Electronic Supplementary Material (ESI) for Food & Function.

Supplementary Information

Probiotic/prebiotic correction for adverse effects of iron fortification on intestinal resistance to *Salmonella* infection in weaning mice

Feifei Lin [a], Haohao Wu [a,*], Mingyong Zeng [a,*], Guangli Yu [b], Shiyuan Dong [a], Huicheng Yang [c]

[a] *College of Food Science and Engineering, Ocean University of China, 5 Yushan Road, Qingdao, Shandong Province, 266003, China*

[b] *School of Medicine and Pharmacy, Ocean University of China, 5 Yushan Road, Qingdao, Shandong Province, 266003, China*

[c] *Zhejiang Marine Development Research Institute, No.10, Tiyu Road, Zhoushan, Zhejiang Province 316021, PR China*

[*] Authors to whom correspondence should be addressed; E-mails: wuhaohao@ouc.edu.cn (Wu, H.); mingyz@ouc.edu.cn (Zeng, M.); Tel.: +86-532-8203-2400

Table S1. Taxa with different abundance in the basal diet group and the 250 ppm-$FeSO_4$ group across the LEfSe algorithm.

Taxon	LAD Effect size	LEfSe *P*-value	Increased in:
Bacteria.Cyanobacteria	2.08	0.0236	250 ppm-$FeSO_4$
Bacteria.Cyanobacteria.Melainabacteria	1.98	0.0186	250 ppm-$FeSO_4$
Bacteria.Cyanobacteria.Melainabacteria.Gastranaerophilales	1.98	0.0186	250 ppm-$FeSO_4$
Bacteria.Tenericutes	4.01	0.0472	250 ppm-$FeSO_4$
Bacteria.Tenericutes.Mollicutes	4.01	0.0472	250 ppm-$FeSO_4$
Bacteria.Tenericutes.Mollicutes.Mollicutes_RF9	4.01	0.0472	250 ppm-$FeSO_4$
Bacteria.Firmicutes.Clostridia	4.90	0.0283	250 ppm-$FeSO_4$
Bacteria.Firmicutes.Clostridia.Clostridiales	4.90	0.0283	250 ppm-$FeSO_4$
Bacteria.Firmicutes.Clostridia.Clostridiales.Christensenellaceae.Christensenellaceae_R_7_group	3.25	0.0283	250 ppm-$FeSO_4$
Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae	4.71	0.0283	250 ppm-$FeSO_4$
Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Lachnospiraceae_bacterium_610	2.18	0.0459	250 ppm-$FeSO_4$
Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnoclostridium	4.12	0.0472	250 ppm-$FeSO_4$
Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae._Eubacterium__ventriosum_group	2.80	0.0129	250 ppm-$FeSO_4$
Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_NK4A136_group.Lachnospiraceae_bacterium_10_1	2.05	0.0144	250 ppm-$FeSO_4$
Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.unidentified_Lachnospiraceae.Clostridium_sp__Clone_17	3.22	0.0361	250 ppm-$FeSO_4$
Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_NK4A136_group.Clostridiales_bacterium_CIEAF_020	3.55	0.0088	250 ppm-$FeSO_4$
Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Tyzzerella_3	2.55	0.0259	250 ppm-$FeSO_4$
Bacteria.Firmicutes.Clostridia.Clostridiales.Ruminococcaceae	4.41	0.0283	250 ppm-$FeSO_4$
Bacteria.Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_UCG_013	4.11	0.0472	250 ppm-$FeSO_4$
Bacteria.Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_UCG_014	4.03	0.0472	250 ppm-$FeSO_4$
Bacteria.Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_NK4A214_group	3.58	0.0283	250 ppm-$FeSO_4$
Bacteria.Firmicutes.Clostridia.Clostridiales.Christensenellaceae	3.27	0.0361	250 ppm-$FeSO_4$
Bacteria.Firmicutes.Erysipelotrichia.Erysipelotrichales.Erysipelotrichaceae.Erysipelatoclostridium	2.28	0.0095	250 ppm-$FeSO_4$
Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacterales.Helicobacteraceae.Helicobacter.Helicobacter_mastomyrinus	2.41	0.0278	Basal diet
Bacteria.Proteobacteria.Alphaproteobacteria.Rhodospirillales	2.86	0.0465	250 ppm-$FeSO_4$
Bacteria.Proteobacteria.Gammaproteobacteria.Aeromonadales	1.43	0.0495	250 ppm-$FeSO_4$
Bacteria.Proteobacteria.Gammaproteobacteria.Aeromonadales.Aeromonadaceae	1.43	0.0495	250 ppm-$FeSO_4$
Bacteria.Proteobacteria.Gammaproteobacteria.Aeromonadales.Aeromonadaceae.Aeromonas	1.43	0.0495	250 ppm-$FeSO_4$
Bacteria.Proteobacteria.Gammaproteobacteria.Aeromonadales.Aeromonadaceae.Aeromonas.Aeromonas_hydrophila	1.43	0.0495	250 ppm-$FeSO_4$

[a] Arbitrarily chosen numbers to define which taxa are parts of the same branch.

Abbreviations: LDA, linear discriminant analysis; LEfSe, the LDA effect size.

Table S2. Taxa with different abundance in the basal diet group and the 500 ppm-$FeSO_4$ group across the LEfSe algorithm.

Taxon	LAD Effect size	LEfSe P-value	Increased in:
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae	3.80	0.0283	Basal diet
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides	3.80	0.0283	Basal diet
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Bacteroides_acidifaciens	3.71	0.0283	Basal diet
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Dysgonomonas	2.50	0.0063	500 ppm-$FeSO_4$
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Dysgonomonas.Dysgonomonas_mossii	2.50	0.0063	500 ppm-$FeSO_4$
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Petrimonas	2.82	0.0132	500 ppm-$FeSO_4$
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella_9	2.14	0.0092	Basal diet
Bacteria.Bacteroidetes.Flavobacteriia	2.62	0.0132	500 ppm-$FeSO_4$
Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales	2.62	0.0132	500 ppm-$FeSO_4$
Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae	2.62	0.0132	500 ppm-$FeSO_4$
Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Chryseobacterium	2.62	0.0071	500 ppm-$FeSO_4$
Bacteria.Bacteroidetes.Sphingobacteriia	3.54	0.0236	500 ppm-$FeSO_4$
Bacteria.Bacteroidetes.Sphingobacteriia.Sphingobacteriales	3.54	0.0236	500 ppm-$FeSO_4$
Bacteria.Bacteroidetes.Sphingobacteriia.Sphingobacteriales.WCHB1_69	3.20	0.0406	500 ppm-$FeSO_4$
Bacteria.Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Lactobacillus_animalis	3.96	0.0472	Basal diet
Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae	2.41	0.0259	Basal diet
Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus	2.41	0.0259	Basal diet
Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_danieliae	2.38	0.0236	Basal diet
Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae._Eubacterium__ventriosum_group	1.93	0.0343	500 ppm-$FeSO_4$
Bacteria.Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Intestinimonas	2.52	0.0129	500 ppm-$FeSO_4$
Bacteria.Proteobacteria.Alphaproteobacteria	3.87	0.0472	500 ppm-$FeSO_4$
Bacteria.Proteobacteria.Alphaproteobacteria.Rhizobiales	3.81	0.0472	500 ppm-$FeSO_4$
Bacteria.Proteobacteria.Alphaproteobacteria.Rhodospirillales	2.65	0.0160	500 ppm-$FeSO_4$
Bacteria.Proteobacteria.Alphaproteobacteria.Rhodospirillales.Rhodospirillaceae	2.47	0.0138	500 ppm-$FeSO_4$
Bacteria.Proteobacteria.Alphaproteobacteria.Rhodospirillales.Rhodospirillaceae.Azospirillum	2.20	0.0071	500 ppm-$FeSO_4$
Bacteria.Proteobacteria.Alphaproteobacteria.Rhodospirillales.Rhodospirillaceae.Azospirillum.Azospirillum_brasilense	2.20	0.0071	500 ppm-$FeSO_4$
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Comamonadaceae	3.01	0.0264	500 ppm-$FeSO_4$
Bacteria.Proteobacteria.Deltaproteobacteria.Desulfuromonadales	3.91	0.0236	500 ppm-$FeSO_4$
Bacteria.Proteobacteria.Deltaproteobacteria.Desulfuromonadales.Geobacteraceae	3.91	0.0236	500 ppm-$FeSO_4$
Bacteria.Proteobacteria.Deltaproteobacteria.Desulfuromonadales.Geobacteraceae.Geobacter	3.91	0.0236	500 ppm-$FeSO_4$
Bacteria.Proteobacteria.Deltaproteobacteria.Desulfuromonadales.Geobacteraceae.Geobacter.Geobacter_sp__GSS01	3.91	0.0236	500 ppm-$FeSO_4$

Table S2. Continued.

Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacterales.Campylobacteraceae	3.08	0.0132	500 ppm-$FeSO_4$
Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacterales.Campylobacteraceae.Arcobacter	3.08	0.0132	500 ppm-$FeSO_4$
Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacterales.Campylobacteraceae.Arcobacter.Arcobacter_butzleri	3.08	0.0132	500 ppm-$FeSO_4$
Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacterales.Helicobacteraceae.Helicobacter.Helicobacter_mastomyrinus	2.41	0.0361	Basal diet
Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales	2.52	0.0445	500 ppm-$FeSO_4$
Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae	2.52	0.0445	500 ppm-$FeSO_4$
Bacteria.Spirochaetes	2.60	0.0236	500 ppm-$FeSO_4$
Bacteria.Spirochaetes.unidentified_Spirochaetes	2.60	0.0236	500 ppm-$FeSO_4$
Bacteria.Spirochaetes.unidentified_Spirochaetes.Spirochaetales	2.60	0.0236	500 ppm-$FeSO_4$
Bacteria.Spirochaetes.unidentified_Spirochaetes.Spirochaetales.Spirochaetaceae	2.60	0.0236	500 ppm-$FeSO_4$
Bacteria.Spirochaetes.unidentified_Spirochaetes.Spirochaetales.Spirochaetaceae.Sphaerochaeta	2.57	0.0406	500 ppm-$FeSO_4$

[a] Arbitrarily chosen numbers to define which taxa are parts of the same branch.

Abbreviations: LDA, linear discriminant analysis; LEfSe, the LDA effect size.

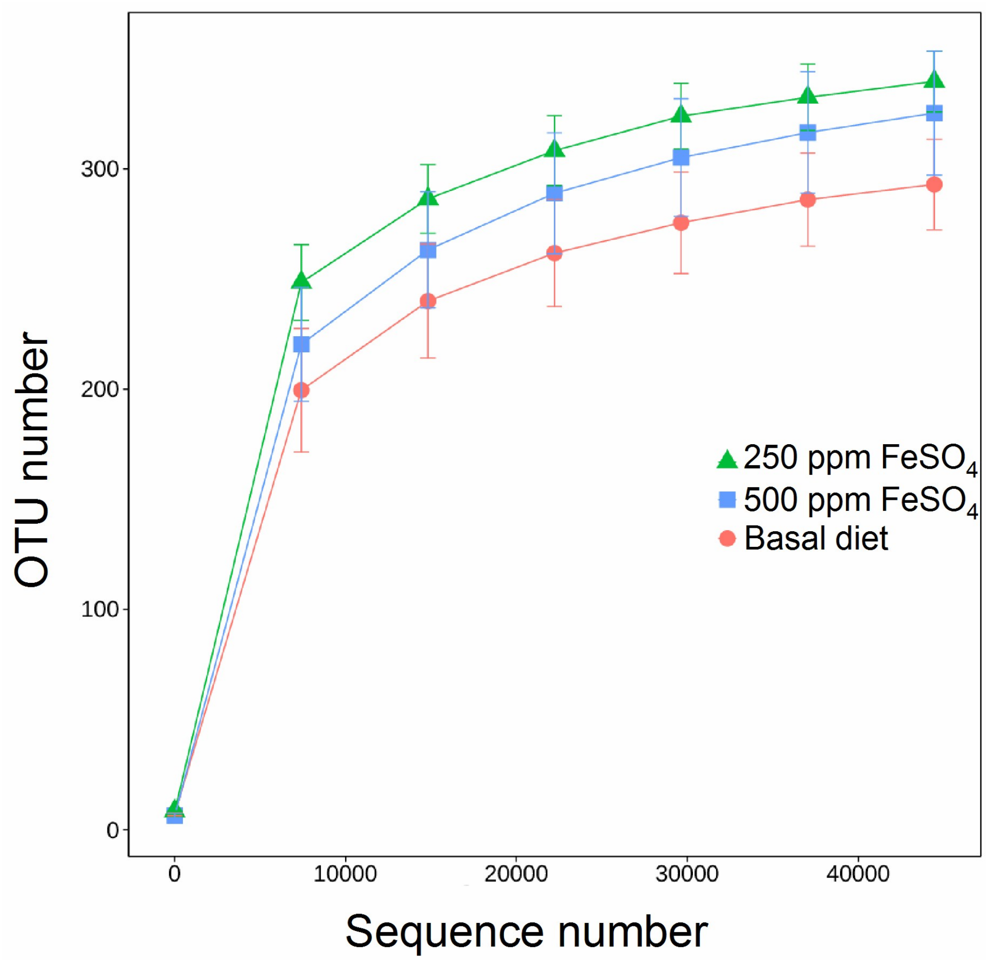

Figure S1. Rarefaction curves calculated for each sample.