

Table S5. Pearson's product-moment correlation between the composition of bacterial phyla found in horses' fecal microbiota and clinical alterations related to acute laminitis in animals from starch-saline and starch-buffer treatments.

SS												
Observed												
Parameters	Euryarcheota		Actinobacteria		Bacteroidetes		Firmicutes		Proteobacteria		Spirochaetes	
	r	p	r	p	r	p	r	p	r	p	r	p
HR	0.2	.248	0.0	.639	0.1	.583	0.0	.977	-0.1	.478	0.0	.800
T°C	-0.1	.739	0.5	.011	-0.1	.501	0.1	.716	-0.2	.333	0.0	.830
Diarrhea	-0.3	.139	0.4	.017	0.3	.157	0.5	.004	0.6	.001	-0.3	.080
Inappetence	-0.2	.461	0.0	.991	-0.1	.513	0.5	.004	0.6	.002	-0.1	.479
Decubitus	0.0		0.0		0.0		0.0		0.0		0.0	
Dehydration	-0.2	.231	0.0	.867	0.6	.002	0.2	.207	0.5	.005	-0.1	.581
N° steps	-0.2	.317	0.5	.006	-0.1	.438	0.1	.585	0.3	.160	0.0	.852
Obel Grade	0.1	.672	0.1	.653	-0.1	.594	0.2	.267	0.3	.124	-0.1	.445

SB												
	Euryarcheota		Actinobacteria		Bacteroidetes		Firmicutes		Proteobacteria		Spirochaetes	
	r	p	r	p	r	p	r	p	r	p	r	p
HR	0.1	.735	0.6	.002	-0.1	.783	0.3	.073	-0.1	.777	-0.4	.017
T°C	0.5	.010	-0.3	.144	-0.1	.464	0.3	.069	-0.3	.170	-0.2	.337
Diarrhea	-0.1	.682	0.1	.550	-0.4	.057	0.7	.001	-0.2	.406	-0.3	.105
Inappetence	0.0	.912	0.4	.052	0.1	.710	0.3	.173	0.3	.154	-0.2	.217
Decubitus	0.0	.847	0.4	.019	-0.1	.496	0.3	.158	-0.1	.701	0.1	.452
Dehydration	-0.2	.333	0.5	.003	-0.4	.041	0.5	.003	-0.2	.387	-0.3	.070
N° steps	-0.2	.391	0.3	.071	0.3	.060	0.2	.428	0.3	.115	-0.3	.094
Obel Grade	-0.3	.168	0.7	.001	0.1	.757	0.0	.934	0.0	.989	-0.3	.148

SS = starch-saline; SB = starch-buffer; HR = heart rate (beats/minute); T°C = rectal temperature; N° steps = number of steps; r = correlation (negative - $r < 0.1$ [beige]; weak - $0.1 < r < 0.3$ [light blue]; moderate - $0.4 < r < 0.6$ [blue]; strong - $0.7 < r < 1.0$ [dark blue]).

Table S6. Pearson's product-moment correlation between the composition of bacterial families found in horses' fecal microbiota and clinical alterations related to acute laminitis in animals from starch-saline and starch-buffer treatments.

SS								
Observed Parameters								
		HR	T°C	Diarrhea	Inappetence	Decubitus	Dehydration	N° steps
								Obel Grade
Ruminococcaceae	r	0.5	0.1	-0.5	-0.4	0.0	-0.4	-0.3
	p	.010	.617	.010	.056		.049	.088
Lachnospiraceae	r	0.2	-0.2	-0.3	-0.3	0.0	-0.1	-0.4
	p	.424	.348	.187	.102		.638	.036
Lactobacillaceae	r	-0.3	0.0	0.5	0.6	0.0	0.2	0.4
	p	.185	.910	.005	<.001		.317	.049
Prevotellaceae	r	0.0	-0.1	0.2	-0.1	0.0	0.5	-0.2
	p	.643	.516	.293	.476		.010	.339
Methanobacteriaceae	r	0.2	0.0	-0.3	-0.1	0.0	-0.2	-0.2
	p	.269	.839	.178	.503		.283	.336
Spirochaetaceae	r	0.0	0.0	-0.4	-0.2	0.0	-0.1	-0.2
	p	.810	.868	.043	.359		.519	.358
Streptococcaceae	r	-0.1	0.1	0.6	0.3	0.0	0.5	0.0
	p	.567	.595	<.001	.115		.004	.663
Bifidobacteriaceae	r	-0.1	0.4	0.5	0.0	0.0	0.0	0.6
	p	.615	.015	.010	.821		.917	.002
Erysipelotrichaceae	r	0.0	0.4	0.4	0.0	0.0	0.0	0.4
	p	.919	.016	.045	.673		.886	.035
Eubacteriaceae	r	0.0	0.0	-0.5	-0.3	0.0	-0.4	-0.3
	p	.690	.742	.006	.089		.045	.072
SB								
Ruminococcaceae	r	-0.6	-0.4	-0.7	-0.4	0.0	-0.6	-0.3
	p	<.001	.019	<.001	.024	.957	<.001	.116
Lachnospiraceae	r	-0.6	-0.3	-0.6	-0.4	0.0	-0.7	-0.4
	p	<.001	.110	<.001	.046	.899	<.001	.035
Lactobacillaceae	r	0.2	0.0	0.6	0.3	-0.2	0.6	0.0
	p	.335	.809	.001	.090	.385	<.001	.886

Prevotellaceae	r	-0.1	-0.1	-0.3	0.0	-0.1	-0.4	0.3	0.0
	p	.542	.535	.058	.791	.470	.033	.155	>.999
Methanobacteriaceae	r	0.1	0.5	-0.1	0.0	0.0	-0.2	-0.2	-0.3
	p	.669	.008	.643	.854	.883	.344	.408	.183
Spirochaetaceae	r	-0.4	-0.1	-0.3	-0.2	0.2	-0.3	-0.3	-0.3
	p	.041	.588	.169	.310	.389	.114	.155	.168
Streptococcaceae	r	0.2	0.4	0.5	0.2	-0.2	0.3	-0.1	-0.2
	p	.314	.019	.003	.368	.268	.124	.605	.284
Bifidobacteriaceae	r	0.5	-0.3	0.1	0.3	0.4	0.5	0.3	0.7
	p	.002	.148	.576	.059	.020	.003	.098	<.001
Erysipelotrichaceae	r	0.4	0.0	0.1	0.1	0.1	0.2	0.8	0.5
	p	.014	.963	.612	.468	.688	.294	<.001	.002
Eubacteriaceae	r	-0.6	-0.4	-0.7	-0.4	0.0	-0.6	-0.3	-0.2
	p	<.001	.019	<.001	.024	.957	<.001	.116	.265

SS = starch-saline; SB = starch-buffer; HR = heart rate (beats/minute); T°C = rectal temperature; N° steps = number of steps; r = correlation (negative - $r < 0.1$ [beige]; weak - $0.1 < r < 0.3$ [light blue]; moderate - $0.4 < r < 0.6$ [blue]; strong - $0.7 < r < 1.0$ [dark blue]).

Table S7. Pearson's product-moment correlation between the composition of bacterial genera found in horses' fecal microbiota and clinical alterations related to acute laminitis in animals from starch-saline and starch-buffer treatments.

SS									
		Observed Parameters							
		HR	T°C	Diarrhea	Inappetence	Decubitus	Dehydration	N° steps	Obel Grade
Clostridium_XIVa	r	0.2	-0.2	-0.3	-0.3	0.0	-0.1	-0.3	-0.4
	p	.421	.387	.107	.077		.539	.091	.059
Ruminococcaceae*	r	0.4	0.0	-0.3	-0.3	0.0	-0.3	-0.3	-0.1
	p	.032	.866	.067	.114		.098	.083	.608
Lactobacillus	r	-0.3	0.0	0.5	0.6	0.0	0.2	0.4	0.3
	p	.187	.930	.005	<.001		.315	.053	.138
Methanobrevibacter	r	0.2	0.0	-0.3	-0.1	0.0	-0.2	-0.2	0.1
	p	.262	.805	.182	.502		.295	.329	.599
Prevotella	r	0.0	-0.2	0.3	-0.1	0.0	0.5	-0.2	-0.2
	p	.828	.400	.176	.575		.004	.410	.406
Treponema	r	0.0	0.0	-0.3	-0.1	0.0	-0.1	0.0	-0.1
	p	.800	.830	.080	.479		.581	.852	.445
Lachnospiraceae*	r	0.2	0.0	-0.2	-0.3	0.0	-0.2	-0.4	-0.1
	p	.266	.741	.192	.157		.403	.038	.451
Streptococcus	r	-0.1	0.1	0.6	0.3	0.0	0.5	0.1	0.1
	p	.539	.566	<.001	.125		.006	.609	.626
Bifidobacterium	r	-0.1	0.5	0.5	0.0	0.0	0.0	0.5	0.1
	p	.666	.013	.012	.869		.954	.002	.509
Clostridium_III	r	0.2	0.0	-0.5	-0.3	0.0	-0.4	-0.4	-0.3
	p	.409	.912	.005	.070		.034	.043	.093
Erysipelotrichaceae*	r	0.0	0.4	0.4	-0.1	0.0	0.0	0.4	0.1
	p	.875	.053	.024	.750		.819	.031	.529
Ruminococcus	r	0.0	0.0	-0.3	-0.2	0.0	-0.2	-0.1	-0.2
	p	.900	.995	.080	.298		.322	.774	.202
Eubacterium	r	0.1	-0.1	-0.5	-0.3	0.0	-0.4	-0.3	-0.3
	p	.707	.767	.006	.113		.034	.103	.127
SB									
Clostridium_XIVa	r	-0.6	-0.3	-0.5	-0.4	0.0	-0.5	-0.6	-0.3
	p	<.001	.124	.006	.020	.860	.002	.012	.075
Ruminococcaceae*	r	-0.6	-0.2	-0.5	-0.5	0.0	-0.5	-0.5	-0.3
	p	<.001	.253	.008	.005	.853	.006	.010	.068
Lactobacillus	r	0.2	0.0	0.6	0.3	-0.2	0.6	0.0	0.0
	p	.351	.806	.001	.102	.365	<.001	.864	.793
Methanobrevibacter	r	0.1	0.5	-0.1	0.0	0.0	-0.2	-0.2	-0.2
	p	.655	.007	.672	.852	.866	.352	.428	.193
Prevotella	r	-0.1	-0.1	-0.3	0.1	-0.1	-0.4	0.3	0.0
	p	.688	.575	.085	.703	.441	.050	.120	.895
Treponema	r	-0.4	-0.2	-0.3	-0.2	0.1	-0.3	-0.3	-0.3
	p	.017	.337	.105	.217	.452	.070	.094	.148
Lachnospiraceae*	r	-0.6	-0.2	-0.6	-0.6	0.0	-0.6	-0.5	-0.3
	p	<.001	.247	.001	<.001	.909	<.001	.009	.073

Streptococcus	r	0.2	0.4	0.5	0.2	-0.2	0.3	-0.1	-0.2
	p	.329	.021	.003	.358	.264	.120	.587	.269
Bifidobacterium	r	0.5	-0.3	0.1	0.4	0.4	0.5	0.3	0.7
	p	.002	.152	.558	.056	.019	.003	.095	<.001
Clostridium_III	r	-0.6	-0.2	-0.5	-0.5	0.0	-0.5	-0.5	-0.3
	p	<.001	.213	.009	.006	.952	.006	.006	.058
Erysipelotrichaceae*	r	0.4	0.0	0.1	0.1	0.1	0.2	0.8	0.5
	p	.013	.944	.599	.459	.710	.289	<.001	.002
Ruminococcus	r	-0.6	-0.3	-0.5	-0.5	-0.1	-0.5	-0.5	-0.3
	p	.001	.180	.009	.009	.447	.004	.013	.083
Eubacterium	r	-0.5	-0.4	-0.6	-0.4	0.0	-0.6	-0.2	-0.2
	p	.004	.033	<.001	.036	.831	<.001	.200	.366

SS = starch-saline; SB = starch-buffer; HR = heart rate (beats/minute); T°C = rectal temperature;

N° steps = number of steps; r = correlation (negative - $r < 0.1$ [beige]; weak - $0.1 < r < 0.3$ [light blue];

moderate - $0.4 < r < 0.6$ [blue]; strong - $0.7 < r < 1.0$ [dark blue]).