Abstract: A total of 1,789 pigs (PIC; 337×1050; initial BW 108.9 ± 1.14 kg) were used to determine the effects of increasing L-Lys-HCl and AA ratios on performance of late finishing pigs fed corn-soybean meal diets without DDGS. The study used 2 groups of pigs and each study lasted 18 and 27 d, respectively. Pigs were housed in mixed gender pens with 20 to 25 pigs/pen and 19 replications/treatment (10 and 9 replications/group, respectively). Pens of pigs were blocked by BW and randomly allotted to 1 of 4 dietary treatments. Treatment diets were formulated to 0.70% digestible Lys and consisted of low, medium, or high levels of feed-grade AA and moderate or high AA ratios relative to Lys. Low, medium and high feed-grade AA treatments had increased L-Lys-HCl (0.15, 0.30 and 0.39%) replacing soybean meal to achieve CP levels of 13.6, 12.0, and 11.0. Minimum AA:Lys ratios were 53% Ile, 128% Leu, 58% Met&Cys, 66% Thr, 18.5% Trp, 68% Val, and 34% His in Moderate AA ratio diets and 60% Ile, 128% Leu, 60% Met&Cys, 70% Thr, 21.2% Trp, 72% Val, and 33% His for the high AA ratio treatment. Overall, there was a marginally significant increase in ADFI (quadratic, \( P = 0.097 \)) observed in pigs fed medium feed-grade AA and moderate AA ratios. Treatment diets had no effect on ADG or G:F. At the end of group 2, carcass data was collected with no differences (\( P > 0.10 \)) observed for HCW, carcass yield, backfat depth, loin depth or percentage lean. In summary, differing levels of feed-grade AA and AA ratios used in this study did not impact growth performance or carcass characteristics of late finishing pigs with the exception of a marginally significant increase in ADFI.

### Keywords
- amino acids, finishing pig, growth
Abstract: The objective of this study was to investigate the fecal microbiota of weaned pigs when supplemented with different botanical blends while being experimentally infected with a pathogenic E. coli. A total of 60 weaned pigs (7.17 ± 0.97 kg) were individually housed and randomly assigned to 1 of the 5 treatments (12 pigs/treatment): sham control (CON-), challenged control (CON+), challenged botanical blend 1 with 100 ppm (BB1_100), challenged BB2 with 50 ppm (BB2_50), and challenged BB2 with 100 ppm (BB2_100). Both botanical blends were composed of capsicum oleoresin but different garlic extract varieties. The experiment lasted for 28 d including a 7-d habituation period followed by an E. coli oral inoculation of $10^8$ CFU/dose for 3 consecutive days. Fecal samples were collected on d -7, 0, 5 and 21 post inoculation (PI) to perform 16S rRNA sequencing at the V4 hypervariable region. Downstream analysis was performed using QIIME2 (v. 2020.8) and R. No difference was observed among treatments throughout the experiment in alpha diversity. Bray-Curtis PCoA displayed pronounced clusters by days but also displayed overlaps when looking into day and treatment interaction. *Firmicutes* was more abundant (P < 0.05) in the botanical treatments while *Bacteroidetes* and *Proteobacteria* were more abundant (P < 0.05) in BB1_100 and BB2_50 than in CON- on d 5 PI. *Firmicutes* was less abundant (P < 0.05) in BB2_50 and *Proteobacteria* was more abundant (P < 0.05) in BB1_100 than in CON+ on d 21 PI. *Lachnospiraceae* was less abundant (P < 0.05) in BB2_50 than in CON- on d 5 PI and less abundant (P < 0.05) in BB1_100 than in CON- on d 21. In conclusion, the botanical treatments have modified the fecal microbiota of weaned pigs challenged with an enteropathogenic E. coli.

**Keywords:** botanical blends, fecal microbiota, weaned pigs