2422V Improved, expanded, and automated ancestor discovery. D. J. Null*[1], G. R. Wiggans[2], E. O.O Ogwo[1], and P. M. VanRaden[1], [1]*USDA, Agricultural Research Service, Animal Genomics and Improvement Laboratory, Beltsville, MD,* [2]*Council on Dairy Cattle Breeding, Bowie, MD.*

Maternal grandsires (MGS) and maternal great grandsires (MGGS) can be discovered using percentages of haplotypes shared after removing paternal haplotypes in each generation. Accuracy of ancestor discovery was originally tested with 2011 data, published in 2013, and was retested here with 2021 data to account for more markers, different chips, revised imputation, faster generation intervals, and many more candidate grandsires. Accuracy was determined from a random sample of 88,995 calves whose dams, granddams (MGD), MGS, and MGGS were genotyped and already confirmed to have correct parent-progeny relationships. The genotypes and pedigrees of the dam and MGD were removed to determine how often the correct MGS and MGGS could be discovered within each breed. In all 5 breeds (Holstein, Jersey, Brown Swiss, Ayrshire, and Guernsey) about 92% of true grandsires were automatically filled correctly, about 5% of true grandsires were suggested but not filled, and <2% of the added ancestors were incorrect. Most incorrect ancestors were the dam's MGS instead of her sire or the MGD's MGS instead of her sire. Counts across all test animals were 78,492 MGS and MGGS correctly added, 7,576 in 1st place but not added, 402 incorrectly added, and 2,525 other cases. The other cases were mostly where the true grandsire was in second place or was less than 2 years older than the dam and no grandsire was automatically added. Discovery was further improved by adjusting the birth year and haplotype sharing limits to accept and add more of the first-place candidates because most were correct. This automated system has already added hundreds of thousands of MGS for known dams and will add >1.3 million more ancestors for animals with unknown dams or MGD using virtual dam IDs to connect calves to their MGS and / or MGGS. Any discovered ancestors thought to be incorrect can be set back to missing by animal owners. Full implementation is expected in 2022.

Key Words: genomics, grandsires, pedigrees

2423V Deep sequencing of Murciano-Granadina goats for variant detection and insights into potential loss-of-function variants. K. Wang*[1,2], M. G. Luigi-Sierra[1], A. Martínez[3], J. V. Delgado[3], J. F. Álvarez[3], A Noce[1], M. Wang[1], J. Jordana[4], and M. Amills[1,4], [1]*Centre de Recerca Agrigenòmica (CRAG), Campus Universitat Autònoma de Barcelona, Bellaterra, Spain,* [2]*College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, China,* [3]*Departamento de Genética, Universidad de Córdoba, Córdoba, Spain,* [4]*Departament de Ciència Animal i dels Aliments Universitat Autònoma de Barcelona, Bellaterra, Spain.*

Livestock species have accumulated deleterious mutations at high frequencies due to the processes of domestication and artificial selection. Loss-of-function mutations have not been characterized in depth in goats despite the fact that embryo lethality has probably a noticeable impact on the reproductive success and economic profitability of goat farms. In this work, we have sequenced the genomes of 15 bucks with an average coverage of 32.92x ± 1.45x. After performing variant calling following GATK (v 4.1.8.0) best practices, we have predicted the functional consequences of polymorphisms with SnpEff and Ensembl-VEP. Potential loss-of-function mutations, comprising SNPs cataloged as stop-gained, stop-lost, splice-acceptor, splice-donor, and start-lost, were filtered out with strict selection criteria and those consistently identified by both programs were taken into account. In total, 2029 potential LoF were detected out of the whole-genome sequencing results (Table 1). Functional enrichment analyses of the genes harboring LoF will be performed. Moreover, we will also analyze the segregation of LoF mutations with an expected harmful effect in the offspring of the 15 bucks, and statistical methods will be employed to determine whether any of the mutations show a depletion of individuals with homozygous genotypes for the harmful polymorphism. This research project should provide valuable information to discriminate potentially harmful mutations with abnormal transmission patterns to offspring and could be used in selection schemes to avoid the use of bucks carrying mutations with adverse effects on embryo and fetal viability.

Key Words: loss-of-function mutations, goats, variant calling

2424V Identification of goat mammary gland long noncoding RNAs and characterization of their expression in lactating and dry individuals. M. Wang*[1], M. G. Luigi-Sierra[1], A. Noce[1], A. Martínez[2], J. V. Delgado[2], J. Fernández-Álvarez[2], A. A. K. Salama[3], X. Such[3], J. Jordana[3], and M. Amills[1,3], [1]*Centre de Recerca Agrigenòmica (CRAG), Campus Universitat Autònoma de Barcelona, Bellaterra* [08193]*, Spain,* [2]*Departamento de Genética, Universidad de Córdoba, Córdoba* [14071]*, Spain,* [3]*Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra* [08193]*, Spain.*

Long noncoding (lncRNAs) modulate biological processes by regulating transcription, chromatin remodeling, and RNA splicing. Lactation involves dramatic changes in the gene expression patterns of the mammary gland in goats, but we do not know yet which lncRNAs are expressed in this tissue and their exact biological roles. In this work, we aimed to characterize caprine mammary lncRNAs in lactating and dry

Table 1 (Abstract 2423V). SNP filtering of Murciano-Granadina goats

SnpEFF		VEP		Intersection	
Mutation type	Count	Mutation type	Count	Bedtools	Vcf-compare
Stop gain	1,049	Stop gain	989	989	989
Stop lost	163	Stop lost	49	57	49
Start lost	136	Start lost	146	92	92
Splice acceptor	584	Splice acceptor	361	361	361
Splice donor	893	Splice donor	3,992	598	538
Total	2,825		5,537	2,097	2,029