Table 1
Distribution of particle size in feed and feces expressed on % DM basis

Feed PS (mm)	Diet				*P*-value
	HA	HO	HOP	HP	
>19.0	82	33	33	33	
8.1–19.0	9	4	4	4	
4.1–8.0	5	46	24	2	
1.18–4.0	4	12	7	1	
<1.18	1	5	33	60	
Fecal PS (mm)					
4.8	22 ± 3^a	30 ± 4^b	27 ± 2^b	10 ± 4^c	<0.001
2.4	10 ± 3^{ab}	9 ± 2^b	7 ± 2^a	8 ± 1^{ab}	<0.05
1.6	14 ± 3^a	11 ± 2^{ab}	10 ± 1^b	13 ± 3^a	<0.05
Cheesecloth[1]	23 ± 2^a	18 ± 3^b	20 ± 2^b	31 ± 4^c	<0.001
Remainder[2]	32 ± 6^a	32 ± 5^a	38 ± 5^a	39 ± 7^a	<0.05

[1] Cheesecloth was folded 4 times.
[2] Calculated % of DM that was not caught on any of the layers.

gastrointestinal disease. It was hypothesized that diets with decreasing DPS would result in decreased fecal particle size (FPS) and fecal pH. Eight geldings (528 ± 54 kg BW) ranging from 3 to 15 yr were used in a Latin Square design. Four dietary treatments fed at 2% BW were 100% hay (HA), 40% hay and 55% whole oats (HO), 40% hay, 27.5% whole oats, and 27.5% pellets (HOP), and 40% hay and 55% pellets (HP). Differences in DPS are clarified by the % feed particles <1.18 mm in the HA, HO, HOP, and HP diets (1, 5, 33, and 60%; respectively). Pellets were formulated to have similar nutrient makeup to whole oats. To meet nutrient requirements, HO, HP, and HOP diets had a balancer pellet added at 5%, that was unneeded for HA diet. Treatments were divided into 4 14 d periods; each proceeded by a 14 d hay only washout period. The DPS profiles of feed were obtained using the Penn State Particle Separator and feed company data. These values were used to calculate DPS distribution of the 4 diets (Table 1). Fresh fecal samples were collected from the stall on d 10 during treatment periods and pH was analyzed. Remaining feces were frozen at −20°C until FPS was measured by a modified Nasco Digestion Analyzer sieving method (Table 1). A mixed ANOVA was used to investigate differences due to fixed effects of diet and period. Differences were defined at $P < 0.05$. There was an overall effect of diet on fecal pH and fecal pH was different between each diet group (HA 6.7 ± 0.3, HO 6.3 ± 0.1, HOP 6.0 ± 0.1, and HP 5.8 ± 0.1). The range of pH may be due to different availability of dietary NSC across diets. The horses fed whole oats had the largest % of 4.8 mm (largest diameter sieve) fecal particles, a characteristic that may be due to the indigestible oat hulls. This study reports feasible methods to quantify FPS and DPS and results indicate that certain characteristics of whole oats may increase hindgut pH.

Key Words: pH, Oats, particle size

125
Equine microbiome project: Understanding differences in the horse gut microbiome related to diet

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In the hindgut of a horse, changes in the bacteria levels through dietary disruption, seasonal changes, stress, or age can lead to colic and laminitis, causing lameness or even death in severe cases. In this study, we profiled bacterial communities from fecal samples collected and submitted by horse-owners participating in the Equine Microbiome Project (EMP) and correlated differences in community structure with feed type, specifically horses eating exclusively hay, pasture, a hay-concentrate mix, or a combination of pasture, hay, and concentrate as reported in EMP metadata surveys. Feed categories were based on reported diet, and no surveys reported feeding a hay and pasture diet, thus the absence of a hay/pasture group. To participate in the EMP, horse owners submitted a fresh fecal sample collected in a provided kit according to standard instructions, and were required to complete an informational survey including horse diet, past medical history, and other metadata. Genomic DNA from fecal samples from 184 horses were analyzed using the 16S rRNA gene. Sequences were clustered against the Greengenes database, and β diversity was calculated using weighted UniFrac metric in QIIME. Significant differences in bacterial community structure of pasture fed horses were found using PERMDISP (999 permutations, *P*-value <0.05). Spearman rank correlation (999 permutations, *P*-value <0.05) identified *Christensenellaceae*, *Oscillospira*, and *Prevotella* taxa to be more highly abundant in only pasture whereas RFN20, *Streptococcus*, and *Lactobacillus* taxa were differentially represented in hay/concentrate. These results point to functional differences in these communities that could lead to understanding how diet affects normal microbiome structure and hypotheses regarding functional differences leading to equine digestive disorders such as colic, laminitis, and equine metabolic syndrome.

Key Words: diet, microbiome, multivariate analysis

126
Morphometric comparisons of draft, pony, and horse breeds

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Estimating body fatness is an important measurement tool; however, some measurements are subjective and even repeated trainings fail to increase accuracy. Objective measurements, including equations based off morphometric measurements, may provide a better estimate. Ponies (n = 30), horses (n = 32), and draft horses (n = 27) were evaluated for neck length (NL), neck circumference (NC), heart girth (HG), belly girth (BG), wither height (WH), body length (BL), and body condition score (BCS). Calculations included the ratio of NC to NL (NCNL), BG to HG (BGHG), BG to WH (BGWH), and BG to BL (BGBL) and body condition index (BCI). Breed types differed by BCS, with draft horses (6.0 ± 0.2) averaging higher ($P < 0.001$) scores than horses (5.2 ± 0.2) or ponies (5.2 ± 0.2). The ability of the BCI equation to accurately predict BCS scores across breed type was evaluated by classifying animals as having acceptable agreement (absolute difference ≤ 1; AGR) or having unacceptable agreement (absolute difference > 1; NAG), and were analyzed using Chi Square. Agreement between the BCI and BCS was noted for 66% of horses,

Table 1
Number of horses with agreement between BCS and BCI scores using different equations

Type	Original BCI			Adjusted BCI		
	AGR	NAG	*P*-value	AGR	NAG	*P*-value
Horse	22	10	0.034	28	4	0.001
Pony	16	14	0.715	23	7	0.004
Draft	9	18	0.083	22	5	0.001

53% of ponies, and 33% of drafts horses (Table 1). To improve the rate of acceptable agreement, morphometric comparisons were made within breed type. For horses, the HGWH ratio tended ($P = 0.085$) to be greater for NAG horses (1.22 ± 0.04) than AGR horses (1.13 ± 0.03), and in horses where the HGWH ratio was > 1.16, altering the BCI equation to $[(HG^{0.5}+BG+NC^{1.2})/WH^{1.06})]^{2.2}$, resulted in 88% agreement between BCI and BCS (Table 1). For ponies, the NCNL was greater ($P = 0.016$) in NAG (1.37 ± 0.04) than AGR (1.23 ± 0.04) ponies, and in ponies were the NCNL was > 1.30, altering the BCI equation to $[(HG^{0.5}+BG+NC^{1.155})/WH^{1.05})]^{2.2}$ resulted in a 77% agreement between BCI and BCS (Table 1). In drafts, the BGHG ratio was greater ($P = 0.039$) in NAG (1.07 ± 0.01) than AGR (1.03 ± 0.01), and in drafts with a BGHG > 1.051, altering the BCI equation to $[(HG^{0.5}+BG^{0.95}+NC^{1.2})/WH^{1.05})]^{2.2}$ resulted in 81% agreement between BCI and BCS (Table 1). Equations to predict BCS have the potential to improve nutritional management across all equine types, especially for equine managers with minimal training. Further evaluation is warranted.

Key Words: body condition, body fat, morphometrics