

Article

Effects of Fumonisin B and Hydrolyzed Fumonisin B on Growth and Intestinal Microbiota in Broilers

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Table S1. FBs and HFBs affect the body weight of broilers.

	ANOVA with Tukey's multiple comparisons test	Significant	P-Value
Week 6	Control vs. L-FBs	ns	0.9315
	Control vs. H-FBs	ns	0.1385
	Control vs. L-HFBs	ns	0.9991
	Control vs. H-HFBs	ns	0.1507
	L-FBs vs. H-FBs	*	0.0174
	L-FBs vs. L-HFBs	ns	0.9783
	L-FBs vs. H-HFBs	*	0.0196
	H-FBs vs. L-HFBs	ns	0.0600
	H-FBs vs. H-HFBs	ns	>0.9999
	L-HFBs vs. H-HFBs	ns	0.0666
Week 7	Control vs. L-FBs	ns	0.7984
	Control vs. H-FBs	***	0.0002
	Control vs. L-HFBs	ns	0.8260
	Control vs. H-HFBs	***	0.0006
	L-FBs vs. H-FBs	*	0.0129
	L-FBs vs. L-HFBs	ns	>0.9999
	L-FBs vs. H-HFBs	*	0.0278
	H-FBs vs. L-HFBs	**	0.0059
	H-FBs vs. H-HFBs	ns	0.9992
	L-HFBs vs. H-HFBs	*	0.0140
Week 8	Control vs. L-FBs	ns	0.8592
	Control vs. H-FBs	****	<0.0001
	Control vs. L-HFBs	ns	0.9819
	Control vs. H-HFBs	****	<0.0001
	L-FBs vs. H-FBs	****	<0.0001
	L-FBs vs. L-HFBs	ns	0.9887
	L-FBs vs. H-HFBs	***	0.0009
	H-FBs vs. L-HFBs	****	<0.0001
	H-FBs vs. H-HFBs	ns	0.9241
	L-HFBs vs. H-HFBs	****	<0.0001

Table S2. Differentially expressed bacteria after FBs and HFBs treatment.

	ANOVA	Kruskal Wallis
Phylum		Elusimicrobia Planctomycetes
Class	Elusimicrobia Phycisphaerae	Elusimicrobia Phycisphaerae Subgroup_22
Order	WD260	WD260
Deltaproteobacteria_Incertae_Sedis	Subgroup_13	Deltaproteobacteria_Incertae_Sedis
Reyranellales	Gastranaerophilales	Subgroup_13
Gastranaerophilales	Subgroup_2	Reyranellales
Acetobacterales	Actinomarinales	Gastranaerophilales
Actinomarinales	SJA-28	Subgroup_2
Mollicutes_RF39	MVP-88	Acetobacterales
uncultured_Acidobacteriales_bacterium		JG36-TzT-191
Family	SAR324_clade(Marine_group_B)	SAR324_clade(Marine_group_B)
Candidatus_Nitrosoarchaeum_limnia_SFB1	Rickettsiales	Rickettsiales
SM2D12		R7C24
uncultured_Bradyrhizobiaceae_bacterium	Enterobacteriales	Enterobacteriales
Prolixibacteraceae	KF-JG30-C25	KF-JG30-C25
uncultured_forest_soil_bacterium	uncultured_soil_bacterium	uncultured_soil_bacterium
Mycobacteriaceae	Izimaplasmatales	Izimaplasmatales
Geodermatophilaceae	Rhodospirillales	Rhodospirillales
Magnetospirillaceae	Lactobacillales	Lactobacillales
Rhizobiales_Incertae_Sedis		
Reyranellaceae	Candidatus_Nitrosoarchaeum_limnia_SFB1	Candidatus_Nitrosoarchaeum_limnia_SFB1
Tannerellaceae	SM2D12	SM2D12
S15-21	uncultured_Bradyrhizobiaceae_bacterium	uncultured_Bradyrhizobiaceae_bacterium
Unknown_Family	Prolixibacteraceae	Prolixibacteraceae
Chitinimonadaceae	uncultured_forest_soil_bacterium	uncultured_forest_soil_bacterium
Ilumatobacteraceae	Mycobacteriaceae	Mycobacteriaceae
Genus	Geodermatophilaceae	Geodermatophilaceae
GOUTA6	Magnetospirillaceae	Magnetospirillaceae
Magnetospirillum	Rhizobiales_Incertae_Sedis	Rhizobiales_Incertae_Sedis
uncultured_Rickettsiales_bacterium	Reyranellaceae	Reyranellaceae
	Clostridiales_vadinBB60_group	Clostridiales_vadinBB60_group
	uncultured_Acidothermaceae_bacterium	uncultured_Acidothermaceae_bacterium
	Acetobacteraceae	Acetobacteraceae
	Arcobacteraceae	Arcobacteraceae
	Paenibacillaceae	Paenibacillaceae
	Saccharospirillaceae	Saccharospirillaceae
	Rs-E47_termite_group	Rs-E47_termite_group
	metagenome	metagenome
	Nitrosococcaceae	Nitrosococcaceae
	SAR116_clade	SAR116_clade
	Enterobacteriaceae	Enterobacteriaceae
	Inquilinaceae	Inquilinaceae
	Acidothermaceae	Acidothermaceae
	A21b	A21b
	URHD0088	URHD0088
	Phaseolus_acutifolius_(tepary_beans)	Phaseolus_acutifolius_(tepary_beans)
	Lactobacillaceae	Lactobacillaceae
	GOUTA6	GOUTA6
	Magnetospirillum	Magnetospirillum
	uncultured_Rickettsiales_bacterium	uncultured_Rickettsiales_bacterium

Candidatus_Nitrosoarchaeum_limnia_SFB1	Candidatus_Nitrosoarchaeum_limnia_SFB1
Sunxiuqinia	Sunxiuqinia
uncultured_Bradyrhizobiaceae_bacterium	uncultured_Bradyrhizobiaceae_bacterium
Lachnospiraceae_UCG-010	Lachnospiraceae_UCG-010
Erysipelotrichaceae_UCG-003	Erysipelotrichaceae_UCG-003
Klebsiella	Klebsiella
uncultured_forest_soil_bacterium	uncultured_forest_soil_bacterium
Clostridium_sensu_stricto_1	Clostridium_sensu_stricto_1
Lachnospiraceae_UCG-006	Lachnospiraceae_UCG-006
Anaerostipes	Anaerostipes
Deferrisoma	Deferrisoma
Ornithinimicrobium	Ornithinimicrobium
Chitiniphilus	Chitiniphilus
Erysipelothrix	Erysipelothrix
Mycobacterium	Mycobacterium
Undibacterium	Undibacterium
Granulicella	Granulicella
uncultured_Nitrosomonadales_bacterium	uncultured_Nitrosomonadales_bacterium
Flavonifractor	Paenibacillus
PAUC26f	wb1-P19
Draconibacterium	Segetibacter
Azovibrio	Lachnospiraceae_NK4B4_group
Chitinimonas	WCHB1-32
Pseudolabrys	Lechevalieria
Amycolatopsis	Lachnospiraceae_AC2044_group
Conexibacter	Polaromonas
[Eubacterium]_ventriosum_group	Duganella
Azohydromonas	Rosearcus
Ruminococcaceae_UCG-010	Azospirillum
Parabacteroides	uncultured_proteobacterium
Ruminococcaceae_UCG-003	Kibdelosporangium
	Plesiomonas
	Blyi10
	Roseburia
	Mycoplasma
	GAS113
	Rheinheimera
	Edaphobacter
	[Eubacterium]_brachy_group
	Glutamicibacter
	Roseomonas
	Blastococcus
	Inquilinus
	Acidothermus
	Eggerthella
	Lactobacillus
	Phaseolus_acutifolius_(tepary_beans)
	Anaerofilum
	Sandaracinus
	uncultured_Rhizomicrobium_sp.
	Xanthobacter
	Fournierella
	Lachnospiraceae_NK4A136_group
	Oleibacter
	Dyella
	Triticum_aestivum_(bread_wheat)
	Arcobacter
	Acidipila
	Turneriella
	uncultured_Acidothermaceae_bacterium

Species	uncultured_Nitrosomonadaceae_bacterium uncultured_Hyphomicrobiaceae_bacterium Clostridium_sensu_stricto_8
	uncultured_Rickettsiales_bacterium
	Candidatus_Nitrosoarchaeum_limnia_SFB1
	uncultured_forest_soil_bacterium
	Bacteroides_acidifaciens_JCM_10556
	Lactobacillus_salivarius
	uncultured_rumen_bacterium
	uncultured_Nitrosomonadales_bacterium
	uncultured_spirochete
	uncultured_organism
	uncultured_soil_bacterium
	uncultured_Rickettsiales_bacterium
	Candidatus_Nitrosoarchaeum_limnia_SFB1
	uncultured_forest_soil_bacterium
	Bacteroides_acidifaciens_JCM_10556
	Lactobacillus_salivarius
	uncultured_rumen_bacterium
	uncultured_Nitrosomonadales_bacterium
	uncultured_Dongia_sp.
	uncultured_Acidothermaceae_bacterium
	uncultured_Nitrosomonadaceae_bacterium
	uncultured_Burkholderia_sp.
	Rhizobium_leguminosarum
	uncultured_Desulfovibrio_sp.
	uncultured_Polaromonas_sp.
	uncultured_Gemmimonadaceae_bacterium
	Lactobacillus_gasseri
	uncultured_Hyphomicrobiaceae_bacterium
	Phaseolus_acutifolius_(tepary_beans)
	uncultured_Rhizomicrobium_sp.
	uncultured_Bradyrhizobiaceae_bacterium
	Other
	uncultured_Lactobacillaceae_bacterium
	uncultured_Allobaculum_sp.
	Lactobacillus_vaginalis
	Triticum_aestivum_(bread_wheat)

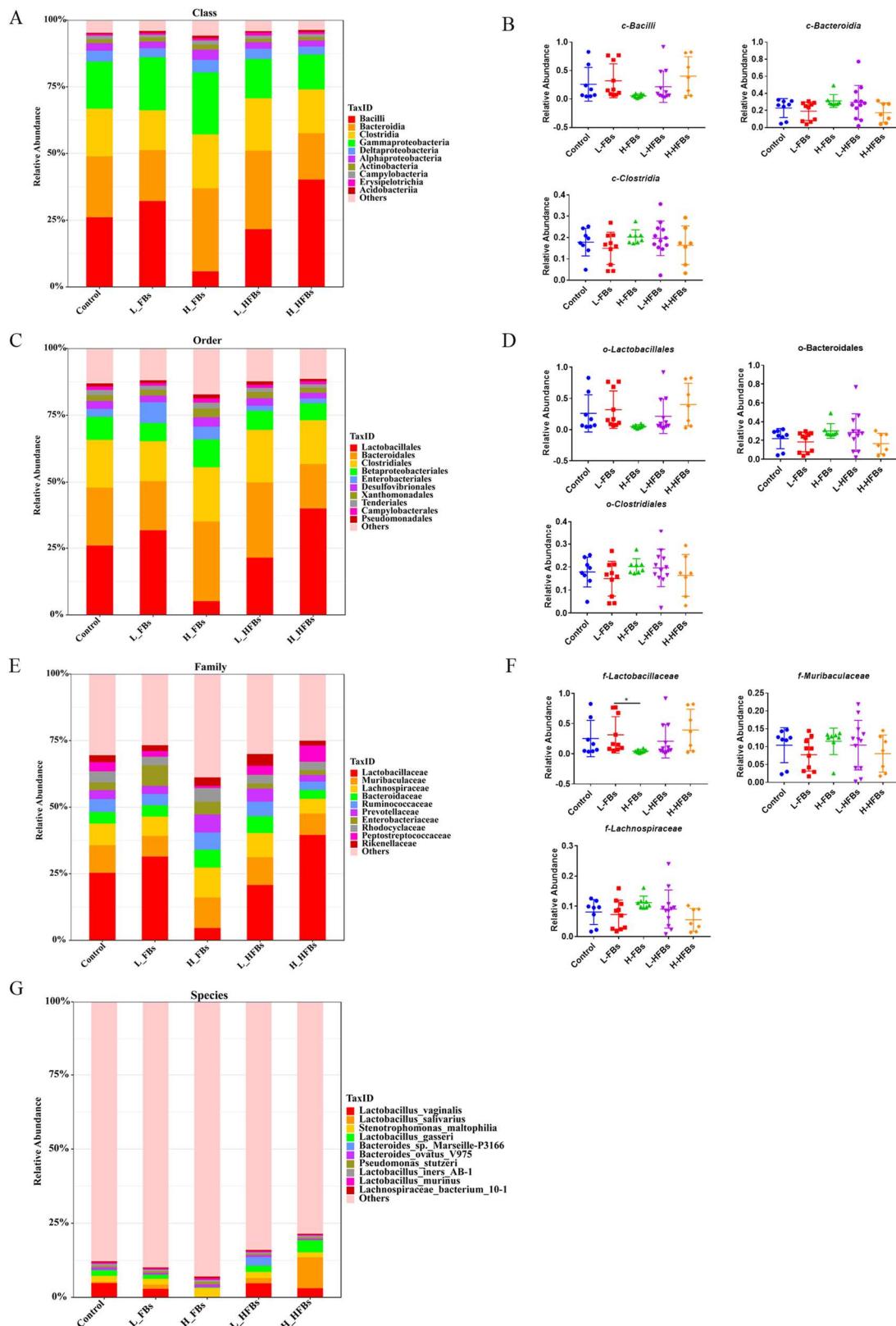


Figure S1. Relative abundance of bacteria and analysis of dominant bacteria at Class (**A-B**), Order (**C-D**), Family (**E-F**) and Species (**G**) level.

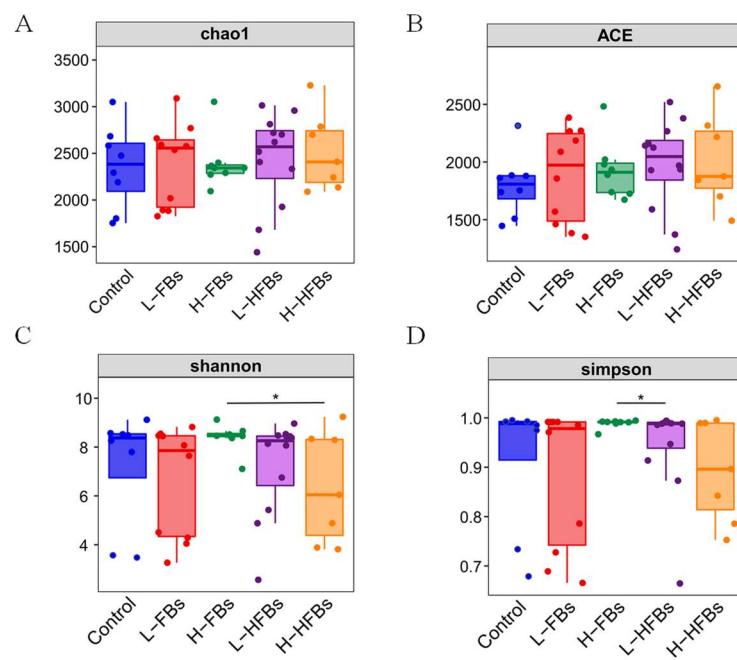


Figure S2. Alpha analysis of intestinal microbiota after FBs and HFBs treatment. (A) chao 1 analysis. (B) ACE analysis. (C) shannon analysis. (D) simpson analysis.