874 Understanding the signaling pathways that regulate muscle mass in horses throughout the lifespan. K. L. Urschel*[1], A. L. Wagner[1], L. M. Mastro[1], C. M. M. Loos[1], A. A. Adams[2], and K.M. Brennan[3], *[1]Department of Animal and Food Sciences, University of Kentucky, Lexington, KY, [2]Department of Veterinary Science, University of Kentucky, Lexington, KY, [3]Alltech Inc., Nicholasville, KY.*

Skeletal muscle makes up ~50% of body weight in horses, with protein being the largest nonwater component. Muscle mass is largely determined by the balance of rates of muscle protein synthesis and breakdown. In an athletic species such as the horse, where muscle mass has been associated with performance, there is a need to understand how the underlying signaling pathways are regulated. In horses, similar to other species, activation of the downstream factors (4E-BP1, rpS6, S6K1) in the mechanistic target of rapamycin (mTOR) signaling pathway regulating protein synthesis is increased following feeding and insulin administration. The activation in response to feeding decreases with age in growing horses, with the muscle of yearlings being more responsive to feeding than that of 2 year olds. When horses are in an unfed state, there is no effect of age on the activation of mTOR signaling factors, either during growth or when comparing mature to old (> 20 yr old) horses. When comparing 2 populations of old horses: those that are relatively healthy and those with pituitary pars intermedia dysfunction, a condition that has been associated with a loss of muscle mass and insulin resistance, there were no differences between groups in the muscle activation or abundance of any of the mTOR signaling factors, myostatin (a factor related to muscle loss), or factors associated with the protein degradation signaling pathways (FoxO, atrogin-1, MuRF1), in response to either feeding or insulin infusion. Changes that occur in the muscle signaling pathways of old horses is an area where additional research is needed. In a dexamethasone-induced model of insulin resistance, where glucose uptake in response to insulin infusion was decreased by ~75%, there were profound decreases in the activation of mTOR signaling factors. These findings indicate that, in addition to being a risk factor for the development of laminitis and equine metabolic syndrome, insulin resistance may also impair the ability of the horse to maintain muscle mass, although additional research in other equine models of insulin resistance is needed. Understanding the factors that regulate the signaling pathways of muscle protein synthesis and breakdown will allow the development of management and feeding strategies to promote muscle mass accretion and maintenance throughout the lifespan.

875 The unexplored part of the rumen microbiome: Exploring the adaptive roles of bacteriophage auxiliary metabolism genes during dietary intervention in the rumen. Christopher L. Anderson[1,2], Galen Erickson[1], and Samodha C. Fernando*[1], *[1]Department of Animal Science, University of Nebraska-Lincoln, Lincoln, NE, [2]School of Biological Science, University of Nebraska-Lincoln, Lincoln, NE.*

Viruses are the most abundant biological entity, yet the roles of viruses within ecosystems are poorly understood. Work from other environments demonstrates that bacteriophage populations contain auxiliary metabolism genes thought to increase host fitness by altering host metabolism. As an attempt to better understand the viral influence on host bacterial populations, we investigated viral and total microbial community structure and function using culture-independent metagenomic approaches under 4 different dietary conditions. Using a shared read approach based on median k-mer profiling, the structure of total microbial communities significantly differed based on diet and host, whereas enriched viral metagenomes differed only by diet. The majority of differences between viral populations from different diets were metabolic in nature. Using community level metabolic networks, we further explored why different diets enrich phage communities for specific metabolic pathways. Enzymes differentially abundant in the total metagenome and virome had significantly higher betweenness centrality and a lower average shortest path length compared with nondifferential genes in the network. In addition, differential viral genes had a significantly higher total degree and in-degree compared with nondifferential genes. This ongoing work begins to suggest that diet, rather than host factors, has a stronger influence on the structuring of rumen phage populations and that phages encode for an adaptive repository of central metabolic functions related to selection pressures driven by altering environmental conditions. Current efforts are focused on better understanding what governs why certain central metabolic genes are enriched and how this is related to the flow of information through metabolic networks.