399 Data collection and determination of factors affecting efficiency and profitability of beef cattle production systems. R. Jones[1] and M. Langemeier*[2], [1]*Oklahoma State University*, *Enid*, [2]*Kansas State University*, *Manhattan*.

This paper summarizes a series of research examining the relative efficiency and profitability of various beef cattle production systems. This type of research has historically been very common in the social sciences, particularly economics, where scientists rely on population data and population research tools and techniques rather than controlled experiments. Much of the particular research referenced in this paper has been conducted using a combination of production and financial data from a sample of actual beef producers. A variety of specific techniques are available, and more than one technique may need to be utilized in the same study to provide answers to the questions at hand. For example, it is quite common to use one technique to quantify the magnitude of relative efficiency (inefficiency) exhibited within a given data set, and then use another technique to identify factors that contribute to that relative efficiency and their magnitudes. The study of important economic outcomes (efficiency, profits, costs, etc.) lends itself particularly well to this type of analysis. Given appropriate data, a wide variety of beef industry research questions can be addressed using similar techniques. We discuss specific data required to conduct various types of population analysis, and suggest potential sources and appropriate collection techniques. In addition, we provide examples of previous and ongoing research projects to illustrate the wide variety of issues that can be addressed using alternative techniques. Finally, we address potential shortcomings and other issues that need to be considered when collecting data and performing economic analyses of beef production systems.

Key Words: efficiency, economic analysis, profit

400 Applications of population data analysis in on-farm dairy trials. M. Engstrom*[1], W. Sanchez[2], W. Stone[2], and N. R. St-Pierre[3], [1]*DSM Nutritional Products, Inc.*, *Parsippany, NJ*, [2]*Diamond V Mills*, *Cedar Rapids, IA*, [3]*The Ohio State University*, *Columbus*.

With appropriate statistical designs and management controls, research trials done on-farm can generate good data, speed up technology interchange, and in some cases couldn't be done anywhere else. Useful designs include split-herd ("pen vs. pen") trials where pen comprises the experimental unit, and crossover or switchback designs where treatments are imposed on a schedule over one or more experimental groups. We've also used a "paired-herd" design, where two switchback studies are run in tandem, but with the treatments out-of-phase to neutralize environmental variation. A multi-site design utilized 35 dairies to compare milk responses to a protein source, using individual cow records to evaluate differences in milk production. Recently, we have used statistical process control techniques (SPC) to evaluate current management changes, using repeated measures on the dairy. Although a drawback to SPC might be the lack of traditional statistics to test differences, standard rules can be used to demonstrate that a process or variable has changed, or to characterize a seasonal change. Meta-analysis techniques are the most powerful tools to evaluate many similar trials for low-frequency or subtle effects. Meta-analysis can be used to segment a database to validate and compare trial methods or to investigate for publication bias. Additional design concerns for reproduction studies include the need for adequate numbers of observations and planning for the lag time between an experimental treatment and response measurement (i.e. pregnancy confirmation).

Key Words: trial design, statistical process control, meta-analysis

401 Application of statistical process control techniques to monitor changes in animal production systems. A. De Vries*, *University of Florida*, *Gainesville*.

Statistical process control (SPC) involves using statistical techniques to measure and analyze the mean and variability in process observations. Emerging trends in animal production systems can be detected with the aid of SPC techniques. The conceptual idea is that variability in process observations comes from 2 basic sources. Common cause variability includes all sources of random variability that can be removed only by changing the process. Special cause variability results from some potentially identifiable source that can be removed if needed. Production processes that are influenced by special cause variability are said to be out of control. The goal of SPC is to detect when a process moves from in control to out of control, and possibly suggest the way it went out of control. A process that is out of control warrants further investigation, at a cost of time and effort, to identify the special cause of the shift or drift. On the other hand, processes that are in control should be left alone, unless the process is intentionally changed. Statistical techniques, primarily control charts, are needed to determine if there is enough evidence that the process has changed. The amount of evidence depends on the relative cost of type I (false positive) and type II (false negative) decision errors. Control charts have their origin in manufacturing in the 1920s but there are now abundant applications in health care and epidemiology. Various types of control charts have been applied in animal production systems, with examples in poultry, swine, dairy, and beef. Examples include monitoring of growth, disease incidence, water intake, and reproductive performance. Common challenges for applications in animal production systems are the identification of the best statistical model for the common cause variability, grouping of data, selection of type of control chart, the cost of type I and II errors, and difficulty identifying the special causes when a change is signaled. Nevertheless, carefully constructed SPC applications are powerful methods to monitor animal production systems.

Key Words: monitoring, statistics, system

Breeding and Genetics: Dairy Breeding III - Parameter Estimation

402 Estimates of heritability of feed intake in Canadian Holsteins. J. Song*, J. F. Hayes, and R. I. Cue, *McGill University, Macdonald Campus*, *Ste-Anne de Bellevue, Quebec, Canada*.

95,678,311 feed records from January 2000 to May 2007, corresponding to 16,866,117 test-day records were obtained from the Quebec Dairy Herd Improvement agency, Valacta. Each feed record contained information on animal identification, test-day date, feed type, quantity of feed intake for each feed, percentage composition of each feed for dry matter (DM), crude protein (CP), net energy for lactation (NEL), acid detergent fibre (ADF), etc. Weight of each different feed type fed to a cow on a test-day was recorded by the producer except for forage which was measured on a cow group basis according to production. Any test-day feed record with at least one feed variable outside the range of the

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feed composition (DM%, CP%, ADF%, etc) stored in the Valacta Feed Reference Library for that particular feed was deleted as well as all other associated records for the same cow on that test-day. There remained 72,290,760 feed records corresponding to 11,798,912 test-day records. Thereafter, records with missing information (e.g. missing information in pedigree files), abnormal total DM intake or lactation length, and records of cows that were sold, died or culled were removed, leaving 2,527,442 test-day records in first parity, 1,801,004 in second parity, and 1,229,436 in third parity, corresponding to 258,759, 187,871 and 128,592 lactation records in first, second and third parity respectively. Further editing to ensure that age at first calving was between 18 and 42 months, that each herd-year-season (hys) had at least 3 records, and that sires had at least 10 progeny in 5 herds reduced the data sets to 119,628 cow records in parity 1, 27,628 in parity 2, and 28,840 in parity 3. Heritabilities of feed intake traits were then estimated using an animal model which included hys at calving, age at calving, male and female phantom groups as fixed effects, and animal and residual as random effects. The model was fitted by Restricted Maximum Likelihood and relationships among animals were taken into account on both the male and female side of the pedigree. Heritability estimates ranged from 0.06 to 0.10 for total DM, from 0.08 to 0.12 for NEL, and from 0.06 to 0.11 for CP intake.

Key Words: feed intake, heritability, Holsteins

403 Heritability of body condition score and relationships with milk production traits in Canadian Ayrshires. S. Loker*[1], C. Bastin[2], F. Miglior[3], A. Sewalem[3], J. Fatehi[1], L. R. Schaeffer[1], and J. Jamrozik[1], [1]*CGIL, University of Guelph*, *Canada*, [2]*Gembloux Agricultural University*, *Belgium*, [3]*Agriculture and Agri-Food Canada, Canadian Dairy Network*, *Guelph, Canada*.

The overall objective of this study is to develop a genetic evaluation for body condition score (BCS) in Canadian dairy cattle breeds using two sources of data: a) BCS collected in Quebec by DHI, and b) BCS collected nationally by type classifiers. The specific objective of this preliminary study were to estimate genetic parameters of BCS from Quebec herds and to estimate relationships between BCS and production traits in Canadian Ayrshires. After preliminary edits, there were 32,317 BCS records on 10,067 cows and 547,450 milk production records (which included milk, fat and protein yield, and somatic cell score) on 34,462 cows. There were 45,817 milk urea nitrogen (MUN) records on 9,490 cows and 47,603 lactose percentage records on 9,890 cows. Body condition scores were not always taken on the same test-day as milk production, MUN, or lactose records. Phenotypic correlations were estimated based on the entire data set (parities 1 to 3) after preliminary edits. They were calculated on an overall basis and also by lactation stage (with about 30 days per stage). Overall, BCS was significantly correlated with all traits. Per lactation stage, BCS was significantly negatively correlated with milk, fat and protein yield, and fat:protein ratio toward the end of lactation (correlations between -0.05 and-0.21). Across lactation, BCS was significantly positively correlated with protein percent (between 0.12 and 0.21). For variance component estimation data was edited further, leaving 4,641 first lactation BCS records on 1,338 cows. Body condition score was analyzed longitudinally with a random regression model with Legendre polynomials of the third order. The analysis was attempted with fourth order Legendre polynomials but resulted in the same residual variance as the third order model, so the model with fewer parameters was chosen. The overall heritability for BCS was 0.30 ± 0.06. Heritability across the lactation ranged between 0.17 at 5 days in milk

(DIM) and 0.36 at 275 DIM. Heritability estimates were reasonable considering the literature.

Key Words: body condition score, genetic parameter, random regression model

404 Effect of test-day records beyond 305 days in milk on variance components and 305-d estimated breeding values for production traits and somatic cell score of Canadian Holsteins. J. Bohmanova*[1], F. Miglior[2,3], and J. Jamrozik[1], [1]*Centre for Genetic Improvement of Livestock*, *University of Guelph, Guelph, ON, Canada*, [2]*Agriculture and Agri-Food Canada*, *Sherbrooke, QC, Canada*, [3]*Canadian Dairy Network*, *Guelph, ON, Canada*.

The Canadian Test-Day Model (CTDM) includes test-day (TD) records from 5 to 305 days in milk (DIM). Because 47% of Holstein cows have longer lactation than 305 DIM there is a significant number of TD records beyond 305 DIM that could be included in the genetic evaluation. The additional information could increase accuracy of 305-d estimated breeding values (EBV). On the other hand, extending range of TD records beyond 305 DIM can cause a lack of fit due to inability of regression functions to properly fit the peak or end of the lactation curve when fitting longer lactations. The aim of this study was to investigate the optimal range of TD records for estimation of 305-d EBV for milk, fat and protein yield and somatic cell score (SCS). Three multiple-trait (milk, fat, protein and SCS), multiple-lactation (first three lactations) random regression models fitting TD records up to 305 DIM (M305), 335 DIM (M335) and 365 DIM (M365) were used. The effects common to all models were fixed effects of herd x test-date, DIM class and fixed regression on DIM nested within age × season class, and random regressions for additive genetic (G) and permanent environmental (PE) effects. Legendre polynomials of order 6 and 4 were fitted for fixed and random regressions, respectively. Milk, fat and protein yields were pre-adjusted for the effect of pregnancy. Three data sets were created for variance component estimation by random sampling of 50 herds. Variance components were estimated using Gibbs sampling. Full data sets were used for estimation of breeding values. Overestimation of G and PE variances at extremes of lactations was observed with all three models. The increase of G and PE variances was at earlier DIM with M305, resulting in higher variances at 305 DIM with M305 than M335 and M365. M305 had the best ability to predict TD yield from 5 through 305 DIM. This model had also the smallest Error of Prediction of 305-d EBV and smallest decline of 305-d EBV of bulls. TD records from 5 through 305 DIM only should be used in the CTDM.

Key Words: random regression model

405 Genetic variability of test-day stearoyl coenzyme-A desaturase 9 activity. V. M.-R. Arnould*[1], N. Gengler[1,2], and H. Soyeurt[1], [1]*Gembloux Agricultural University, Animal Science Unit*, *Gembloux, Belgium*, [2]*National Fund for Scientific Research*, *Brussels, Belgium*.

Milk fatty acid (FA) profile is far from the optimal fat composition in regards to human health. Different natural sources of variation such as feeding or genetics could be used to modify the contents of unsaturated fatty acids. The impact of feeding is well described; however, genetics effects on the milk FA composition are not well studied. Increasing the unsaturated fatty acids contents of bovine milk could have the potential to raise the nutritive and therapeutic values of dairy products. The stearoyl Coenzyme-A desaturase 9 (delta-9) gene was identified

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as a potential functional candidate gene affecting milk fat composition in dairy cattle. The objective of this research was to study the genetic variability on this enzyme activity across lactations. A total of 199,977 test-day records were obtained from 29,603 Holstein cows in first lactation, 154,267 records from 23,453 Holstein cows in second lactation, and 173,244 records from 75,887 Holstein cows in third and later lactations. The used model was a multiple-trait random regressions test-day model. Fixed effects were: herd × date of test, and class of age. Random effects were: herd × year of calving, permanent environmental, additive genetic, and residual effects. The studied traits were milk yield, protein content, percentage of fat, monounsaturated fatty acids estimated by mid-infrared spectrometry, and the ratios reflecting the delta-9 activity. Obtained heritability estimates of delta-9 as well as the genetic and phenotypic correlations varied across lactations. These results suggest potential improvements of milk fat composition based on delta-9 activity using animal selection and appropriate management practices.

Key Words: stearoyl coenzyme A desaturase, genetic variability

406 Influence of non-coagulating milk records on estimates of genetic parameters of milk coagulation properties. A. Cecchinato*, M. De Marchi, L. Gallo, G. Bittante, and P. Carnier, *University of Padova, Legnaro, Padova, Italy*.

Milk coagulation properties (MCP: clotting time, curd firmness) of dairy cows have been studied because of its association with cheese yield. Exploitable additive genetic variation exists for milk clotting time (RCT, min) and curd firmness (a30, mm) and, thereby, enhancement of these traits through breeding is a viable option. A critical feature of MCP data is the presence of non coagulating milk (NCM) records. These records, originating when milk does not coagulate at all in a standard 30-min testing time, are usually discarded from statistical analyses. A possible alternative is to consider NCM as censored records while the value of RCT may occurs outside the range of a measuring instrument (i.e. 30 min). The aim of this study was to evaluate the effect of including or not including NCM records on the estimates of genetic parameters of MCP. A total of 1,290 Brown Swiss cows (progeny of 50 sires) and 1,025 Italian Holstein cows (progeny of 54 sires), reared in 38 and 34 herds, respectively, were milk sampled once. Individual milk samples were collected during the morning milking and analyzed for RCT and a30, The percentage of NCM was 10% and 4% for Holstein and Brown Swiss cows, respectively. A Bayesian standard linear model (LMO) and a censored linear model (LMC) were implemented via Gibbs sampling. For LMC, data were augmented from a truncated normal distribution for samples that did not coagulate within 30 min since rennet addition, corresponding to a censoring of those observations, whereas for LMO those records were excluded from the statistical analysis. For RCT, marginal posterior means (SD) of heritabilities using LMO were 0.26 (0.09) and 0.25 (0.07) for Holstein and Brown Swiss cows, respectively. For LMC, corresponding estimates were slightly lower. Estimates of heritabilities for a30 were close to 0.17 (0.06) for both cattle breeds and both models. Results indicate that inclusion of NCM in the estimation of genetic parameters of MCP has limited effects on the magnitude of the estimated parameters.

Key Words: milk coagulations properties, non-coagulating milk, genetic parameters

407 Estimates of genetic parameters among body condition score and fertility traits in first-parity Canadian cows. C. Bastin*[1], S.

Loker[2], N. Gengler[1,3], and F. Miglior[4,5], [1]*Animal Science Unit, Gembloux Agricultural University, Gembloux, Belgium*, [2]*CGIL, Dept. of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada*, [3]*National Fund for Scientific Research, Brussels, Belgium*, [4]*Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, [5]*Canadian Dairy Network, Guelph, ON, Canada*.

The objective of this research was to estimate genetic correlations between body condition score (BCS) and female fertility traits using random regression animal models. Fertility traits were a) days between calving and first service (CTFS), b) days between first service and conception (FSTC), and c) days open (DO). The data analyzed included first-parity Ayrshire and Holstein BCS records collected between 2001 and 2008 by field staff in herds from Québec. On average 2.4 BCS observations were available per cow. Fertility records were extracted for herds with at least one BCS record. For Ayrshire, data included 9,739 BCS observations and from 10,613 to 11,942 fertility records depending on the trait. For Holstein, data included 197,583 BCS observations and from 185,464 to 207,553 fertility observations. (Co)variances were estimated by REML on the whole data set for Ayrshire and on a herd-based random sub set for Holstein. For each breed, genetic parameters were estimated with 3 two-trait models. For BCS, regression curve of genetic and permanent environmental effect were modelled using Legendre polynomials of order 3. All genetic correlations were negative: a genetically low BCS increases the number of days when the cow is not pregnant. The shape of the correlation curve between BCS and fertility varied among traits and breeds. Overall, genetic correlations changed significantly across lactation. For CTFS and FSTC in Ayrshire, genetic correlations were the highest (about -0.8) in the middle of the lactation (220 days in milk) and lower at the extreme of the lactation curve. Concerning DO in Ayrshire and all the traits in Holstein, correlations were high at calving (about -0.6) then slightly increased to be the highest around 180 days in milk (-0.8) and were the lowest at the end of the lactation. This suggested that the BCS measured at mid-lactation is the best indicator of fertility. Although analyses need to be extended to other traits and to later parities, these preliminary results indicated the interest of using BCS in indirect selection for better reproductive performances in Canadian dairy cows.

Key Words: body condition score, fertility, random regression

408 The influence of genetic selection and feed system on milk production and fertility performance of spring-calving dairy cows. J. Coleman*[1,2], K. M. Pierce[2], D. P. Berry[1], A. Brennan[1], and B. Horan[1], [1]*Teagasc, Moorepark Dairy Production Research Centre, Fermoy, Co. Cork, Ireland*, [2]*UCD, School of Agriculture Food Science and Veterinary Medicine, Belfield, Dublin 4, Co. Dublin, Ireland*.

The objective of Irish pasture based dairy production systems is to maximise profitability per hectare through excellence in grassland management within low cost feed systems (FS). Reproductive wastage within such systems results in additional financial losses due to a reduction in pasture utilisation and lower milk productivity from extended calving intervals. The objective of this study was to investigate the influence of genetic selection using the Irish total merit index (Economic Breeding Index; EBI) and intensive pasture based FS on milk production and fertility performance. Three genetic groups were compared: 1) LowNA, national average herd genetic potential; 2) HighNA, high genetic potential North American Holstein-Friesian (HF) and 3) HighNZ, high genetic potential New Zealand HF. Animals were randomly allocated to one of two FS: Moorepark (MP) pasture system

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(2.64 LU/ha and 500 kg concentrate/cow) and a high output per hectare (HC) pasture system (2.85 LU/ha and 1,200 kg concentrate/cow). A total of 126, 128 and 140 animals were used during the years 2006, 2007 and 2008, respectively. HighNA had the greatest milk and solids corrected milk (SCM) yields, HighNZ had the lowest milk yield but similar SCM yield to LowNA group. Increased stocking rates combined with concentrate supplementation increased milk production per cow and overall farm output. HighNA and HighNZ genotypes had greater odds of being served within the first 24 days of the breeding season, becoming pregnant to first service and being pregnant after 42 days of the breeding season compared to the LowNA group. Both HighNA and HighNZ animals also had a lower hazard of being culled compared to the LowNA animals. Concentrate supplementation at pasture had no effect on fertility performance. There was no genotype by FS interaction for any measures recorded. These results demonstrate the EBI as a total merit index to improve reproductive capacity while maintaining milk production performance.

Key Words: genotype, feed system, fertility performance

409 Consequence on reproduction of two feeding levels with opposite effects on milk yield and body condition loss in Holstein and Normande cows. E. Cutullic*[1], L. Delaby[1], G. Michel[2], and C. Disenhaus[1], [1]*INRA UMR1080 Dairy Production*, *Rennes, France*, [2]*INRA UE326 Le Pin-au-Haras*, *Exmes, France*.

The objective of this study was to evaluate the respective effects of milk yield and body condition (BC) loss on cows' postpartum reproductive status taking breed differences into account. 105 Normande (dual-purpose) and 98 Holstein cows were assigned to a low or high feeding level (L-group: 50% grass silage and 50% haylage in winter, no concentrate at grazing; H-group: 55% maize silage, 15% alfalfa hay and 30% concentrate, 4kg concentrate at grazing). Milk progesterone assays led to determine commencement of luteal activity (CLA), postpartum ovarian activity profile, ovulation detection rate and late embryo mortality. Data were analysed by variance-covariance and logistic regression models. In both breeds, L-group cows had a lower 100-day average daily milk yield (MY) than the H-group cows but lost more BC (0-5 scale) (21.5 vs. 30.9 kg/day, -1.38 vs. -0.94 unit, N=102 and 101; P<0.001). Feeding level effect on MY was greater for Holstein than for Normande cows (+10.9 vs. +8.0 kg/day; P<0.05). As expected, Normande cows had shorter CLA, less prolonged luteal phase cycles and higher calving rate than Holstein cows (P<0.01). Feeding level had little effect on CLA and ovarian activity profile. In both breeds, ovulation detection rate was higher in the L-group (77% vs. 60%, N= 254 and 282; P<0.001). At 1st and 2nd inseminations, conception rate was improved in the H-group (74% vs. 57%, N=125 and 138; P<0.01), especially for Holstein cows (73% vs. 48%; P<0.01). As late embryo mortality frequency was very high in the H-Group Holstein cows (30% vs. 9%, N= 64 and 64; P<0.01), difference in calving rate was not significant between feeding groups (P>0.25). Owing to feeding level effects, MY and BC loss could affect reproduction at different stages. Consistent with the literature, a greater BC loss coincides with reduced conception rate. High milk yield coincides with depressed ovulation detection and embryo survival.

Key Words: reproduction, milk yield, body condition loss

Breeding and Genetics: Swine Breeding

410 Performance and carcass composition of pigs selected for residual feed intake on restricted and ad libitum diets. N. Boddicker*, D. Nettleton, N. Gabler, M. Spurlock, and J. C. M. Dekkers, *Iowa State University*, *Ames*.

Understanding the biology behind genetic differences in feed efficiency is important to develop selection strategies to improve efficiency. To this end, a line of Yorkshire pigs selected for lower residual feed intake (LRFI) was developed. The objective of this study was to evaluate the 5th generation of the LRFI line against a random control line (CTRL) for performance, carcass and chemical composition, and overall efficiency. Forty barrows from each line were paired by age (~132 d) and weight (74.8±9.9 kg), and randomly assigned to 1 of 4 feeding levels in individual pens in 10 replicates: 1) ad libitum (adlib), 2) 75% of adlib (A75%), 3) 55% of adlib (A55%) and 4) weight stasis (WS). Pigs were on test for 6 weeks with feed intake adjusted once or twice per week for each pig. Although initial BW did not differ between lines (p=0.49), all results were adjusted for initial BW. The adlib LRFI consumed 8% less feed (p=0.15) with no difference in growth rate versus the CTRL. However, the A55% LRFI gained 10% more (p<0.01) than the CTRL on the same amount of feed. Despite attempts to hold the WS pigs at constant BW for six weeks, the LRFI gained BW while consuming 11% less feed than the CTRL (p=0.05). The LRFI line also had a higher dressing percentage (p<0.03) and lower visceral weights than the CTRL, but this was significant only for the A75% level (p<0.02). Based on chemical analysis of the empty carcass, the LRFI line had lower fat% and greater water% than the CTRL, but this was significant only for the adlib level (p=0.08). There were no line differences in protein% and ash%. In conclusion, pigs selected for LRFI consumed less feed for the same rate of gain but differed in carcass composition, indicating differences in the partitioning of energy. LRFI pigs also had lower viscera weights and required less energy to maintain BW, indicating possible differences in maintenance requirements. Further analysis will focus on differences between retained and consumed energy. *This research was funded by grants from the National Pork Board and the Iowa Pork Producers Association.*

Key Words: residual feed intake, performance, carcass composition

411 Effect of selection for residual feed intake on feeding behavior and daily feeding patterns in pigs. J. M. Young*, W. Cai, and J. C. M. Dekkers, *Iowa State University*, *Ames*.

Residual feed intake (RFI) is a measure of feed efficiency defined as the difference between observed and predicted feed intake based on average requirements for growth and maintenance. The objective of this study was to evaluate the effect of selection for lower RFI on feeding behavior traits (FBT) and to estimate the relationship between FBT and RFI. Data were from 3 parities from the 4th and 5th generations of a selection experiment for lower RFI (LRFI) and a random control line (CTRL) were analyzed by parity. Lines were mixed in pens of 16 and evaluated for FBT obtained from a single-space electronic feeder (FIRE©) over a growing period of ~3 months prior to ~115 kg. The following FBT were evaluated as averages over the entire test period (TP) and over the first (TP1) and second half (TP2) of the test period: number of visits per day (NVD) and per hour (NVH), occupation time per day (OTD), per visit (OTV) and per hour (OTH), feed intake per day (DFI), per visit (FIV) and per hour (FIH), and feeding rate per visit

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