 ± 0.44kg respectively. In the Holstein breed, the males were 1.67kg