wn the hotspots. Variants within these regions were annotated with the VEP software. On chromosome 4, two novel tolerated missense iants in the Lysine (K)-Specific Methyltransferase 2E (*KMT2E*) gene were found. The gene was previously shown to be associated with natal and postnatal lethality and reduced fertility and growth. In the glutathione peroxidase 4 (*GPX4*) gene, located on the chromosome 7 tspot, we found four rare missense mutations, two of which are predicted to cause changes to the protein structure based on SIFT scores. Th ion was also previously found to be highly divergent between *Bos taurus* and *Bos indicus*. *GPX4* is deemed to protect cells against membra id peroxidation and it was also associated with early embryonic death. The chromosome 12 region is a desert gene region and therefore no ididate variants were annotated.

545: Genome Mapping, Tagging & Characterization: Cattle

arch for Causal Mutations in Meat Tenderness Candidate Genes in Nellore Cattle

mila Urbano Braz[1], Jerry Taylor[2], Tiago Bresolin[1], Rafael Espigolan[1], Daniel Gustavo Mansan Gordo[1], Fernando Baldi[1], Luc lvão de Albuquerque[1] and Henrique Nunes de Oliveira[1], (1)São Paulo State University, Jaboticabal, Brazil, (2)University of issouri, Columbia, MO

e objective of this study was to identify genes with significant effects on meat tenderness and to search for the causal mutations in Nellore tle. Phenotypic and genotypic data on 1,616 animals from two Brazilian animal breeding programs were used. All animals were genotyped th the Illumina BovineHD panel. Association analyses were performed to identify significant genes. Two haplotypes located in the *ASAP1* *PN1* genes were significant after Bonferroni correction. To find new SNPs, six regions spanning these genes were sequenced from 298 imals. Seven new SNPs were found in *CAPN1* and four in *ASAP1*. The new SNPs were imputed into the 1,318 remaining animals using AGLEv3.3.2. FastPhase and HaploView were used for haplotype reconstruction and linkage disequilibrium analyses, respectively. Statisti alyses were performed using the MIXED procedure of SAS 9.3. Statistical model included fixed effects for contemporary groups (farm, ye birth, management group, month and year of slaughter), number of alleles in each haplotype as covariable (linear effect) and sire as randon ect. For *ASAP1*, the haplotypes had no effect on tenderness. For *CAPN1*, 14 SNPs were found to be in strong linkage disequilibrium with t st significant haplotype region (exon 14 to intron 19). The SNP *rs17871051* is located in exon 14 and results in a substitution of valine for leucine. This SNP is known from other studies to influence meat tenderness and may also be a causal mutation in Nellore cattle. However, lowing Bonferroni correction, the haplotype was not found to significantly affect meat tenderness. Acknowledgements: FAPESP 013/00035-9, #2014/23013-3 and #2009/16118-5.

546: Genome Mapping, Tagging & Characterization: Cattle

entification of Genomic Regions Related to Tenderness in Nellore Beef Cattle

inos E. Carvalho[1], Fernando Baldi[2], Miguel H. A. Santana[3], Ricardo Ventura[4], Gerson A. Oliveira Junior[1], Rachel S. Bueno[1], arina N. Bonin[5], Fernanda M. Rezende[6] and José B. S. Ferraz[3], (1)University of São Paulo, Pirassununga, Brazil, (2)São Paulo ate University, Jaboticabal, Brazil, (3)University of Sao Paulo, Pirassununga, Brazil, (4)Beef Improvement Opportunities, elph, ON, Canada, (5)Embrapa Beef Cattle, Campo Grande, Brazil, (6)Federal University of Uberlandia, Uberlandia, Brazil

e aim of this study was to identify, by ssGWAS, genomic regions that potentially have association with tenderness in Nellore cattle. enotypes were obtained according to standard USDA Quality Grade (1999), from longissimus thoracis muscle between the 12th and 13th rib the right half-carcass and aged for 7 days. Data of 909 Nellore bulls were analyzed. Those animals were genotyped with Illumina Bovine adchip HD® GGPi (74K). Based on another Nellore population genotyped for Illumina beadchip BovineHD® (777K), genotypes were imp FImput software. Analyses were performed using a pedigree composed by 6,276 animals and, assuming contemporary group (farm and ughter batch) as fixed effect and age at slaughter as a covariate. Single step analyses were realized by Blupf90 program considering windo 10 markers (SNP) to estimate their effects, this procedure enables the identification of regions associated with tenderness along the omosomes. After quality control (MAF <0.05%, call rate <90%), 463,995 SNPs in autosomal chromosomes were used in the association alyses. Based on that, 18 regions in 14 different chromosomes (1, 4, 6, 7, 8, 10, 18, 19, 20, 21, 22, 25, 26 and 29), that explained more than the additive variance, were explored and some genes were identified in these regions, as AVEN, SHISA7, UBE2S, CDC42EP5, C16orf96 ORA1 and FAM119A. With ssGWAS method using high density panel was possible to identify regions related to tenderness in Nellore ca steriorly, those genes and their pathways will be investigated to evaluate their importance for meat quality traits.

547: Genome Mapping, Tagging & Characterization: Cattle

enome-Wide Association Study in Reproductive Trait of Nellore Heifers

erson A. Oliveria Junior[1], Ricardo Ventura[2], Bruno G. de Freitas[3], Miguel H. A. Santana[4], Marcos Vinicius Barbosa da Silva sé B. S. Ferraz[4] and Dorian J. Garrick[6], (1)Iowa State University, Ames, IA, (2)Beef Improvement Opportunities, Guelph, ON nada, (3)University of Sao Paulo, São Pualo, Brazil, (4)University of Sao Paulo, Pirassununga, Brazil, (5)EMBRAPA Dairy ttle – MG, Juiz de Fora, Brazil, (6)Department of Animal Science, Iowa State University, Ames, IA

nsidering the economic importance of sexual precocity in the production system of beef cattle, the project aims to use genome wide ociation study (GWAS) to find possible genomic regions that could explain the genetic variability of this trait.
e database consist of information from 1499 Nellore heifers, from four different herds in Brazil. Heifers, approximately fifteen months old re inseminated using fixed time artificial insemination with pregnancy being confirmed by ultrasound examination. They were genotyped ng GeneSeek Genomic Profiler (GGP-HDi) that features nearly 78,000 SNPs. The quality control analyses were performed by PreGSF90 ckage (MISZTAL et al., 2002) discarding SNPs with minor allele frequency < 0.02; call rate < 0.95; Hardy-Weinberg equilibrium test > 0 *nCall Score* < 0.15 and monomorphic SNPs. Individual genotype call rates lower than 0.90 were also not considered in the analysis. The WAS analyses were conducted by GenSel software (FERNANDO; GARRICK, 2013). Bayes B methodology was applied to estimate poste an proportion of variance explained by one megabase SNP windows. The proportion of no effect SNPs (π) was set at 0.997 in each round e genomic heritability was estimated at 0.09. The GWAS results appointed for one window in chromosome 5 with 22 SNPs that explained 7% of the genetic variance of the trait. This region harbors three genes (ISX, HMGXB4 and TOM1) which are involved in eight biologica ocesses that could affect sexual precocity in Nellore cattle.


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