1475V Current state of inbreeding, genetic diversity, and selection history in all major breeds of US dairy cattle. E. A. Lozada-Soto*[1], C. Maltecca[1], J. B. Cole[2], P. M. VanRaden[3], and F. Tiezzi[4], [1]*Department of Animal Science, North Carolina State University, Raleigh, NC,* [2]*URUS Group LP, Madison, WI,* [3]*Animal Genomics and Improvement Laboratory, Henry A. Wallace Beltsville Agricultural Research Service, USDA, Beltsville, MD,* [4]*Department of Agriculture, Food, Environment and Forestry (DAGRI), University of Florence, Florence, Italy.*

This study aimed to characterize autozygosity, assess the current state of pedigree and genomic inbreeding, and identify trends in genetic diversity in 5 breeds of US dairy cattle. Pedigree information and imputed genotypes for 76,389 autosomal markers were obtained for 4,173,679 animals of the Ayrshire (AY), Brown Swiss (BS), Guernsey (GU), Holstein (HO), and Jersey (JE) breeds. Inbreeding was calculated using pedigree information (F_{PED}), genomic information via a marker-based approach (F_{GRM}), and genomic information using runs of homozygosity (F_{ROH}). The average pedigree inbreeding ranged from 0.06 (AY, BS) to 0.08 (JE), F_{GRM} ranged from 0.22 (HO) to 0.29 (GU, JE), and F_{ROH} ranged from 0.11 (AY) to 0.17 (JE). In addition, we assessed genetic diversity for sires and dams born before genomic selection (P1; 2000–2009), during the implementation of genomic selection (P2; 2010–2014), or after the widespread adoption of GS (P3; 2015–2018). The rate of yearly inbreeding accumulation (ΔF_{year}) and effective population size (N_e) were calculated in each period. For AY, BS, and GU, no clear trends in ΔF_{year} and N_e were observed between periods. For HO and JE sires and dams, we observed a significant increase in inbreeding rate after genomic selection, resulting in effective population sizes that ranged from 14 to 29 for HO sires, from 20 to 55 for HO dams, from 35 to 74 for JE sires, and from 102 to 276 for JE dams. We performed QTL enrichment of genomic regions with high autozygosity. We found high homozygosity on or near QTLs for milk, production, and health in all 5 breeds, for conformation traits in 3 breeds (except HO and GU), for meat and carcass in 3 breeds (except BS and HO), and for reproduction in all breeds except GU. This serves as evidence of direct selection or a correlated response for these traits. We show how recent selection strategies have contributed to the observed levels of autozygosity, rate of inbreeding accumulation, and genetic diversity in the major US dairy populations.

Key Words: dairy cattle, inbreeding, genetic diversity

1476V FoxO1 controls lipolysis via directly binding to adipose triglyceride lipase promoter in dairy goat mammary epithelial cells. Q. He* and J. Luo, *Northwest A&F University, Yangling, Shaanxi, China.*

Goat milk is rich in short- and medium-chain fatty acids and unsaturated fatty acids. Exploring the transcriptional regulating mechanism of fatty acid metabolism in goat mammary gland is of paramount scientific significance to understand the genesis of goat milk flavor formation and milk composition manipulation. Adipose triglyceride lipase (ATGL) is the key enzyme for catalyzing the initial step in adipose triglyceride lipolysis to release fatty acids (FAs) and diacylglycerol (DG). In the liver of mammals, FoxO1 promotes the expression of ATGL to increase the degradation of fatty acids, the mechanism underlying of *ATGL* regulation in goat mammary epithelial cells (GMECs) remains unclear. To explore the regulatory mechanism of ATGL on lipolysis, *ATGL* 5′flanking region were cloned and sequenced. Also, FoxO1 overexpression adenovirus and small interference RNA targeting FoxO1 were designed. Results showed that the mRNA expression of *ATGL* and *ATGL* promoter activity were significantly downregulated after knockdown of FoxO1. Consistently, content of triglycerides was significantly decreased in *FoxO1* overexpression cells. To further confirm the effect of FoxO1 on ATGL promoter activity, cells were transfected with 5 promoter fragments of various lengths. We found that core region of the ATGL promoter was located between −882 bp and −524 bp and there were 2 FoxO1 binding sites (FKH1 and FKH2) in the core region. Moreover, the results of double luciferase activity experiment indicate that overexpression of FoxO1 markedly increased *ATGL* promoter activities after transfected with −882 bp/+216 constructs. In addition, single mutation of FKH element could significantly downregulate the activity of ATGL promoter and weaken the activation of FoxO1 on *ATGL* promoter. Chromatin immunoprecipitation experiments showed that FoxO1 could directly bind to the FKH element of the *ATGL* promoter in vivo, and had a higher affinity for FKH2 than FKH1. In conclusion, our study revealed the regulatory role of FoxO1 on the lipolysis through modulating *ATGL* activities in GMECs.To elucidate the transcriptional regulation mechanism of fatty acid metabolism in mammary gland of dairy goats, and provide a novel target for studies on mechanism of goat milk fatty acid composition manipulation and improving the goat milk quality.

Key Words: FoxO1, ATGL promoter, GMECs