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0317 Molecular breeding values distribution in slick male and female Senepol cattle differing in musculature. C. L. González-Berrios¹, A. Rivera-Serrano¹, A. Casas-Guérmina¹, T. Sonstegard², and M. Pagán-Morales¹,
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Recently, the polymorphisms responsible for double muscling [MSTN: exon 3 11bp indel (NT821)] and slick coat phenotype (PRLR: exon 10 cytosine indel) in Senepol cattle were described. However, the genomic implications of segregating animals according to PRLR and MSTN genotypes have not been elucidated for economically relevant traits (ERTs), especially in tropically adapted beef cattle. Thus, purebred Senepol cattle (males/females) were genotyped for both indel and molecular breeding values (MBV) were obtained through a commercially available marker panel (Igenuity, Neo- gen Corp.). Three MBV categories were established: low (L), intermediate (I) and high (H) based on standard deviations of +1 (L), +2 (I) or +3 (H) from the average MBV for 12 ERTs. Statistical differences were determined using the Chi² test [sex, genotype (MSTN; PRLR) and double and triple combinations]. Genotypic proportions observed were: double muscle (DM): 6/NT821-NT821, 95/NT821-WT, and normal musculature (NM): 273/WT-WT (P < 0.0001) and slick coat (SC): 256/BB, 99/BA, and normal coat (NC): 4 = AA (P < 0.0001). Proportional differences were observed within BB for MBV-average daily gain between MSTN genotypes: NT821/WT: (11.76 H, 72.06 I, 16.18 L) and NM: (26.06 H, 53.72 I, 20.21 L) (P < 0.05). Also, within BB, differences in MBV categories distribution were: males: (20.90 H, 79.10 I, 0.00 L)/females: (33.33 H, 56.08 I, 10.58 L) and females: (16.93 H, 68.78 I, 14.29 L)males: (4.48 H, 77.61 I, 17.91 L) for average daily gain and calving ease, respectively (P < 0.05). Significant differences in MBV-tenderness were observed within females for: NT821/WT (7.46% H, 68.66% I, 23.88% L) and NM: (14.22% H, 73.04% I, 12.75% L) (P < 0.05). Moreover, females BB (n = 189) significantly differed in MBV category distribution depending on musculature for: residual feed intake [NT821/WT: (26.83 H, 68.29 I, 4.88 L)/NM: (18.92 H, 60.14 I, 20.95 L), yield grade [NT821/WT: (24.39 H, 70.73 I, 4.88 L)/NM: (14.19 H, 66.89 I, 18.92 L)], backfat thickness [NT821/WT: (57.14 H, 38.10 I, 4.76 L)/NM: (27.70 H, 50.01 I, 22.30 L)], pregnancy rate [NT821/WT: (4.88 H, 78.05 I, 17.07 L)/NM: (25.00 H, 66.22 I, 8.78 L)] and Stay-ability [NT821/WT: (9.76 H, 63.41 I, 26.83 L)/NM: (18.24 H, 70.27 I, 11.49 L)] (P < 0.05). In the present study, a higher proportion of Senepol cattle with SC and NM were observed and intermediate MBV for all ERTs were predominant, with the exception of backfat thickness (NT821/WT-BB-Females). Therefore, genomic selection in slick Senepols segregating

MSTN alleles are needed to improve their ERTs-MBV.
Key Words: slick, myostatin, Senepol

0318 PRUNE2 gene has a potential effect on residual feed intake in Nellore cattle. A. O. D. Lima¹, P. S. N. Oliveira², P. C. Tiziot², A. L. Somavilla³, W. J. S. Diniz¹, J. V. D. Silva¹, S. C. S. Andrade⁴, C. Boschiero³, A. S. M. Cesar³, M. M. Souza³, M. I. P. Rocha³, J. Afonso², C. E. Buss³, M. A. Mudadu⁵, G. B. Mourao⁶, L. L. Coutinho⁶, and L. C. A. Regitano⁷, ¹Federal University of São Carlos, São Carlos, Brazil, ²Embrapa Southeast Livestock, São Carlos, Brazil, ³Universidade Estadual Paulista “Júlio de Mesquita Filho,” Jaboticabal, Brazil, ⁴Genetics and Evolutionary Biology Department-IB, University of São Paulo, Brazil, ⁵Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, Brazil, ⁶Animal Biotechnology Laboratory-ESALQ, University of São Paulo, Piracicaba, Brazil, ⁷Federal University of São Carlos, Brazil, ⁸Embrapa Pecuária Sudeste, São Carlos, Brazil, ⁹Embrapa Southeast Livestock, São Carlos, Brazil.

Residual feed intake (RFI) can increase the profitability of producers, reduce methane emission and land allocation to livestock production. However, this trait has late and costly measurements. Identifying gene expression changes combined with polymorphisms that affect residual feed intake variation is important for identify target regulatory polymorphisms that can be used in animal breeding programs. Diverse studies performed by our research group in a Nellore population, such as genome-wide association (GWA), association weight matrix (AWM) and RNA-seq analysis of liver tissue have been pointed Prune homolog 2 (Drosophila) (PRUNE2) as a potential candidate gene influencing feed efficiency. For this reason, we select this gene for a more detailed analysis considering haplotypes consisting of SNPs presented in the Illumina Bovine HD Bead Chip. For this, we used a population consisted of 591 steers with genotypes and RFI estimates available. After quality control filtering, performed by PLINK and Bioconductor/R, we used a total of 449,203 SNPs in our haplotype analysis. Genotype phasing and missing genotype imputation were performed using BEAGLE and the LDexplorer software was used for haplotype block recognition. After adjust the RFI estimates for fixed effects of contemporary group, which included type of pen, birth place, feedlot location and age of the animal effect as covariate, the genetic effects of haplotypes in PRUNE2 gene was estimated by PLINK using a linear regression method. We identified 1 haplotype constituted of 4 SNPs: rs136298898 (C/T); rs133593644 (C/T); rs137799737 (A/C); rs132675549 (C/T), for which two out of 4 haplotype combinations had significant effect (P ≤ 0.05) on RFI. Haplotype variation (1111) (p-value
with 35.29% frequency was associated to lower RFI ($\beta = -0.0776$). On the other hand, haplotype variation (1112) ($p$-value = 0.0351) presenting 11.13% frequency was associated with high RFI ($\beta = 0.0846$). The PRUNE2 gene has a potential role in biological processes, such as oxidation-reduction, metal ion and polyphosphate catabolic. Our findings indicated that this gene influence genetic variation of RFI, it is a strong candidate gene to be incorporated in Nellore breeding programs, nevertheless more studies considering this gene should be realized to understand better its biological role on feed efficiency in beef cattle.

**Key Words:** haplotype, feed efficiency, functional gene enrichment

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**0319** A genome-wide association study for changes in dry matter intake due to temperature variation in an admixed beef cattle population. R. Ghebremwold$^1$ and M. L. Spangler$^2$, $^1$University of Nebraska, Lincoln, $^2$University of Nebraska, Lincoln.

Environmental conditions, such as changes in ambient temperature, can cause changes in animal behavior and performance. In general it is believed that as ambient temperature increases, dry matter intake (DMI) of beef cattle decreases. However, our hypothesis was that the degree to which animals adjust their daily DMI due to changes in ambient temperature is partially controlled by underlying genetic effects. Consequently, the objective of this study was to estimate the genetic component of the regression of DMI on ambient temperature using an admixed beef cattle population consisting of various crosses of Angus, Simmental, and Piedmontese ($n = 207$). Ambient temperatures were received from a local weather station and DMI was collected via Calen gates. The feeding period averaged 155 d with a range of 114 d to 189 d depending on the management group. Individual animal regressions of DMI on ambient temperature were performed using either daily high or low temperatures over the entirety of the feeding period. Daily high temperatures ($^°C$) averaged 15.07 with a range of $-17.21$ to 38.25. Daily low temperatures ($^°C$) averaged 2.37 with a range of $-28.33$ to 15.26. The corresponding intercept and regression coefficient for each animal were used as phenotypes for a genome-wide association study (GWAS). Animals were genotyped with the BovineSNP50 Beadchip. Data were analyzed using GenSel software and a Bayesian model fitting contemporary group ($n = 4$) and initial body weight (IBW) as fixed effects. A MCMC chain of 100,000 iterations was used with the first 40,000 samples discarded as burn-in. The proportion of SNPs having null effect ($\gamma$) was set to 0.995. Posterior mean heritability estimates (SD) for the analysis when daily high temperature was considered in the regression were 0.64 (0.07) and 0.46 (0.08), for the intercept and slope, respectively. Similarly, posterior mean heritability estimates (SD) for the intercept and slope when the daily low temperature was considered in the regression were 0.69 (0.06) and 0.52 (0.07), respectively. These results suggest that changes in DMI due to changes in ambient temperature are under genetic control. Admittedly the population under study is small and admixed, suggesting that the genomic heritability estimates contained herein are potentially biased upward. However, the concept of applying this same procedure in larger populations warrants further investigation as a means of identifying animals that are less sensitive to environmental extremes.

**Key Words:** beef cattle, GWAS, feed intake

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**0320** An international effort to improve feed efficiency and reduce methane emissions in dairy cows through genomics. A. M. Wilson$^1$, A. M. Butty$^1$, C. Baes$^1$, A. Cánovas$^1$, M. P. Coffey$^2$, E. E. Connor$^1$, M. De Pauw$^3$, B. Gredler$^4$, E. Goddard$^4$, G. Haile$^5$, V. R. Osborne$^1$, J. E. Pryce$^6$, M. Sargolzaei$^7$, F. S. Schenkel$^8$, R. Stothard$^9$, E. Wall$^1$, Z. Wang$^1$, T. C. Wright$^{10,11}$, and F. Miglior$^{10,12}$. 

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Increasing international demand for high quality dairy and meat products as well as greater awareness of climate change has put pressure on the livestock industry to deliver quality products while reducing its environmental impact. Enteric methane from cattle is a major contributor to greenhouse gas emissions and is a target of reduction through improving cow feed efficiency (FE) and reducing methane emissions (ME). The overall goal of this project is to produce genomic predictions for FE and ME that are ready for breeding application in the dairy cattle industry. Breeding for improved FE and less methane emitted will lower feed costs and reduce the industry’s environmental footprint. Collecting phenotypes required for genetic improvement is presently very difficult and expensive, and to date, there has been limited to no direct selection for these traits in dairy cattle breeding. Recent genomic approaches provide the opportunity to finally select for these traits, but require a large reference population with accurate phenotypes. Data of individual feed intake and ME are being