15 d, with fecal samples taken on d 0, 5, and 15. The number of eggs/g feces were determined by a modification of the McMaster technique. Larvae were cultured for 10 d at 27^{o}C by placing 20 g of fresh feces inside a small glass container within a larger container holding free water (20 ml) to maximize humidity. Larvae were collected using a modified Baermann$'$s procedure and counted. Mean fecal egg counts (2,722 *vs* 1,162 eggs/g) and TFEO (173 *vs* 45 x 104 eggs/d) were lower ($P<0.01$) for RC *vs* SL. Larvae development from eggs to infective stage of larvae (L3) by 15 d was 88% (3,432 *vs* 421 larvael/20 g feces; $P<0.001$) lower for RC *vs* SL. In conclusions that CT in forages such as SL may reduce pasture contamination with infective larvae and be a valuable tool for parasite control.

Key Words: condensed tannins, gastrointestinal parasite

124 Minimally invasive diagnostic procedures and measures of test performance in BVD infected cattle. N Cook*[1], A Schaefer[1], S Tessaro[2], D Deregt[2], G Desroche[3], and P Dubeski[4], [1]*Agriculture and AgriFood Canada*, [2]*Animal Disease Research Institute*, [3]*Public Works, Edmonton*, [4]*Alberta Agriculture Food and Rural Development*.

The objective was to compare minimally invasive measures for diagnosis of bovine viral diarrhea (BVD). Heifers (n = 10) were infected with 2 * 10^7 TCID type 2 strain 24515A BVD virus, with 5 seronegative animals as controls. Infrared thermographic (IRT) images of the eye were recorded each day for 21 days. Saliva samples were collected every third day. Clinical assessment was conducted every day and utilized a 4-symptom classification system, each on a scale of 0 # 4. Scores for clinical assessment identified infected animals from Day 9 post-infection. Infrared images of the maximum eye temperature were statistically higher for infected animals by Day 7 post#infection ($p<0.001$) and remained statistically different from control levels up to Day 11 ($p<0.05$). Salivary cortisol levels were elevated in infected animals by Day 7 post-infection ($p<0.004$) and remained so until Day 14 ($p<0.02$). Comparisons between tests were made using measures of test performance. Clinical assessment score = 2 had a maximum test efficiency of 50%. Maximum test efficiency for IRT eye temperature was 60.3% at 32.4C and for salivary cortisol was 83% at 8 nmol/L. Diagnostic tests were compared at referent levels giving maximum test efficiency. IRT eye temperature provided a test sensitivity of 98.5%, compared to 87.8% for salivary cortisol and 19.7% for clinical assessment. However, IRT test specificity was 10% compared to 100% for clinical assessment and 47.2% for salivary cortisol. Risk factor (RF) was represented as the ratio of false negative to true negative test results. Clinical assessment RF = 1.05 was higher than for salivary cortisol (RF = 0.35) and IRT eye temperature (RF = 0.2). Minimally invasive diagnostic tests are capable of earlier diagnosis of BVD infection than clinical assessment. Additionally, measures of test performance vs. test referents can be used to objectively manage risk associated with diagnostic testing.

Key Words: Bovine Viral Diarrhea, Infrared Thermography, Salivary Cortisol

Breeding and Genetics

Genetic Prediction and Selection in Cattle

125 Detection and adjustment of abnormal test day yields. G. R. Wiggans*, P. M. VanRaden, and J. C. Philpot, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

Milk, fat, and protein yields on test-day (**TD**) were investigated to develop a method to detect abnormal yields for exclusion from calculation of lactation yields as an alternative to using producer-reported sick code. A TD yield was considered to be abnormal if it was $<$ 60 or $>$ 150% of predicted TD yield. These limits were selected to identify the low and high 1% of the distribution. The new cow specific upper limit replaced the previous limit of 123 kg milk. Predicted TD yield was calculated from previous TD yield adjusted by a daily change (slope) based on days in milk (**DIM**), DIM^2, previous TD yield, and interaction between DIM and previous TD yield. To accommodate changes in slope at peak yield, separate coefficients were estimated for $\leq$50 and $>$50 DIM. Because yield from more than one TD may be abnormal, the last previous normal TD yield was retained for assessing subsequent TD yield. To be identified as abnormal, TD yields that were abnormal based on the previous TD yield also were required to be abnormal when checked against a prediction based on last previous normal TD yield and subsequent TD yield. Herd mean was used when fewer than three TD were recorded and to determine an acceptable range for component percentages. The procedure was applied in reverse for the first test with the predicted yield calculated from the second TD. When the outlier detection method was applied to $>$93 million TD records of cows that calved in 1997 or later, 1.8% of milk, 3.4% of fat, and 1.9% of protein TD yields were identified as abnormal. The higher percentage of outliers for fat reflects its greater variability. Lactation yields were calculated after replacing abnormal TD yields with a floor or ceiling of 60 or 150% , respectively, of yield predicted from the last previous normal TD. For cows that had lactation records with one abnormal TD yield or more and a subsequent lactation record, the correlation between consecutive lactations increased from 0.692 to 0.693 for milk (561,063 lactations), from 0.653 to 0.660 for fat (951,387 lactations), and from 0.686 to 0.694 for protein (488,653 lactations). The outlier detection method identifies both high and low abnormal TD yield and improves the correlation between consecutive lactation yields.

Key Words: Test-day yield, Abnormal yield, Outlier detection

126 Examination of methods to correct for preferential treatment among AI bull dams. N.R. Zwald* and K.A. Weigel, *University of Wisconsin - Madison, Madison, WI.*

The objective of this study was to quantify the magnitude of preferential treatment among dams of AI sires, and to identify methods that can be used to reduce selection errors. Accurate selection of the most elite animals from the population is essential in maximizing genetic progress. Preferential treatment in some dairy herds has made this selection increasingly complex. To examine this problem, test-day data from dams of 1,972 AI bulls born between 9/1/94 and 9/1/97 and their herd-mates were obtained. These data included 641 herds, 188,031 cows, and 1,634,441 test-day records from cows calving between 1/1/90 and 12/31/97. Data were analyzed using a standard sire model, sire-maternal grandsire model, animal models with various assignment of management group classes, and test-day models. Breeding values of bull dams for milk, fat, and protein were regressed on daughter yield deviations of their sons to determine the magnitude of preferential treatment, and to determine which model best corrects for preferential treatment in bull dam herds. Correlations between initial sire PTA and pedigree values were calculated for AI sires receiving their first evaluation during 1998. Correlation between initial PTA was calculated for the following pedigree information at bull birth date: parent average (0.37), sire PTA milk (0.42), dam PTA milk (0.29), maternal grandsire PTA milk (0.36), sire-MGS PTA milk (0.44). This research shows that considerable preferential treatment occurs in many herds, which can lead to incorrect selection of bull dams and inflated parent averages on many young sires.

Key Words: Preferential treatment, Test-day model

127 Data sub-setting and assessment of bias in estimation of genetic correlations among countries. H. Jorjani*, *Interbull Centre, Dept. of Anim. Breed. and Genet., Swedish University of Agricultural Sciences.*

The objective of this study was to assess the effects of different data sub-settings for simultaneous estimation of genetic correlations among a large number of countries. For this purpose dairy cattle populations in 6 countries, with heritability values of 0.15-0.40 and genetic correlations between 0.50 and 0.90, were simulated. Exchange of selected young bulls among countries started at generation 2 and continued until the end of experiment at generation 10. Two different population structures, small and mixed, with 20 bulls and 2000 cows, and 20-640 bulls and 2000-64000 cows per generation, respectively, were simulated. For estimation of genetic correlations either all bulls or only a sub-set of bulls were used. There were two different sub-setting criteria: only bulls with at least 2 proofs and bulls with an effective number of proofs larger than 2.0 (approximately equivalent to 2-4 proofs). Estimated correlations for country combinations with high genetic correlations (0.90) were in good agreement with the simulated values and only occasionally differed by more than 3%. For country combinations with low genetic correlations (0.50) there was almost always a noticeable difference between simulated and estimated values. In the small population structure, simulated correlations were generally overestimated (by up to 35%), irrespective of the sub-setting criteria. In the mixed population structure, simulated correlations were both over and underestimated (by up to 20%). However, the results from the two sub-setting criteria in the mixed population structure were generally in very good agreement with each other and only in few cases differed by more than 3%. The main conclusion of this study was that a shift from current sub-setting criterion (use of common bulls only) to a situation where bulls with high effective number of proofs are used is not the source of any increase in bias and can be adopted for routine international estimation of genetic correlations in the future to reduce the time and computational burden of estimating genetic correlations.

Key Words: Data sub-setting, Genetic correlation, International evaluation

128 Selection differentials from national Holstein bull progeny test programs estimated from international data.

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Genetic progress in dairy cattle is largely determined by the merit of bulls used to sire the next generation, which is influenced by merit of parents, progeny-test (**PT**) accuracy, and intensity of subsequent selection. For 10 national Holstein bull populations, percentage of PT bulls returned to artificial-insemination service and selection differentials for yield traits were computed. All PT bulls were <7 yr old. Selection of PT bulls was assumed to have taken place based on a bull's second evaluation. Where earlier data were not available to identify an evaluation as the second, additional age limits were applied. Data for PT selection evaluations were from the routine genetic evaluation files for Holstein bulls from the International Bull Evaluation Service (Interbull) for 1995 through 1996. A bull was considered to have been returned to service based on the addition of 200 or more daughters in the interval between evaluations 3 and 5 yr after the PT selection evaluation. Selection differentials were computed as differences between mean evaluations of PT bulls returned to service and all PT bulls, divided by sire standard deviations from Interbull. Percentages of PT bulls returned to service were 3 to 17% (mean of 8%). However, some PT bulls that actually were returned to service may not have had 200 additional daughters. Alternative criteria for determining return to service (100, 500, or 1000 additional daughters) impacted proportion selected considerably (up to 10%) for some countries but little ($<2\%$) for others. Selection pressure was highest for protein yield. Selection differentials for estimated breeding value, in standard deviation units, ranged from 0.53 to 1.47 for milk yield, 0.37 to 1.15 for fat yield, and 0.58 to 1.61 for protein yield. For the US, results were 1.02, 0.64, and 1.05. Selection differentials for yield are affected by selection for other traits. Differences in percentage of PT bulls returned to service may be due to the intensity of parental selection, number of PT bulls and PT accuracy, and semen importation policies and export opportunities. These results document the intensity of genetic selection for yield, the differences in trait emphasis across countries, and the US position relative to other countries.

Key Words: Selection differential, Progeny testing, International evaluation

129 Improvements in dystocia national genetic evaluation system and data processing.

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The Animal Improvement Programs Laboratory (AIPL) of USDA assumed responsibility for conducting the national genetic evaluation for dystocia and maintaining the associated database in 1999. Current evaluations use a sire model. Adding a maternal grandsire (MGS) effect to the model is expected to improve accuracy by partially accounting for merit of mates and differences in maternal ability of the dams. Dystocia data were migrated to a relational database integrated with the AIPL production database. This database design was implemented to allow more rigorous data edits by comparing with the production data and to improve MGS identification (ID) rate by utilizing pedigree records from production records with dam ID sufficiently unique to match production pedigrees. Improvements in MGS ID rate are important for implementation of a sire-MGS model. Processing information for 8,861,363 records is available: 568,396 were duplicates or updates of existing records; 33,378 records were rejected; and, the remaining 8,259,589 records ($>93\%$) were accepted. MGS ID increased from 57.2% to 73.1% by integrating the dystocia and production data. Sire and sire-MGS models were compared using data from the August 2001 national genetic evaluation. These data included over 5 million birth score records after requiring sire and MGS ID, dam and sire breed of Holstein or Red and White, single birth, and birth 1980 or later. The sire model included herd-year, year-season, sex of calf, parity of dam, birth year group of sire, and sire. MGS and birth year group of MGS were added to the sire-MGS model. Herd-year, sire and MGS were random effects. Variance for herd-year was set to 10% of residual variance, residual variance was set to 1, heritability to .16, maternal variance to 40% of the direct genetic variance, and correlation between direct and maternal effects to -.3. Correlation between sire solution from the two models was .93. For the sire-MGS model, the range of solutions for sire effects was 1.36 and for MGS solutions the range was .42. Integration of dystocia data with production data resulted in substantial increase in MGS ID rate. A sire-MGS model is feasible for the dystocia data set and provides similar sire evaluations to a sire model.

Key Words: Dystocia, Threshold model, Genetic evaluation

130 A mixed effects heteroskedastic threshold model analysis of calving ease in Italian Piedmontese cattle.

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Genetic evaluations of calving ease scores based on threshold models typically invoke the assumption of homogeneous residual variances on the underlying liability scale. Nevertheless, residual heteroskedasticity across sexes or herds has been firmly established for many production traits. Ignoring residual heteroskedasticity may lead to biased breeding values predictions. Heteroskedastic threshold models have been recently proposed for the analysis of ordinal categorical data; however, the proposed procedures invoke analytical approximations that may be somewhat tenuous. We define a multiplicative structural model for residual variances as a function of "fixed" (e.g. sex of calf) and "random" (e.g. herd) effects using Markov Chain Monte Carlo (MCMC) methods. After validating our procedure in a simulation study, we applied a sire and maternal grandsire model version to the analysis of calving ease records on 8,847 first Italian Piemontese cows from 66 herds, each with at least 100 records. Using the Deviance Information Criterion (DIC), a residual heteroskedastic threshold model (DIC = 16753) was deemed to be better fitting than a regular homoskedastic threshold model (DIC = 17349) to the data. The 95% equal-tailed posterior probability intervals (PPI) of the residual variances for males and females were 0.9268-1.2898, and 0.6061-0.8392, respectively, with the corresponding 95% PPI for the difference being 0.2822-0.4915, thereby confirming significant residual heteroskedasticity across sexes. This difference further translated to small differences in both direct and maternal heritabilities between calf sexes. The inferred degree of residual heteroskedasticity across the 66 herds was such that the 95% PPI of the standard deviation of residual variances across herds was 0.5351-1.0732, with posterior means of individual herd residual variances ranging from 0.34 to 2.97 times the mean herd residual variance. Nevertheless, the Pearson and rank correlations between posterior means of breeding values and between their standard deviations using homogeneous versus heterogeneous models always exceeded 0.98. We have therefore established that both sex of calf and herds are significant sources of residual heteroskedasticity for calving ease scores in Italian Piedmontese cattle.

Key Words: Heterogeneity, Threshold model, MCMC

131 Investigating the value of birth weight as a predictor of perinatal mortality and dystocia.

J.M. Johanson*[1] and P.J. Berger[1], [1]*Iowa State University.*

Birth weights of Holstein cattle are rarely recorded, so the effect of birth weight on perinatal mortality (alive or dead) and dystocia (assisted or unassisted) has been difficult to determine. This research explores the effect of birth weight and other factors on mortality and dystocia. The Iowa State University dairy research farm in Ankeny, IA, collected 5166 records of births between 1968 and 1999. The frequencies of mortality and dystocia were 9.8% and 26.0%, respectively. Due to the binary nature of the observations, the logistic regression was used to predict both perinatal mortality and dystocia. The model including birth weight was a better predictor of **perinatal mortality** than without birth weight. Linear and quadratic effects of birth weight were significant. Probabilities of mortality for birth weights of 27, 33, 40, 46, and 52 kg were 5.0, 2.9, 2.6, 3.5, and 7.0%, respectively. Other significant factors were year of birth, season, dystocia, parity and gestation length (quadratic). The model including birth weight was a better predictor of **dystocia** than without birth weight. The model included a significant quadratic effect of birth weight ($P=0.058$), but not a significant linear effect. Probabilities of dystocia for birth weights of 27, 33, 40, 46, and 52 kg were 5.0, 7.4, 11.6, 19.2, and 31.7%, respectively. Other significant factors were year of birth, sex of calf, parity, and perinatal mortality. Birth weight was necessary to predict the outcome of both perinatal mortality and dystocia. Fewer factors were necessary to predict dystocia than to predict perinatal mortality.

Key Words: Birth weight, Dystocia, Perinatal mortality

132 Repeatability of birth weight of calves in Holstein dams of Southern Nigeria.

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One of the methods by which repeatability of a trait on an individual animal can be estimated is through the variance components method, where repeatability $R= \sigma^2{}_D / \sigma^2{}_D + \sigma^2{}_W$. The General Linear Model of SPSS was used for both the Analysis of Variance and variance components estimation. Factors studied included the season of birth, year of birth, sex of calf and parity of dam as fixed factors, while the dam was used as a random factor. A total of 229 birth weight records from 47 Holstein dams (with minimum of 4 calves per dam) covering a period of 12 years, recorded at Ibadan, Oyo State, Nigeria, were analyzed in this study. All year round calving occurred at the farm across the four climatic seasons. The late dry period (January - March) had 29.7 percent of the births recorded; the early wet period (April - June) had 25.3 percent; the late wet period (July - September) had 17.0 percent, and the early dry period (October - December) had 27.9 percent of the births. The observed differences in the number of births recorded significantly deviated from the expected distribution of births across the seasons ($X^2 = 8.642$). However, the sex ratio was not significantly different from expectation; males calves accounted for about 47.2 percent of the births. Of the factors studied, only season of birth ($P<0.05$) and dam ($P<0.01$) exerted significant influence on the birth weights of Holstein calves. The mean birth weight of Holstein calves on the farm was 33.49 ± 0.29 kg. The heaviest calves were born during the late wet season (34.33 ± 0.70 kg), while the lightest were born during the late dry season (32.38 ± 0.53 kg). Repeatability of calves' birth weight was 0.22 ± 0.07. The low estimate may be due to the large number of dams with relatively small number of offspring. This estimate can be used to select dams for future breeding on the farm.

Source	Degree of Freedom	Mean Square
Season of Birth	3	58.388*
Year of Birth	11	18.607^{ns}
Sex of Calf	1	1.585^{ns}
Parity of Dam	7	21.933^{ns}
Dam	46	42.280**
Error	160	

* = $P<0.05$, ** = $P<0.01$, ns = not significant

Key Words: Repeatability, Holstein dam, Nigeria

133 Additional evaluation of the parameters of the glucose tolerance test (GTT) in connection with pedigree performance (PBV) in growing young bulls.

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Breeders are interested in early information for the estimation of genetic merit of young bulls. High milk performance connected with sound health regarding metabolism and sufficient fertility in dairy cows depends on a well balanced distribution of energy in the body. Glucose concentration in the blood stays almost constant. Insulin plays an important role based on its central position in energy metabolism. The function of insulin was recorded by means of the intravenous glucose tolerance test (GTT) on 329 breeding bulls. They were injected with 1 g of glucose per $kg^{0.75}$ metabolic body weight. The aim was an additional contribution to the assessment of breeding bulls before the start of the offspring's test. The parameter estimates for the glucose tolerance test were a variation of s-%=9, a $h^2=0.20\pm0.12$, and a mean correlation between the physiological indicator and estimated breeding value of 0.40 to 0.50. These relationships were affected by factors such as experimental conditions, age and nutritional state of animals. In the age group 6 to 18 mo (n = 52 bulls), the glucose half-life (GHWZ) and glucose area (GA) were superior to insulin concentration for the estimation of the predicted protein yield. On the basis of multiple linear and nonlinear regression between pedigree- (PBV), as well as GTT-information, and the estimated breeding value of the offspring (EBV), an additional recommendation can be given before the start of the offspring's test by the use of the GTT-parameters. The correlation between the offspring's estimated breeding value (EBV) and the regression calculated breeding value (CBV) for protein-kg of the bulls increased by r = 0.6 to 0.7. The pedigree- and GTT-information alone reached a correlation of r = 0.3 to 0.4 with similar certainty. The correlations between pedigree breeding value (PBV) and GTT-parameters were less than 0.1. Therefore, we can expect additional information about the genetic evaluation of breeding bulls from the use of GTT.

Traits	EBV Milk yield	EBV Fat yield	EBV Prot. yield	EBV Fat-%	EBV Pro-% tein-%	EBV RZM RZM
ln GA	-0.33*	-0.30*	-0.26	+0.10	+0.25	-0.29*
ln GHWZ	-0.37**	-0.33*	-0.36**	+0.10	+0.17	-0.38**
ln GA +GHWZ	+0.48**	+0.31*	+0.45**	-0.23	-0.24	+0.44**
PBV	+0.70**	+0.38**	+0.48**	+0.52**	+0.54**	+0.35*
CBV	+0.83**	+0.65**	+0.70**	+0.73**	+0.67	+0.67**

n = natural logarithm; GA = glucose area equivalent; GHWZ = glucose half-life; PBV = pedigree breeding value; CBV = regression calculated breeding value; EBV = offspring's breeding value; RZM = selection index combining the total breeding values of fat and protein yield using relative economic weights of 1:4

Key Words: Cattle, Glucose, Breeding value

134 Global trends in international selection strategies of Holstein bulls.

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Interbull production files were analyzed to assess trends in international selection strategies of Holstein bulls. The 27 populations included in the Interbull evaluations were divided into 4 groups: a) North America (Canada and United States), b) Europe (all European countries that sample more than 200 Holstein bulls per year: Denmark, France, Germany, Italy and The Netherlands), c) Oceania (Australia and New Zealand), and d) Other (the remaining European countries, Israel and South Africa). A total of 6,215 Holstein bulls were first proven worldwide in 2001. In spite of major efforts of AI organizations, average number of daughters at the bull's first proof was relatively low (49). Partly due to seasonal calving, Australia and New Zealand had the highest average number of daughters at bull's first proof (60) and the youngest average age at first proof (55 months). Of bulls born in 1984, 60% had a sire that already had a second crop proof. This figure dropped to less than 5% for bulls born in 1997 reflecting an increased usage of newly proven bulls as sires of sons. Consequently, generation interval in the sire of son pathway had drastically reduced over time, from almost 10 years in 1984 born bulls to 6.5 years in 1997 born bulls. Within a year from the bull's first proof, all major selection decisions are already made. Average number of sons per sire has been quite constant over time for North America (15 sons per sire), while Europe has slowly increased from 9-10 in the 1980s to 13-14 sons per sire in recent years. Selection intensity has been increasingly higher over time also in the dam of sons pathway. Genetic level of most recent bulls was highest for milk and protein yield in North America, and for fat yield in Oceania. Genetic progress in the last 5 years was strongest for milk in North America, for fat in Oceania, and for protein yield in Other countries. Fast development of Interbull evaluations has allowed a rapid evolution from local to global selection. Superior genetics expressed on local scales is widely available and the best bulls have been chosen as sires of sons independent of their origin, thus providing strong genetic progress, even in countries with small breeding programs.

Key Words: Dairy bulls, International evaluations, Breeding strategies

135 The effect of producer goals on sire selection.

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Information from an on-line survey of dairy producers was used to determine how important producers perceived three different objectives in the breeding problem. The objectives were: maximizing expected net merit of the progeny; minimizing the expected progeny inbreeding coefficient; and minimizing semen expenditure. Producers were asked to rank the three objectives and then weight the importance of each objective relative to the others. This information was then used to determine weights to be used in a multiple-objective integer program designed to select individual mates for a herd of 76 Jersey cows with known genetic background and cow net merit. The results of the multiple-objective models show that rank and relative importance of producer objectives can affect the portfolio of sires selected. Producers whose primary objective was to maximize expected net merit had a range of average expected progeny net merit of $306 to $310, but the level of expected progeny inbreeding was from 6.99% to 10.45% and a semen cost per conception of $35 to $41. Similar results occurred for producers who selected minimizing progeny inbreeding or minimizing total expenditure on semen as their primary goal in their breeding programs. The results of this research suggest that producer information and goals have a substantial impact on the portfolio of sires selected by that producer to attain these goals.

Key Words: Sire selection, Producer objectives, Mathematical programming

136 Effect of fitting dominance effects on the prediction of genetic values for beef cattle.

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The purpose of this study was to examine differences in direct and maternal breeding values under dominance and additive models using field data. The data consisted of 253,072 and 382,895 adjusted weaning weight records from the American Charolais and American Gelbvieh populations, respectively. In these data sets 10% and 9% of all animals had at least one full-sib, with the largest full-sib family consisting of 16 and 31 animals in the Charolais and Gelbvieh populations, respectively. The dominance model fit to both data sets accounted for dominance covariances, and included contemporary group, animal additive, animal maternal, maternal permanent environment and parental dominance (one-quarter of dominance variance) effects. In addition, a regression coefficient for inbreeding percentage was included. A reduced model was also fit, in which the parental dominance effect was removed. The correlations between direct and maternal breeding values in the two models were >0.99. However, changes were observed for parents whose proportion of total progeny that were full-sibs was large. Direct breeding values under the reduced model (ignoring dominance effects) were inflated for sires and deflated for dams as the proportion of total progeny that were full-sibs increased. For Charolais sires with a large proportion of full-sib progeny (>50%), direct breeding values were 0.65 kg higher and maternal breeding values were 0.35 kg lower under the reduced model, while changes observed for Gelbvieh sires were very small. For dams with a large proportion of full-sib progeny (>50%), direct breeding values were 0.13 and 0.06 kg lower under the reduced model, whereas maternal breeding values were 0.07 and 0.13 kg higher under the reduced model, for Charolais and Gelbvieh dams, respectively. The largest changes in direct (and maternal) breeding values in both breeds were 6.85 (3.98) and 2.53 (1.24) kg for Charolais and Gelbvieh populations, respectively, and were observed for sires with no individual records and many full-sib progeny or relatives. Ignoring dominance effects has the greatest impact on animals with little individual information who rely heavily on pedigree records from large full-sib progeny groups.

Key Words: Dominance, Mating system, Beef cattle

Dairy Foods
Micro

137 Production of Exopolysaccharides from *Streptococcus thermophilus* strains in Batch, Continuous and Fed-batch culture.

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Compared to dextran-producing lactic acid bacteria (LAB) or Gram-negative exopolysaccharide (EPS) producers, the low EPS production by thermophilic LAB is a constraint for both its use as additives (*ex situ*) and the *in situ* production of EPS during yoghurt fermentation. Both approaches implicate the optimisation of physical and chemical factors to enhance bacterial growth and EPS production during fermentation. Secondly, technological factors, like the use of (semi)-continuous fermentations, need to be considered for a higher EPS production. Two high-molecular-mass (MM > 1000 kDa) EPS-producing *S. thermophilus* strains were used to optimise bacterial growth and EPS production during batch, continuous and fed-batch fermentations. Besides the production of high-molecular-mass EPS, also low-molecular-mass EPS material was found in the fermentation broth, possibly degradation products. Physical (pH, T) and chemical (nitrogen source) optimisation of the milk medium resulted in an eleven-fold increase in maximum EPS yields. The influence of combined energy sources on the kinetics of bacterial growth and EPS production was investigated using this optimised milk medium. The EPS yield was clearly dependent on the energy source. Whereas the monomer composition of the EPS was not dependent on the type of monomer used, there was evidence that the molecular mass might be influenced. During batch and continuous fermentations it was further observed that EPS production by *S. thermophilus* followed the bacterial growth. The carbon/nitrogen ratio influenced the biomass formation, the EPS production and the relative concentrations of high-molecular-mass and low-molecular-mass EPS. Fed-batch fermentations using two different feeding strategies (constant feeding and acidification-controlled feeding) did not result in higher maximum EPS concentrations compared to batch fermentations. However, it was shown that a high (constant) lactose concentration was necessary to yield high concentrations (1130 ± 226 mg polymer dry mass per litre) of high-molecular-mass EPS and to prevent their degradation upon prolonged fermentation. Fed-batch fermentations can in this respect be interesting, not only to obtain high concentrations of high-molecular-mass EPS but also to improve their stability.

Key Words: Exopolysaccharides, Thermophilic Lactic Acid Bacteria, Fermentation

138 Effect of milk salts on autolytic behavior of lactococcal starter and wild *Lactobacillus paracasei* strains under cheese conditions.

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The autolysis of starter and, potentially non-starter bacteria, during the ripening process of cheese results in the release of intracellular enzymes into the curd matrix, consequently leading to enhanced flavor development. Previous research defining the autolytic behavior of cheese bacteria has focused on the effect of pH and NaCl concentration by assaying autolysis in various NaCl-adjusted buffer systems. This does not take into account, however, the ionic component of the cheese moisture