

development of novel genomic strategies for improving service sire fertility in Brown Swiss cattle.

Key Words: genomic scan, service sire fertility, sire conception rate

1123 A major QTL for brachygnathia inferior in Brown Swiss cattle. S. Widmer^{*1}, F. R. Seefried², C. Flury³, and C. Drögemüller¹, ¹*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland*, ²*Qualitas AG, Zug, Switzerland*, ³*School of Agricultural, Forest and Food Sciences, Bern University of Applied Sciences, Zollikofen, Switzerland*.

Shortening of the lower jaw (brachygnathia inferior) is a congenital and often inherited malformation in domestic animals including cattle. Viral infections, teratogenic drugs and alkaloids of plants can also lead to such craniofacial malformations. Brachygnathia inferior often leads to reduced growth and poorer health and welfare of the animals, which affects productivity. As it is already described in sheep and buffalo, a complex inheritance is to be assumed. We have observed several cases with a frequency of about 0.1 % in the Brown Swiss cattle population of Switzerland. A simple monogenic dominant model of inheritance can be excluded, as none of the 46 specifically examined offspring of 147 affected cows showed the trait. Therefore, we have suspected that either a simple monogenic-recessive or an oligo- or polygenic inheritance is underlying. We conducted a genome-wide association study with 147 cases and 509 normal controls to decipher the associated genetic regions. The phenotypes were recorded as part of the routine assessment of conformation. The animals were genotyped with different routinely available array chips and imputation was done in a 2-step approach. Using the final high-density 700k data set, we applied single SNP regression analysis to identify a single major QTL for this trait on chromosome 5 between 29 and 33 Mb. Numerous genes and loci are annotated in this 4 Mb interval, including genes of signaling pathways such as Wnt (wingless-related integration site), which are important for the complex regulation of the development of craniofacial structures. The association signal in this genome region was supported by the results of a subsequent run of homozygosity analysis with the same data set. Currently, whole-genome sequencing data from several cases is being performed to achieve both fine mapping and subsequent discovery of associated, potentially causal variants. Our work represents the first comprehensive study of the genetics of brachygnathia inferior in dairy cattle and provides the basis for future DNA-based selection against this undesirable trait.

Key Words: craniofacial anomaly, GWAS, WGS

1124 Evidence of selection against recessive defects. H. D. Norman^{*1}, D. J. Null², and P. M. VanRaden², ¹*Council on Dairy Cattle Breeding, Bowie, MD*, ²*USDA-ARS Animal Genomics and Improvement Laboratory, Beltsville, MD*.

Haplotype tests are effective for differentiating animals with traits of desirable performance, or conversely, those that are carriers of detrimental recessive alleles. Our objective was to show how the frequencies of carriers have changed in US dairy animals over time. Several carriers have haplotypes impacting fertility, first described by P.M. VanRaden and updated by J.B. Cole et al. in USDA AIP Research Report Genomics (12–20). In their homozygous state, embryonic death or stillbirth occurs. The stage of gestation when abortions occur varies, thus the economic losses vary as well. Semen from some carrier bulls continued in use, but selection against their carrier sons followed. Mating programs helped

avoid mating carriers to carriers. Frequencies of carrier by years were derived from genotyped animals; those from 2011 and 2021 are shown. AH1 and AH2 in Ayrshires remains high (18.5 and 19.9%), but below 2011 (31.6 and 20.8%). BH2 in Brown Swiss in 2021 is 5.7%, down from 17.7%. Several haplotypes in Holsteins (HO) have been uncovered. Carriers in 2011 and 2021 respectively were: HH0 5.9 and 0.9%; HH1 4.3 and 1.0%; HH2 3.6 and 1.8%; HH3 6.8 and 1.9%; HH4 0.7 and 0.2%; HH5 4.2 and 6.3%; and HH6 0.7 and 1.9%. JH1 in Jerseys (JE) were 23.3 and 9.7%. Carriers for BLAD, CVM, DUMPS, and mulefoot were 0.6, 2.8, 0.02 and 0.16% in 2011 and 0.1, 0.6, 0.01 and 0.02% in 2021. Recently discovered JNS in Jerseys rose from 3.6 to 7.2%. Alleles considered favorable changed as well. The polled carriers changed in HO from 1.2 to 2.1 and in JE from 4.2 to 3.4. Percentage of detrimental carriers often increased before discovery which made detection easier; after exposure, selection against them followed.

Key Words: abortions, fertility, haplotypes

1125 Gestation length and dystocia of Holsteins mated to Holstein and beef breed service sires. B. L. Basiel^{*}, T. L. Felix, and C. D. Dechow, *Pennsylvania State University, University Park, PA*.

Objectives were to determine if dystocia and gestation length (GL) in Holstein heifers and cows are influenced by beef service sires in comparison to Holstein service sires. Calving records (n = 6,671) of Holsteins from the years 2019 to 2022 were obtained from Pennsylvania dairies (n = 7). Cows were mated to Holstein (n = 5,545 calvings; n = 394 sires), Angus (n = 617 calvings; n = 53 sires), Charolais (n = 114 calvings; n = 3 sires), Wagyu (n = 36 calvings; n = 4 sires), Simmental or SimAngus (n = 292 calvings; n = 14 sires), and crossbred beef (n = 67 calvings; n = 5 sires) bulls. Calving ease (CE) score from 1, indicating no problem, to 5, indicating extremely difficult birth or Cesarean section, was used to quantify dystocia. Records of GL were available for all calvings and CE score was available from a subset (n = 4,424) of records from 5 herds. Linear models were used to analyze GL and CE where sire breed type (beef or dairy) or sire breed was the main effect. Lactation number, twinning incidence, stillbirth incidence (SB), and calf sex were included as fixed effects. The interactions of SB and twinning incidence and of SB and calf sex were included in the CE models. When grouped as breed type, beef-sired calves were carried for 0.9 d longer than dairy-sired calves ($P < 0.05$). However, gestation length of Charolais-sired calves was shorter (271 d) than Holstein-sired calves (272 d, $P < 0.05$) while Angus (273 d), Simmental (274 d), and Wagyu-sired (279 d) calves was longer ($P < 0.05$). Calving ease of Holsteins mated to beef bulls did not differ from those mated to Holstein bulls. The least squares means of CE score of animals mated to Holstein and Angus sires were greater than those mated to Simmental sires. Holsteins mated to Angus sires had poorer CE scores than those mated to crossbred beef sires. Beef-sired calves were carried for the same or a greater number of days than Holstein-sired calves except for those sired by Charolais bulls. Using beef sires did not cause greater incidence of dystocia than Holstein sires. Simmental-sired calves reduced incidence of dystocia when compared with Holstein-sired calves.

Key Words: beef × dairy, dystocia, days carried calf

1126 Changes in herd statistics for dairy cattle in the US. F. L. Guinan^{*1,2}, G. R. Wiggans², H. D. Norman², J. B. Cole³, T. M. McWhorter¹, J. W. Dürr², and D. Lourenco¹, ¹*University of Georgia, Athens, GA*, ²*Council on Dairy Cattle Breeding, Bowie, MD*, ³*URUS, Madison, WI*.