Se)] and nutritional level [control (C) or restricted (R); fed to meet 100% or 60% of NRC recommendations] fed at different times of gestation [Mid (d 50 to 90) or Late (d 90 to 130)]. Blood samples were taken from ewes and fetuses on d 130 of gestation. Amino acids were analyzed in plasma samples, and glucose, NEFA and BUN were analyzed in serum samples. A Se × Late interaction showed the fetal:maternal ratio of glutamate was greater (P = 0.03) in HSe-C compared to ASe-C and HSe-R (2.39 vs. 1.49 and 1.74 ± 0.32) with ASe-R ewes being intermediate. A Se × Late interaction indicated a greater (P = 0.03) fetal:maternal ratio of glutamine in ASe-R compared to ASe-C and HSe-C ewes (2.71 vs. 1.31 and 1.88 ± 0.33). The Late-R group exhibited greater (P = 0.02) serine fetal:maternal ratio compared to Late-CON ewes (9.94 vs. 6.43 ± 1.07). There was a Se x Late interaction on glycine, with ASe-R having a greater (P = 0.03) fetal:maternal ratio compared to all other ewes (1356.61 vs. 1027.64, 1159.92, and 1192.66 ± 74.56 for ASe-C, HSe-C, and HSe-R, respectively). The Late-R ewes had a lower (P = 0.01) NEFA fetal:maternal ratio compared to the Late-C ewes (0.12 vs. 0.19 ± 0.02). The BUN fetal:maternal ratio was lower (P = 0.01) in the HSe compared to the ASe ewes (1.04 vs. 1.19 ± 0.04). The fetal:maternal glucose ratio did not differ (P = 0.14). These data indicate the fetal to maternal concentration gradient of metabolically versatile amino acids, NEFA, and BUN are affected by Se and nutritional level during late gestation, indicating a role for maternal diet impacting placental function.

Key Words: sheep, fetus, maternal nutrition

82 Use of microarray to determine genes differentially expressed in muscle and subcutaneous fat of heifers never treated or considered chronically morbid after a 63-d preconditioning program. J. Johnson*, D. R. Stein, L. O. Burciaga-Robles, B. P. Holland, D. L. Step, U. DeSilva, and C. R. Krehbiel, *Oklahoma State University, Stillwater*.

The objective was to determine gene expression changes in growing heifers due to bovine respiratory disease (BRD) using microarray analysis. Tissue biopsy samples from the LM and s.c. fat (SCF) between the 12th and 13th rib from heifers never treated against BRD (HEALTHY; n = 5) and heifers classified as chronically morbid (CHRONIC; n = 5) were collected after a 63 d preconditioning program. CHRONIC was defined as animals receiving at least three antimicrobial treatments had a loss of BW during the previous 21 d on feed. Hybridizations utilizing a long oligo bovine array were performed. Preprocessing and normalization of data was accomplished using the R-project statistical environment with the Bioconductor and LIMMA packages through the GenePix AutoProcessor (GPAP 3.2). Significance level for differentially expressed genes was set at $P < 0.01$ with a twofold change or greater. Ontology analysis of the differentially expressed genes was carried out using GFINDer with emphasis on biological process and molecular function. To further elucidate the interaction(s) of annotated genes within the context of metabolic or signaling pathways, Ingenuity Pathways Analysis was utilized to identify the most relevant biological mechanisms, pathways and functions of the differentially expressed genes. Of the 186 differentially expressed genes in LM (143 down- and 43 up-regulated) and the 121 differentially expressed genes in SCF (44 down- and 77 up-regulated); 87 and 50, respectively, had known ontology. Differentially expressed genes were mapped to pathways involved in immunological functions, metabolism, catalytic activities, binding, proteolysis, apoptosis, translation, transcription, growth, and transport of nutrients. These differences in gene expression across tissues and between treatment groups will provide a better understanding of the impact BRD has on immune response and animal growth.

Key Words: animal growth, bovine respiratory disease, microarray

83 Efficacy of varying phytase levels and development of a P release curve. C. K. Jones*[1], M. D. Tokach[1], B. W. Ratliff[2], N. L. Horn[3], S. S. Dritz[1], R. D. Goodband[1], J. M. DeRouchey[1], and J. L. Nelssen[1], [1]*Kansas State University, Manhattan,* [2]*Enzyvia, LLC, Sheridan, IN,* [3]*JBS United, Inc., Sheridan, IN*.

Two experiments used 184 pigs (PIC, 10.3 and 9.7 kg BW, respectively) to develop an available P (aP)release curve for commercial phytase products. In Exp. 1 and 2, pigs were fed a basal diet (0.06% aP) and two levels of added aP from inorganic P to develop a standard curve. In Exp. 1, 100, 175, 250, or 500 FTU/kg OptiPhos; or 200, 350, 500 or 1000 FTU/kg Phyzyme XP were added to the basal diet. In Exp. 2, 250, 500, 750, or 1000 FTU/kg OptiPhos; 500, 1000, or 1500 FTU/kg Phyzyme XP; or 1850 or 3700 FYT/kg Ronozyme P were added to the basal diet. Manufacturer guaranteed phytase levels were used in diet formulation. Diets were analyzed for phytase using both the Phytex and AOAC methods. Pigs were blocked by sex and weight and allotted to individual pens with 8 pens per treatment. Pigs were euthanized on d 21 and fibulas were analyzed for bone ash. In Exp. 1 and 2, pigs fed increasing inorganic P had improved (lin, $P \leq 0.01$) G:F, and percentage ash. Pigs fed increasing Optiphos had improved (Exp 1: lin, $P < 0.001$; Exp2: quad, $P \leq 0.01$) percentage ash. Pigs fed increasing Phyzyme XP had improved (lin, $P < 0.001$) percentage ash. In Exp. 2, increasing Ronozyme P improved (quad, $P \leq 0.03$) percentage ash. Using AOAC analyzed values and bone ash as the response variable, aP release for up to 1000 FTU/kg of *E. coli*-derived phytases (Optiphos and Phyzyme) can be predicted by the equation (y = -0.000000125x2 + 0.000236245x + 0.015482000) where x is the phytase level in the diet.

Table 1.

	Exp. 1			Exp. 2		
	Trt	AOAC, FTU/kg	Ash, %	Trt	AOAC, FTU/kg	Ash, %
Added aP, %	0		35.6	0		34.2
′	0.075		39.4	0.07		39.6
′	0.15		41.8	0.14		41.2
OptiPhos, FTU/kg	100	345	36.2	250	674	41.6
′	175	560	38.2	500	1227	41.9
′	250	729	38.6	750	1849	42.7
′	500	1509	41.1	1000	2479	43.6
Phyzyme, FTU/kg	200	214	37.0	500	369	37.1
′	350	407	39.0	1000	708	41.9
′	500	429	37.9	1500	1091	42.0
′	1000	1038	40.0	1850	1694	41.1
				3700	3778	42.3

Key Words: growth, nursery pig, phytase

84 Effects of elevated levels of distiller's grains on performance and carcass characteristics in steers fed up to 70% distillers. S. W. Reader*[1], R. L. Atkinson[1], P. M. Walker[2], J. M. Carmack[2], and B. R. Wiegand[3], [1]*Southern Illinois University, Carbondale,* [2]*Illinois State University, Normal,* [3]*University of Missouri, Columbia*.

The objective of this study was to determine effects of 70% (DM) inclusion of dried distillers grain with soluble (**DDGS**) on performance and carcass characteristics. Additionally, isocaloric and isonitrogenous diets versus 40 % (DM) DDGS were compared to determine effects of equivalent nutrient versus by-product. Ninety-six Angus steers (292 ± 35.83 kg) were used in a completely randomized design, stratified by body weight