439 **Influence of forage inclusion level on growth performance and feeding behavior in finishing steers.** M. C. Ruch*, T. C. Gilbery, S. R. Underdahl, M. L. Bauer, K. C. Swanson, *North Dakota State University, Fargo.*

Forty-four steers (452 ± 4.6 kg) predominately of Angus and Simmental origin were used in a randomized block design to determine the effects of forage inclusion level on growth performance and feeding behavior in finishing steers. Steers were fed dry-rolled corn based diets which included a mixture of hay and corn silage as the forage source. Dietary treatments were 5%, 10%, 15%, or 20% forage. Diets were fed for 84 days. Feed intakes and feeding behavior were measured using the Insentec system. A visit was defined as each time the Insentec system detected a steer at a bunk. A meal was defined as eating periods which may include short breaks separated by intervals not longer than 7 min. Animals were weighed the first 2 days, then every 28 days after, and finally the last two days of the study. Steers were slaughtered with an average weight of 625 kg. There was a linear decrease ($P \leq 0.02$) in DMI intake, ADG, and G:F as forage inclusion increased. Number of visits and meals per day and eating time per visit, per meal, and per day were not affected by forage inclusion. Feed DMI per visit did not differ between treatments but eating rate per meal decreased linearly ($P < 0.001$) with increasing forage inclusion. Eating rate (g/min) responded quadratically ($P = 0.04$) with the greatest eating rate observed in the 10% forage treatment. Hot carcass weight and dressing % decreased ($P = 0.02$) linearly as forage inclusion increased. These results indicate that a decrease in forage inclusion in a finishing diet will increase DMI, ADG, and G:F as well as increase DMI per meal.

Key Words: behavior, finishing steers, forage, growth

440 **Evaluation of further processing methods for soybean meal in diets for nursery pigs.** A. M. Jeffrey*, H. L. Frobose, M. D. Tokach, R. D. Goodband, S. S. Dritz, J. C. Woodworth, J. M. DeRouchey, *Kansas State University, Manhattan.*

A total of 296 mixed sex pigs (PIC 327 × 1,050; 6.5 ± 1.4 kg BW and 21 d of age) were used in a 31-d experiment evaluating the effect of further processing methods for soybean meal on nursery pig growth performance. There were 11 replicate pens per treatment with 6 or 7 pigs per pen. At weaning, pigs were allotted to pens by initial weight to 1 of 4 treatments in a completely randomized design. A 3-phase diet series was used with experimental diets fed during phase 1 (d 0 to 7) and phase 2 (d 7 to 20), and a common diet fed during phase 3 (d 20 to 30). Experimental treatments were: 1) Negative control (NC: 38.5% SBM and 25% dried whey), 2) Fermented soybean meal processing method 1 (FSBM1; Nutraferma, Sioux City, IA), 3) Fermented soybean meal processing method 2 (FSBM2; Nutraferma, Sioux City, IA), and 4) Enzymatically treated soybean meal (ETS; Hamlet Protein, Findlay, OH). Diet formulation was based on a common SID Lys level (1.35%). Diets 2, 3 and 4 contained 28.5% SBM and 25% dried whey and specialty soybean meal sources were added at 5% in both phase 1 and 2. Feed was pelleted in phases 1 and 2, while the phase 3 common diet was fed in meal form. From d 0 to 7, pigs fed FSBM2 had increased ($P < 0.05$) ADG and d 7 BW compared to pigs fed ETS, and increased G:F ($P < 0.05$) compared to all treatments. No other differences ($P > 0.10$) were observed for growth or pig BW during phase 2, phase 3 or for the overall experiment. In summary, further processed soybean meal sources did not improve nursery pig growth compared to traditional soybean meal.

Key Words: fermented soybean meal, nursery pig, protein sources

Table 440.

	NC	FSBM1	FBSM2	ETS	SEM	*P* <
d 0 to 7						
ADG, g	76[ab]	74[ab]	96[b]	64[a]	11.7	0.07
ADFI, g	172	162	162	141	16.5	0.32
G:F	0.415[a]	0.457[a]	0.604[b]	0.445[a]	0.050	0.03
d 0 to 31						
ADG, g	360	351	362	358	12.4	0.81
ADFI, g	541	526	530	525	16.7	0.76
G:F	0.664	0.665	0.680	0.678	0.013	0.46

Table 441.

	NC	Plasma A	Plasma B	Nutri-Gold	SEM	*P* <
d 0 to 10						
ADG, g	82[a]	129[c]	125[c]	102[b]	5.0	0.001
ADFI, g	124[a]	156[c]	141[b]	123[a]	3.0	0.001
G:F	0.660[b]	0.832[a]	0.885[a]	0.821[a]	0.029	0.001
d 0 to 24						
ADG, g	234[a]	252[b]	257[bc]	242[ab]	4.7	0.01
ADFI, g	299[a]	324[b]	321[b]	304[a]	5.7	0.01
G:F	0.785	0.778	0.802	0.798	0.009	0.19

[a,b,c] Means without a common superscript differ $P < 0.05$.

441 **Evaluation of bovine plasma source and whole dried milk in nursery pig diets on growth performance.** C. D. Evans*[1], H. L. Frobose[1], D. W. Dean[2], M. D. Tokach[1], R. D. Goodband[1], S. S. Dritz[1], J. C. Woodworth[1], J. M. DeRouchey[1], *[1]Kansas State University, Manhattan, [2]International Ingredient Corp, Fenton, MO.*

A total of 360 barrows and gilts (PIC 359 × C29; initially 6.2 ± 1.4 kg BW and 19 d of age) were used in a 24-d experiment evaluating different specialty ingredients on nursery pig growth performance. This experiment was conducted in a commercial environment (Cooperative Research Farm Nursery; Sycamore, OH). At weaning, pigs were allotted to pens by initial BW to 1 of 4 treatments in a completely randomized design. There were 9 replicate pens per treatment with 10 pigs per pen. Experimental diets were fed from d 0 to 10 with a

Table 442.

Variable	Treatments					Contrasts			
	16%CP	14.9%CP +EAA	14.9%CP	13.5%CP +EAA	13.5%CP	16 vs 14.9	16 vs 13.5	14.9 vs 14.9 + EAA	13.5 vs 13.5+ EAA
Leucine									
Artery, uM	122.92	104.39	109.74	119.64	107.98	0.0613	0.0432	NS	0.1150
Fractional removal[1], %	35.36	41.91	38.05	44.59	40.67	NS	0.2031	NS	NS
Mammary uptake:milk output	1.14	1.11	1.11	1.21	1.15	NS	NS	NS	NS
Methionine									
Artery, uM	25.92	37.94	23.11	49.08	23.98	NS	NS	0.0003	<0.0001
Fractional removal, %	43.38	27.32	43.32	24.24	40.43	NS	NS	0.0011	0.0014
Mammary uptake:milk output	1.14	1.01	1.01	0.97	0.96	0.0657	0.0171	NS	NS

[1]Fractional removal = arterio-venous difference/arterial concentration

common diet fed from d 10 to 24. Experimental diets were: 1) Negative control (NC; 5% fish meal), 2) NC + 5% bovine plasma A (AP920,APC Inc.; Ankeny, IA), 3) NC + 5% bovine plasma B (Promax; Protena, Nicauragua), and 4) NC + 5% dried whole milk (NutriGold; International Ingredients Corporation Inc., St. Louis, MO). All diets were balanced on SID Lys and lactose and were fed in pellet form. From d 0 to 10, pigs fed Plasma A and Plasma B had greater ($P < 0.01$) ADG and ADFI than pigs fed the NC or NutriGold diets. Pigs fed Nutrigold also had increased ($P < 0.01$) ADG relative to pigs fed the NC diet. Also, G:F was greater ($P < 0.001$) for plasma and NutriGold containing diets compared to the NC. During the common period (d 10 to 24), there were no differences for ADG or ADFI, but pigs previously fed NC had greater (0.810 vs. 0.765; $P < 0.01$) G:F compared to those previously fed Plasma A. Overall (d 0 to 24), pigs fed Plasma A and B had greater ($P < 0.02$) ADG and ADFI than NC pigs. Furthermore, pigs fed Plasma B had increased ($P < 0.04$) ADG relative to pigs fed Nutrigold. In summary, both plasma sources increased intake and growth with no differences between sources. NutriGold also improved performance compared to the NC.

Key Words: animal plasma, milk products, nursery pig

442 **Effect of amount and profile of amino acid supply on mammary amino acid metabolism.** B. M. Dado*[1], M. A. C. Danes[1], G. A. Broderick[2], M. A. Wattiaux[1], [1]*University of Wisconsin, Madison,* [2]*Broderick Nutrition & Research, LLC, Madison ,WI.*

Amino acids function not only as protein building blocks but also as signaling molecules that affect milk protein synthesis and mammary metabolism. In an attempt to expose the mammary gland to different amounts and profile of AA in the arterial blood, ten Holstein cows were blocked by DIM into two 5x5 Latin squares and fed 5 treatments: (1) positive control (16% CP), formulated to meet metabolizable protein requirements; 14.9% CP with (2) or without (3) EAA infusion; or 13.5% CP diet with (4) or without (5) EAA infusion. The AA solutions were prepared according to AminoCow to provide all limiting EAA in each diet and were infused continuously into the abomasum. On the last day of each 14-d period, blood samples were taken from the coccygeal vessel and the mammary vein simultaneously, at four time-points equally spaced between two milkings. Plasma samples were analyzed for AA by GC-MS. Data was analyzed using Proc Mixed, significance was declared at $P < 0.10$ and trend at $P < 0.20$. Contrasts and LS-means are reported in Table 442. All AA are analyzed and responded differently to the treatments. Methionine and Lysine are presented as examples of the two groups of AA according to their post-absorptive metabolism. The changes in AA arterial concentrations were smaller than we attempted to achieve. Nonetheless, some effects were observed. Decreasing dietary CP decreased leucine arterial concentration but fractional removal was numerically increased relative to the positive control, indicating that the mammary uptake process might not be driven by mass action alone. For methionine, fractional removal decreased with AA infusions, even though methionine arterial concentrations were increased. Mammary uptake to milk output ratio was affected by CP levels for methionine, suggesting responses within the mammary gland.

Key Words: amino acid, mammary gland

443 **Novel cecum cannulated pig model to investigate the human microbiota through inter species transfer of gut microbiota from humans to pigs.** M. E. Kaiser*, C. L. Anderson, N. D. Aluthge, T. E. Burkey, P. S. Miller, D. E. Hostetler, S. C. Fernando, *University of Nebraska, Lincoln.*

Recent studies of the human microbiome have helped understand how changes in the microbial community affects human health and physiology, yet they fail to identify the mechanisms and signals underlying how the microbiota impacts human physiology and health. This is mainly because of the lack of a good animal model to investigate the human microbiome over time. The main goal of this research project was to develop a new cecum-cannulated humanized pig model through fecal transplants from humans to pigs to identify the signals of the microbiome that affects the obese phenotype. To this end, we derived 15 germ-free pigs and performed inter- intra-