Breeding and Genetics: Feed efficiency and methods

522 Definition and implementation of a breeding value for feed efficiency. Jennie E. Pryce*[1,2], Oscar Gonzalez-Recio[1], Gert Nieuwhof[1], Bill Wales[1], Michael P. Coffey[3], Ben J. Hayes[1,2], and Michael E. Goddard[1,4], *[1]Department of Economic Development, Jobs, Transport and Resources, Bundoora, VIC, Australia, [2]La Trobe University, Bundoora, VIC, Australia, [3]SRUC, Edinburgh, Midlothian, UK, [4]The University of Melbourne, Melbourne, VIC, Australia.*

The objective was to describe how a new estimated breeding value (EBV) for feed efficiency is calculated. From April 2015, the Australian Dairy Herd Improvement Scheme (ADHIS) has published a new breeding value, called feed saved, that is the amount of feed saved through improved metabolic efficiency and reduced maintenance requirements. The breeding value includes a genomic component for residual feed intake (RFI) combined with either a genomic or pedigree EBV for body weight (BW) predicted using conformation traits. The RFI component of the feed saved EBV has 2 parts: Australian calf RFI and Australian lactating cow RFI. Genomic breeding values for RFI were estimated in a multi-trait analysis (3 traits) that included including Australian growing heifer and lactating cow RFI in addition to overseas (UK and Dutch) lactating cow RFI. The reference population included 50k single nucleotide polymorphism (SNP) genotypes and phenotypes for 234 Australian lactating cows and 843 heifers (approximately 6 mo old) and 958 UK and Dutch lactating cows. In all cases, the RFI phenotypes were trait deviations that were calculated by correcting dry matter intake for bodyweight, growth and yield (in the case of lactating cows). Effects for each SNP were calculated from the output of genomic best linear unbiased prediction and used to predict breeding values of 4,416 sires that were genotyped, but did not have RFI phenotypes themselves. These bulls already had BW breeding values calculated from type traits, from which maintenance requirements in kg of feed per year were inferred. Finally, RFI and the feed required for maintenance (through BW) were combined to construct a feed saved breeding value. Animals with EBVs that are one standard deviation above the mean are predicted to eat 65 kg dry matter less per year at the same level of milk production. The mean reliability associated with the feed saved breeding value was 0.37 in the data set of 4416 genotyped Holstein sires. From April 2015, feed saved has also been included as part of the Australian national selection index published by ADHIS.

Key Words: feed efficiency, residual feed intake, genomic

523 Indices to improve feed efficiency. Kelli J. Retallick*[1], Jennifer M. Bormann[1], Robert L. Weaber[1], Michael D. MacNeil[3], Heather L. Bradford[1], Harvey C. Freetly[2], Daniel W. Moser[1], Warren M. Snelling[2], Richard M. Thallman[2], and Larry A. Kuehn[2], *[1]Kansas State University, Manhattan, KS, [2]USDA-ARS Meat Animal Research Center, Clay Center, NE, [3]Delta G, Miles City, MT.*

Evaluating feed efficiency of beef cattle has evolved from relying on single trait selection for increased gain to extensive use of multiple trait selection combining measures of gain and intake. Postweaning gain (difference between 365-d and 205-d age adjusted weights) is analyzed as part of National Cattle Evaluation programs and could be used in an index with shorter intake tests (currently >70d to accurately measure gain) to select animals for improved feed efficiency. Under this paradigm, producers could decrease costs per animal and increase genetic change by testing a greater number of animals per year. Objectives of this study were to compare 2 alternative indices for feed efficiency and to quantify the genetic response to selection for feed efficiency combining an intake test with PWG data. Strong genetic correlation estimates for steers and heifers between average daily gain (ADG) and postweaning gain (PWG) (0.81, 0.65) suggest PWG is a reliable proxy for ADG. On-test ADFI, on-test average daily gain ADG, and postweaning daily gain (PWG) records on 5,606 growing steers and heifers were obtained from the US Meat Animal Research Center in Clay Center, NE. Genetic (co)variances and EBV were estimated using a 6 trait animal mixed model with ADG, ADFI, and PWG as dependent variables for both steers and heifers. Indices combining EBVs for ADFI and ADG and for ADFI and PWG were evaluated. For each index, the weighting of gain was arbitrarily set to 1.0 and the weighting for ADFI was the negative of the average of the intra-contemporary group ratio of mean gain divided by mean ADFI. Values were combined with EBV to compute 2 index values per animal. Pearson correlations for steers (0.96) and heifers (0.45) indicated a strong relationship for steers between the indices. For steers, using the index with PWG rather than with ADG effectively results in the same genetic gain without additional intake records. Because more animals can be measured for intake, using PWG increases relative annual progress of selection for feed efficiency by 15%. These findings support using PWG data in combination with ADFI to determine efficient steers, lessen costs, and increase feed efficiency genetic change per year.

Key Words: beef, index, efficiency

524 Comparison of actual versus predicted feed intake phenotypes for genetic evaluation of feed efficiency in beef cattle. Kimberly A. Branham*[1], Jonathan E. Beever[2], Dan B. Faulkner[10], Holly L. Neibergs[3], Kris A. Johnson[3], Christopher M. Seabury[4], Dorian J. Garrick[5], Daniel D. Loy[5], Stephanie L. Hansen[5], Harvey C. Freetly[6], Matt L. Spangler[7], Monty S. Kerley[8], Robert L. Weaber[9], Daniel W. Shike[2], Robert D. Schnabel[8], J. E. Decker[8], Jerry F. Taylor[8], and Megan M. Rolf[1], *[1]Oklahoma State University, Stillwater, OK, [2]University of Illinois, Champaign, IL, [3]Washington State University, Pullman, WA, [4]Texas A&M University, College Station, TX, [5]Iowa State University, Ames, IA, [6]USDA- Meat Animal Research Center, Clay Center, NE, [7]University of Nebraska, Lincoln, NE, [8]University of Missouri, Columbia, MO, [9]Kansas State University, Manhattan, KS, [10]University of Arizona, Tucson, AZ.*

Feed efficiency is expensive to measure in beef cattle because of the technology it requires to measure individual animal dry matter intakes (DMI). One potential solution is to develop methods to effectively utilize pen feed intake data for genetic evaluation. Genetic correlations between predicted DMI (pDMI) and actual DMI reported in the literature indicate that pDMI may be useful as an indicator trait. Therefore, the objective of this study is to evaluate whether quantitative trait loci (QTL) mapping approaches identify the same regions of the genome for pDMI and DMI. Because average daily gain (ADG) is a primary driver of the prediction models, the overlap of pDMI and DMI QTL regions with QTL for ADG will also be evaluated. To achieve these objectives, individual animal feed intake, weight, and carcass data was obtained on 849 Hereford steers and heifers fed within a GrowSafe (GrowSafe Systems Ltd.) feed intake system. The Cattle Value Discovery System (CVDS) growth and carcass data model was utilized to obtain pDMI

from DMI pooled within pens and reallocated to individual animals. Phenotypic correlations were 0.64 ($P < 0.0001$) and 0.56 ($P < 0.001$) between pDMI and DMI and pDMI and ADG, respectively. Genotypes were collected using the Illumina BovineHD Beadchip assay (Illumina Inc., San Diego, CA), and after data filtering, a final data set of 648,625 single nucleotide polymorphisms (SNP) were available for analysis. The SNP effects for ADG, pDMI, and DMI were estimated utilizing a BayesB0 model in GenSel. The 5-SNP windows surrounding the 100 largest SNP effects for each phenotype were compared with determine overlap between QTL regions. Concordance of QTL regions was 50% between pDMI and ADG, 26% between pDMI and DMI, and 19% between DMI and ADG. Seven of the QTL regions in common between pDMI and DMI were independent of ADG QTL regions. These results show that there is concordance between genomic regions for pDMI and DMI independent of the model drivers (ADG), and additional research will be conducted to characterize these regions of interest in genomic prediction for feed efficiency.

Key Words: beef cattle, feed efficiency, genomics

525 Hierarchical Bayesian inference on genetic and non-genetic components of partial efficiencies determining feed efficiency in dairy cattle. Yongfang Lu*[1], Mike Vandehaar[1], Diane Spurlock[2], Kent Weigel[3], Louis Armentano[3], Charles Staples[4], Erin Connor[5], Zhiquan Wang[6], Mike Coffey[7], Roel Veerkamp[8], Yvette Haas[8], Nora Bello[9], and Robert Tempelman[1], *[1]Michigan State University, East Lansing, MI, [2]Iowa State University, Ames, IA, [3]University of Wisconsin, Madison, WI, [4]University of Florida, Gainesville, FL, [5]U.S. Department of Agriculture, Beltsville, MD, [6]University of Alberta, Edmonton, AB, Canada, [7]Scottish Agricultural College, Easter Bush, Midlothian, UK, [8]Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Lelystad, the Netherlands, [9]Kansas State University, Manhattan, KS.*

Dairy cattle feed efficiency (FE) can be defined as the ability to convert DMI into milk energy (MILKE) and maintenance or metabolic body weight (MBW). In other words, FE is DMI conditional on MILKE and MBW (i.e., DMI|MILKE,MBW). These partial regressions or partial efficiencies (PE) of DMI on MILKE and MBW can be separately partitioned into genetic or residual PE; furthermore, either PE category might be heterogeneous across various environmental or management factors. We develop a hierarchical Bayesian multivariate mixed model to infer upon such heterogeneity in PE as well as that of variance components (VC) of FE by modeling genetic and residual components of PE and of VC as mixed model functions of various factors such as station (fixed), parity (fixed), days in milk (fixed), and ration within station (random). After validating our proposed model with a simulation study, we applied it to analysis of a dairy consortium data set involving 5,088 Holstein cows from 13 research stations in 4 countries. Although no significant differences were detected across stations for the genetic PE of DMI|MILKE (0.38 kg/Mcal) and of DMI|MBW (0.10 kg/kg$^{0.75}$), as well as the residual PE of DMI|MILKE (0.33 kg/Mcal), the residual PE of DMI|MBW significantly differed across stations ($P < 0.05$), ranging from 0.05 kg/kg$^{0.75}$ to 0.18 kg/ kg$^{0.75}$. Substantial heterogeneity in genetic and residual VC in FE across stations, rations, and parities was also inferred. Estimated heritabilities of FE ranged from 0.16 to 0.46 across stations, whereas the overall estimated heritability of FE was 0.23. These results suggest that FE is more complex than what is currently considered in most quantitative genetic analyses.

Key Words: dairy cattle, feed efficiency, heterogeneity.

526 Thermal imaging as an indicator of feed efficiency in mid-lactation Holstein cows. Lydia C. Hardie* and Diane M. Spurlock, *Iowa State University, Ames, IA.*

Genetic improvement of feed efficiency in dairy cattle through direct selection is a challenge because of costs associated with measuring feed intake on individual cows. The identification of an easy to measure indicator trait of feed efficiency would help alleviate this problem. The objective of this study was to characterize the genetic variability and determine the relationship between surface body temperature and internal body temperature with feed efficiency in mid-lactation Holstein cows. Feed efficiency was measured as residual feed intake (RFI), defined as the difference between the actual intake and predicted intake based on milk energy, body weight change, and maintenance requirements. Individual daily feed intakes and milk production were recorded for 8 weeks on 124 primiparous cows between 50 and 200 d in milk. Weekly body weight and milk component data were also collected, and average RFI throughout the measurement period was calculated. Surface body temperature was measured weekly by thermal images taken of the lower right rear leg using a Fluke hand-held Thermal Imaging Scanner. The mean temperature in a defined region on the image was averaged across days for each cow. Rectal body temperatures were taken on imaging days and averaged for each cow. The ability of the body temperatures to explain variation in RFI was analyzed with a linear model, which included the fixed effect of replicate along with body temperature (surface or rectal) as a covariate. Heritabilities for body temperatures were estimated in ASReml. Rectal temperature did not significantly explain variation in RFI while surface leg temperature accounted for 2.8% of the total variance in RFI ($P < 0.10$). Average leg surface temperatures for the top and bottom quartiles for RFI were 25.3 and 24.9 C (SE 0.3) for high and low RFI, respectively. Rectal temperatures did not differ between high and low RFI quartiles. Leg surface temperature was moderately heritable (0.32 ± 0.32) while the heritability estimate of rectal temperature was 0.16 ± 0.26. This research demonstrates surface leg temperature is a heritable trait that explains a small portion of variation in RFI.

Key Words: feed efficiency, residual feed intake, thermal imaging

527 Genetic correlations of lower gastrointestinal tract microflora taxonomic groups with animal intake and gain. Larry A. Kuehn*[1], Warren M. Snelling[1], Rohita Sinha[2], James E. Wells[1], James L. Bono[1], Harvey C. Freetly[1], Min Seok Kim[1], Jennifer Clarke[2], Stephen D. Kachman[2], Etsuko Moriyama[2], Danielle F. Wells[2], and Andrew K. Benson[2], *[1]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, [2]University of Nebraska-Lincoln, Lincoln, NE.*

Diversity and composition of microorganisms in the lower gastrointestinal tract have been shown to affect health and weight in humans and other mammalian species. At least a portion of the microbial diversity is likely under host genetic control. Our objective was to determine whether animal feed intake and growth were genetically correlated with microbial taxonomic groups as measured in fecal samples from the lower gastrointestinal tract through metagenomic analysis. Fall born animals

(n = 905) of various breed composition (crosses of 18 different breeds) had individual animal feed intake recorded during a 63d period. Steers (n = 491) received a high energy concentrate (finishing) ration, and heifers (n = 414) received a roughage (growing) ration. During these feeding trials, animals were weighed on 2 consecutive days both when feed intake collection began and ended with additional weights recorded at least every 3 weeks. Fecal samples were collected prior (once), during (at least 3 times), and after (once) the feed intake trial period and pooled as a composite sample by animal. Taxonomic composition of the fecal microbiome was quantified from shotgun metagenomic sequencing of total DNA. Common contigs within and among animals were pooled by phylogeny yielding a reference metagenome assembly of 87 taxonomic groups. These groups (each present in at least 75% of the animals) were quantified by mapping reads from individual animals onto the reference assembly. Genetic (co)variance components for feed intake, gain, and individual taxonomic groups were estimated using REML. Data were modeled with fixed effects of contemporary group (sex, year, season) and breed composition covariates. Random effects were animal direct genetic effect (pedigree derived relationships) and error. Seven taxonomic groups were estimated to be heritable ($P \leq 0.10$). Genetic correlations were detected ($P \leq 0.10$) for *Blautia* with feed intake (r = 0.61) and *Cellulosilyticum* with weight gain (r = −0.68). Ration (or sex) specific correlations were not estimable; however, it is likely that ration affects the lower gastrointestinal tract microbial composition. The USDA is an equal opportunity provider and employer.

Key Words: beef cattle, feed efficiency, metagenomics

528 Withdrawn

529 Validating your validation: A consistency check for the R^2 found in a validation to calculate correct reliabilities for genomic EBV in a multi-trait setting. W. Marianne Stoop*, H. Eding, and G. de Jong, *CRV, Arnhem, the Netherlands.*

In 2014, the Netherlands and Flanders implemented a new genomic system, in which direct genomic values (DGV) are used as pseudo-observations to directly affect the conventional trait. For most trait groups, this pseudo-record system is a multi-trait animal model, where the added R^2 from a validation study is used as correlation between DGV and conventional trait, and a covariance matrix holding partial correlations is derived from it. However, validation of the DGV is done in a single trait setting, where a relatively young –and unreliable- group of bulls is used as validation set, often resulting in unstable added R^2, depending on which set of bulls you select as validation set. When the added R^2 of traits within a multi-trait system are not consistent to each other, the multi-trait system is unbalanced, even if the defined covariance matrix is positive definite, resulting in incorrect reliabilities. In this study, a consistency check is done on the validation results of a set of fertility traits (nonreturn56, interval-calving-1st-insemination, calving interval, interval-first-last-insemination, conception rate, conception rate heifers, and age at first insemination) used in a multi-trait animal model, to assess the correctness of the added R^2, the used correlations and the reliability calculated for the GEBV. This consistency check is based on the coefficient of multiple correlations (MCC); where the expectation is that the diagonal of the matrix containing MCC is equal to the corresponding R^2 from the validation. Data of the EuroGenomics consortium was used. The training set varied between 6,000 bulls (for traits with national data only) to 26,000 bulls. Bulls born after 20040630 were considered as validation set. The added R^2 ranged from 0.21 for age-at-first-insemination to 0.64 for interval-first-last-insemination. When the set of added R^2 was consistent, the reliabilities for the validation bulls estimated in the multi-trait model were similar to realized reliabilities. In conclusion, the consistency check is a valuable tool to assess genomic validation.

Key Words: dairy cattle, genomics, validation

530 Genomic heritabilities and SNP associated with lower gastrointestinal tract microflora taxonomic groups and *E. coli* O157:H7 shedding. Warren M. Snelling*[1], Larry A. Kuehn[1], Rohita Sinha[2], James E. Wells[1], James L. Bono[1], Elaine D. Berry[1], Min Seok Kim[1], Jennifer Clarke[2], Stephen D. Kachman[2], Etsuko Moriyama[2], Danielle F. Wells[2], and Andrew K. Benson[2], *[1]USDA-ARS-US Meat Animal Research Center, Clay Center, NE, [2]University of Nebraska-Lincoln, Lincoln, NE.*

Risk of beef contaminated by *E. coli* O157:H7 is affected by prevalence of O157:H7 in cattle feces. Host genetics may influence O157:H7 shedding and overall microbial diversity in the lower gastrointestinal tract. Objectives of this study were to determine influence of animal genotypes on measures of O157:H7 shedding and relative abundance of different taxa in cattle feces, and identify regions of the bovine genome associated with O157:H7 prevalence and microbial diversity. Feces were sampled from fall born animals (n = 1,099) of various breed composition (crosses of 18 different breeds) undergoing trials to measure individual animal intake over 63 to 90 d periods. Steers (n = 574) received a high-energy finishing ration and heifers (n = 525) a high-roughage breeding development diet. Feces were sampled once before, at least thrice during, and once after the feed intake trial period. Individual samples were assessed for enumerable O157:H7. Taxonomic composition of the

fecal microbiome was quantified from shotgun metagenome sequencing of total DNA pooled for each animal. Reads were assembled for each animal individually and contigs pooled within and across animals by phylogeny, yielding a reference metagenome assembly of 87 different taxonomic groups that were detected across > 75% of the animals. These taxa were quantified by mapping reads from each sample onto the reference assembly. Heritability for relative abundance of each taxa and O157:H7 prevalence measure was estimated with REML, using genomic relationships described by imputed BovineHD SNP genotypes. Individual SNP effects were solved from animal solutions after REML converged. Heritability estimates ranged from 0.00 for 35 taxa to 0.21 for *Butyrivibrio,* and were greater than 0.05 for 19 taxa. For O157:H7 traits, estimates were 0.10 for the number of times the animal was prevalence positive, and 0.07 for $\log_{10}$ of the average O157:H7 level. Correlations between SNP effects on O157:H7 and individual taxa were near zero, although a cluster of SNP between *TMEM20* and *PLCE1* on BTA26 was associated with $\log_{10}$[0157:H7] and 11 taxa having heritabilities >0.05.

Key Words: beef cattle, metagenomics, *E. coli* O157:H7

531 Utilizing cattle genetic trends to evaluate the long-term use of gene bank collections. Harvey D. Blackburn*[1], Carrie S. Wilson[1], Samuel Paiva[2], Scott Spiller[1], and Phil H. Purdy[1], *[1]ARS/USDA, Fort Collins, CO, [2]EMBRAPA, Brasilia, Brazil.*

The National Animal Germplasm Program has developed substantial germplasm collections (>800,000 samples) for more than 300 unique livestock populations or breeds. Gene bank utilization is relatively new to the livestock sector and the long-term genetic relevance of such collections has not been documented in terms of how far into the future the captured diversity might be commercially useful. Comparing the annual average PTA or EPD for various traits computed by the respective breed associations with the collection's PTA/EPD statistics (mean, standard deviation, and extremes) may be a comparison that provides insight as to how well the collection mirrors the in situ population. Six breeds selected for comparison were Holstein (n = 5393), Jersey (n = 873), Angus (n = 703), Hereford (n = 252), Charolais (n = 86), and Brangus (n = 70). Birth years for the bulls in each breed spanned: 50, 60, 55, 60, 45, and 35 years, respectively. Trends for PTA or EPD for each trait computed by the respective associations were developed. Breed average (in situ population) vs. collection: average, standard deviation and minimum and maximum values for the respective breeds were compared. The collection average across breeds and traits closely mirrored the in situ populations' PTA or EPD estimates over time. When comparing the repository PTA or EPD outliers of any breed to the mean of its in situ counterpart across traits it was determined that it would take the in situ average PTA/EBV estimates, for a given birth year, 25 to 35 years to reach the collection's maximum or minimum value. This finding was consistent across all breeds regardless of collection size and age. These results demonstrate that animals with samples in gene bank collections could produce progeny that are commercially competitive for at least a quarter century (post collection) and demonstrates that gene bank collections are sufficient to provide protection for the various breeds in the collection. These results demonstrate that continued targeted sampling by gene banks over time will further ensure collection utility. In addition to the issue of genetic security, these findings suggest genetic progress has not advanced as quickly in cattle populations as might have been assumed.

Key Words: genetic resource, cattle, gene bank

532 Estimating the heritability of gene expression profiles using RNAseq data. Deborah Velez-Irizarry*[1], Catherine W. Ernst[1], Ronald O. Bates[1], Pablo Reeb[1], Yeni Bernal Rubio[2], Nancy E. Raney[1], and Juan P. Steibel[1], *[1]Michigan State University, East Lansing, MI, [2]University of Buenos Aires, Buenos Aires, Argentina.*

Estimation of heritability is crucial for breeding purposes and for understanding the genetic basis of phenotypic traits. For the specific case of expression traits, heritability estimates can be used to prioritize expression quantitative trait loci (eQTL) genes. Estimates of heritability are usually obtained by linking phenotypic records with the estimated relationship matrix. The relationship matrices can be derived from pedigree, marker information or both. We propose an approach to estimate heritability of gene expression that takes full advantage of next generation sequencing platforms. A GBLUP-based animal model was used to fit all genetic markers simultaneously to each gene expression profile individually. A preliminary study using longissimus muscle (LM) transcriptome sequence data (RNaseq) for 24 animals from the Michigan State University pig resource population (MSUPRP) showed that more power was needed to identify significant genetic effects when using gene expression profiles as a trait phenotype. A subsequent study involving LM RNaseq for 144 MSUPRP animals was conducted using a similar GBLUP-based model. Results showed great improvement in the detection of significantly heritable expression traits (HET). A total of 226 statistically significant HET were discovered at FDR = 1%. The range of heritability estimates for these significant expression traits was between 0.27 and 1.00. Furthermore, 3 gene expression profiles showed extremely high heritability ($h^2 > 0.99$, with GBV q-values $<1 \times 10^{-8}$). Pathway Analyses of the significant HET revealed multiple genes involved in organismal development and transcriptional regulation emphasizing cellular growth and proliferation. The top genes involved in these molecular processes include *TGFB3*, *BMPR1A* and *MCM8*, the former 2 associated with weight gain. This research shows that genomic prediction models can be effectively used to elucidate the molecular mechanisms driving variations in heritable expression traits and to identify important regulatory gene networks.

Key Words: heritability, RNAseq, quantitative genetics

533 Exploitation of population-wide whole-genome genotyping to identify the founder of a deleterious mutation in cattle. Andreas Kromik[1], Phillip Widmann[1], Frieder Hadlich[1], Dierck Segelke[2], Rosemarie Weikard[1], and Christa Kühn*[1,3], *[1]Leibniz Institute for Farm Animal Biology (FBN), Institute for Genome Biology, Dummerstorf, Germany, [2]Vereinigte Informationssysteme Tierhaltung w.V. (vit), Verden/Aller, Germany, [3]University Rostock, Faculty of Agricultural and Environmental Sciences, Rostock, Germany.*

Genomic selection programs generate deep pedigrees with whole genome genotyping data, which can also be used for the analysis of genetic defects. Recently, studies highlighted the relevance of novel mutations for human health. The use of non-progeny tested very young sires in genomic selection programs increases the danger of an unnoticed, rapid spread of novel mutations, if no respective precautions are taken. Recently, we identified a novel defect (spinal and vertebral malformation, VSD) and its causal mutation in Holstein cattle. Based on 50K SNP data, in our project 73 offspring of a carrier sire for VSD (41 VSD affected, 31 VSD unaffected) were haplotyped using CRIMAP options, and the paternal haplotype carrying the VSD mutation was identified. To further trace the origin of the haplotype associated with VSD, we subsequently haplotyped 50K SNP genotypes of a total of 55,384 indi-

viduals from the German Holstein population including all available relatives of the carrier sire using BEAGLE. Genotypes were provided by VIT Verden, the central database for genomic evaluation in German Holstein cattle. Tracking of haplotypes and haplotype breakpoints through the pedigree excluded the father of the carrier sire as potential source of the mutation and indicated that the mutation was located on the paternally inherited haplotype of the dam. Sequencing of the bovine *brachyury* gene in the maternal grandsire, the dam and the carrier sire itself revealed that the mutation developed de novo in the dam, because the haplotype of the maternal grandsire that was transmitted to the dam contained the wild type allele, whereas the respective haplotype in the dam showed the mutated allele. Additional genotyping of 94 offspring of the maternal grandsire revealed that none of those offspring showed the mutated allele. In conclusion, population-wide SNP genotyping and haplotype tracking enabled exclusion of a major Holstein blood line as source for VSD and confirmed the origin of the defect. Due to the recent de novo mutation and the confirmed knowledge about the founder, the defect can easily be eradicated from the Holstein population before any further outspread.

Key Words: genetic defect, cattle, vertebro-spinal dysplasia