Abstracts of the
2017 American Dairy Science Association® Annual Meeting

June 25–28, 2017
Pittsburgh, PA

Breeding and Genetics II

T44   Polymorphism in the β-casein gene in Zebu dairy cattle.
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The allelic frequency of the CSN2 gene in Gyr and Guzerat pure breed animals was studied in an experiment conducted at the Rio Grande do Norte State, in Brazil, with 88 Guzerat and 68 Gyr animals of different categories. Hair samples from the cow tail tassel were collected and the DNA extraction was performed from the hair follicles, following the precipitation method with salt. Nucleotide sequence readings of the amplified fragment for the β-casein gene (A1 and A2) were aligned and edited. Allele frequencies (Xi) for β-casein alleles (1) and genotypic frequencies for the genotype (2) were obtained using the equations: $Xi = 2n_{ii} + \sum n_{ij} / 2n; x_{ij} = n_{ij} / n$, in which n_{ii} and n_{ij} correspond to the number of homozygotes and heterozygotes observed in the i allele, respectively; and n corresponds to the number of individuals analyzed. Using the Hardy-Weinberg theorem, expected genotypic frequencies at equilibrium were estimated from expanding the binomial: $(x_i + x_j) = x_i^2 + 2x_ix_j + x_j^2$, where x_i^2 is the expected frequency of homozygous for allele i; $2x_ix_j$ is the expected frequency for heterozygotes ij; and x_j^2 is the expected frequency of homozygous for allele j. It was found that Guzerat animals had a higher amount of heterozygous animals compared with Gyr of the population (Table 1). None of the evaluated animals presented homozygosity for A1. The allelic frequency of A2 allele and the genotypic frequency of A2A2 genotypes for β-casein gene in the assessed Zebu breeds indicate that these breeds may produce less allergenic milk for individuals who are sensitive to β-casein protein.

Table 1 (abstract T44). Allelic and genotypic frequencies for the A1 and A2 alleles of the CSN2 gene in Gyr and Guzerat breeds

Breed	Allelic frequency		Genotypic frequency				
	A1	A2	A1A1	A1A2	A2A2	HWE[1]	P-value[2]
Gyr	0.02	0.98	0	0.04	0.96	0.07	0.99
Guzerat	0.03	0.97	0	0.07	0.93	0.23	0.97

[1]HWE = Hardy-Weinberg equilibrium.

[2]Chi-squared test.

Key Words: allelic frequency, nucleotide sequence, Zebu breed

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T45   Bull fertility evaluations for Angus service sires bred to Holstein cows.
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The purpose of this study was to investigate the use of beef service sires bred to Holstein (HO) cows and heifers and to provide a tool for dairy producers to evaluate Angus service-sires. Many US dairy cows are now being bred to Angus sires because beef prices are high and there is a surplus of dairy heifers in many herds. Sire conception rate (SCR), a phenotypic evaluation of service-sire fertility implemented in August 2008, is based on data from the most recent 4 years, conventional-semen breedings up to 7 services, and cow parities 1 through 5. The SCR model and methodology was used in this study, with service-sire inbreeding and expected inbreeding of resulting embryo set to 0 because pedigree data were unavailable. Service-sire age was combined into 3 groups (1.8 to 4.5; 4.6 to 7.5; and >7.5 yr). A total of 97,987 breedings were available and included observations on 947 Angus service-sires and 64,061 HO cows (other beef breeds had too few records to evaluate). A mean conception rate of 30% was observed (46% standard deviation), compared with 32% for breedings with a HO cow mated to a HO sire. Publishable Angus bulls were required to have 100 total matings, 10 matings in the most recent 12 mo, and breedings in 5 or more herds. Mean SCR reliability was 56% for 95 publishable bulls, with a maximum reliability of 97% based on 8,840 breedings. Average SCR was near 0 (on an Angus base), with a range of −3.4 to 3.3. Breedings to HO heifers were also examined, which included 8,446 breedings (399 Angus service-sires and 6,570 HO heifers). A mean conception rate of 49% was observed (50% standard deviation), compared with 57% for breedings with a HO heifer mated to a HO sire. Angus sires were used more frequently for later services on problem breeders, which explains some of the difference. Mean service number was 1.77 and 2.90 for HO and Angus sires mated to HO heifers, respectively, and 2.21 and 3.41 for HO cows. Mating dairy cows to beef bulls may be profitable if the calf price is higher, fertility is better, or if practices such as sexed semen, genomic testing, and improved cow productive life allow herd owners to produce both higher quality dairy calves for replacement and beef calves for market.

Key Words: sire conception rate, beef breed

T46   Genetic and genomic analysis for oocyte number and embryo production traits in Holstein cattle using in vitro fertilization data.
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The modern reproduction technologies ovum-pickup (OPU) and in vitro fertilization (IVF), combined with genomic selection provide a rapid and sustainable route for genetic improvement in both efficiency and productivity in dairy cattle. The aim of this study was to estimate variance components and identify regions of the genome associated with traits related to oocyte number and embryo production in Holsteins. Data collected on a Holstein dairy farm in Wisconsin from 2013 to 2016 included 11346 OPU and in vitro fertilization records from 1505 unique elite females and 216 unique service bulls. Six traits were defined: number of oocytes collected (NOC), number of oocytes on drop (NOD), number of cleaved embryos (NCE), number of unfertilized oocytes (NUO), number of dead embryos (NDE) and number of transferable embryos (NTE). A univariate repeatability animal model analysis was performed for these traits. Because these are count variables following a Poisson distribution, generalized linear mixed models (GLMM) with a log link function were employed in ASREML. Of the 1505 unique females, 580 were genotyped using a variety of chips. All genotyped animals were imputed to include those markers used for official US genomic evaluations based on a large genotyped population. 58275 SNPs (after quality control) and EBVs from the GLMM models were used for genome-wide association studies by fitting all the SNPs as random effects using a linear mixed model in GCTA. NOC and NOD only depends on a donor's maternal genetic effect, whereas paternal fertility must be considered for other embryo traits. Estimates of maternal heritability were 0.158 for NOC, 0.134 for NOD, 0.162 for NUO, 0.104 for NCE, 0.175 for NDE, and 0.139 for NTE, whereas the relative