Seeking to improve feed efficiency in pigs through microbial modulation via fecal microbiota transplantation in sows and dietary supplementation of offspring with inulin

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Running title: Microbial modulation to alter feed efficiency in pigs

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Table S1. Significant differences in parameters in offspring due to the effect of the interaction between fecal microbiota transplantation (FMT) in sows and dietary supplementation of offspring with inulin for 42 days post-weaning[1]

Sow treatment	**Control[2]**		**FMTp[3]**		**S.E.M.**	**P-value**		
Offspring treatment	**Control[4]**	**Inulin[5]**	**Control**	**Inulin**		**Interaction**	**Sow**	**Offspring**
Weaning								
G_*Streptococcus*	0.73^{b}	0.31^{b}	2.24^{a}	3.71^{a}	0.134	<0.001	<0.001	0.68
G_*Butyricimonas*	0.04^{b}	0.21^{b}	0.08^{b}	2.56^{a}	0.018	<0.001	<0.001	<0.001
G_*Bifidobacterium*	0.09^{b}	0.07^{b}	0.10^{b}	2.07^{a}	0.027	0.001	0.04	0.03
G_*Faecalibacterium*	0.89^{a}	0.20^{b}	0.23^{b}	0.16^{b}	0.099	<0.001	0.003	0.001
G_*Dorea*	0.20^{a,b}	0.57^{a}	0.03^{b}	0.31^{a}	0.009	<0.001	0.01	<0.001
G_*Terrisporobacter*	0.13^{a,b}	0.03^{b}	0.31^{a}	0.12^{a,b}	0.012	0.003	0.007	0.005
Caffeine metabolism	0.0011^{a}	0.0003^{b}	0.0014^{a}	0.0007^{a,b}	0.00014	0.001	0.001	0.005
Day 50								
P_*Proteobacteria*	2.95^{a}	1.10^{b}	4.68^{a}	2.65^{a,b}	0.789	0.004	<0.001	<0.001
1,1,1-Trichloro-2,2-bis(4-chlorophenyl)ethane (DDT) degradation	0.0013^{b}	0.0005^{b}	0.0017^{a,b}	0.0034^{a}	0.00026	0.001	<0.001	0.61
Day 65								
Alpha-linolenic acid metabolism	0.0012^{a,b}	0.0008^{b}	0.0028^{a}	0.0007^{b}	0.00041	<0.001	0.15	<0.001
Day 100								
Body weight (kg)	59.0^{a}	58.6^{a}	51.2^{b}	53.7^{a,b}	1.31	<0.001	<0.001	0.41
P_*Actinobacteria*	0.19^{b}	0.64^{a,b}	1.15^{a}	0.50^{a,b}	0.170	0.004	0.03	0.76
G_*Campylobacter*	1.07^{b}	0.85^{b}	3.22^{a}	1.38^{a,b}	0.567	<0.001	0.002	0.01
G_*Peptococcus*	0.08^{b}	1.18^{a}	0.95^{a}	0.19^{b}	0.032	<0.001	0.49	0.24
G_*Bifidobacterium*	0.03^{a,b}	0.04^{a,b}	0.23^{a}	0.01^{b}	0.004	0.006	0.39	0.05
G_*Sutterella*	0.002^{b}	0.127^{a}	0.158^{a}	0.189^{a}	0.0003	0.004	0.005	0.01
Day 130								
P_*Fibrobacteres*	0.37^{a}	0.35^{a}	0.01^{b}	0.39^{a}	0.001	<0.001	<0.001	0.008

Sow treatment	Control[2]		FMTp[3]		S.E.M.	P-value		
Offspring treatment	Control[4]	Inulin[5]	Control	Inulin		Interaction	Sow	Offspring
G_*Sphaerochaeta*	18.00^{a}	9.96^{a,b}	4.51^{b}	13.38^{a,b}	2.442	0.008	0.07	0.41
G_*Oribacterium*	2.76^{a}	1.80^{a,b}	0.73^{b}	1.80^{a,b}	0.434	0.004	0.01	0.37
G_*Blautia*	1.39^{a,b}	1.36^{a,b}	0.61^{b}	2.06^{a}	0.374	0.006	0.13	0.02
G_*Faecalitalea*	0.42^{a}	0.20^{a,b}	0.06^{b}	0.27^{a,b}	0.031	0.001	0.02	0.29
G_*Fibrobacter*	0.367^{a}	0.351^{a}	0.004^{b}	0.092^{a}	0.001	<0.001	<0.001	0.008
G_*Bifidobacterium*	0.03^{b}	0.46^{a,b}	0.82^{a}	0.30^{a,b}	0.007	0.004	0.02	0.15
G_*Acetanaerobacterium*	0.10^{a,b}	0.02^{b}	0.90^{a}	0.11^{a,b}	0.005	0.007	0.004	0.007
Limonene and pinene degradation	0.22^{b}	0.31^{a}	0.29^{a}	0.27^{a,b}	0.198	<0.001	0.14	0.01
Fatty acid metabolism	0.57^{b}	0.72^{a}	0.69^{a,b}	0.66^{a,b}	0.527	0.001	0.32	0.03
Purine metabolism	5.0^{a}	4.7^{b}	4.6^{b}	4.8^{b}	4.511	0.002	0.05	0.65
Day 140								
Body weight (kg)	104.9^{a}	103.9^{a}	94.3^{b}	96.8^{b}	1.29	<0.001	<0.001	0.59
Carcass weight (kg)	81.0^{a}	80.1^{a}	72.1^{b}	75.0^{b}	1.62	0.01	<0.001	0.54
Carcass muscle depth (mm)	53.5^{a,b}	52.1^{b}	52.5^{a,b}	53.8^{a}	0.71	0.05	0.61	0.92
White blood cells (×10^{3} cells/µL)	28.4^{a}	21.6^{b}	24.7^{a,b}	26.2^{a,b}	1.54	0.01	0.78	0.09
Hemoglobin (g/dL)	13.9^{a,b}	13.6^{a,b}	12.7^{b}	14.0^{a}	0.39	0.05	0.31	0.16
Day 35 – 140								
RFI[7] (g/day)	13.7^{a}	25.2^{a}	-13.9^{b}	-20.9^{b}	15.96	0.05	0.02	0.88

Sow treatment	**Control**[2]		**FMTp**[3]		**S.E.M.**	**P-value**		
Offspring treatment	**Control**[4]	**Inulin**[5]	**Control**	**Inulin**		**Interaction**	**Sow**	**Offspring**
Jejunum								
Number of goblet cells per µm villus height	$0.14^{a,b}$	0.13^{b}	0.16^{a}	0.16^{a}	0.007	0.001	<0.001	0.93
Ileum								
G_*Prevotella*	0.36^{b}	3.35^{a}	2.99^{a}	4.54^{a}	0.164	<0.001	0.004	0.002
G_*Sphaerochaeta*	2.78^{a}	0.32^{b}	0.30^{b}	1.04^{b}	0.143	<0.001	0.16	0.19
G_*Chlamydia*[6]	2.61^{a}	0.20^{b}	0.63^{b}	0.30^{b}	0.086	<0.001	0.22	<0.001
Glycosphingolipid biosynthesis - ganglio series	0.08^{b}	0.13^{a}	0.08^{b}	0.14^{a}	0.063	<0.001	0.76	<0.001
Glycosphingolipid biosynthesis - globo series	0.18^{b}	0.24^{a}	0.19^{b}	0.26^{a}	0.159	<0.001	0.36	<0.001
Nitrotoluene degradation	$0.08^{a,b}$	0.06^{b}	0.10^{a}	$0.08^{a,b}$	0.047	0.008	0.02	0.01
Biosynthesis of ansamycins	$0.15^{a,b}$	0.14^{b}	$0.17^{a,b}$	0.18^{a}	0.129	<0.001	<0.001	0.64
Secondary bile acid biosynthesis	0.002	0.012	0.008	0.019	0.0009	<0.001	0.001	<0.001
Porphyrin and chlorophyll metabolism	1.73^{a}	1.43^{b}	1.60^{b}	1.34^{b}	1.206	0.007	0.22	0.001
Selenocompound metabolism	0.86	0.82	0.81	0.78	0.755	<0.001	<0.001	0.002
Ether lipid metabolism	0.002^{b}	0.001^{b}	$0.006^{a,b}$	0.009^{a}	0.0005	<0.001	<0.001	0.64
Various types of N-glycan biosynthesis	0.0022^{a}	$0.0009^{a,b}$	0.0005^{b}	$0.0013^{a,b}$	0.00025	0.001	0.04	0.69
1,2,1-Trichloro-2,2-bis(4-chlorophenyl)ethane (DDT) degradation	0.002^{a}	0.001^{b}	0.001^{b}	0.002^{a}	0.0002	0.002	0.04	0.69
Acetic acid (µmol/g digesta)	14.9^{b}	10.9^{c}	10.4^{c}	16.7^{a}	1.65	0.02	0.85	0.52
Propionic acid	5.5^{a}	1.8^{b}	4.1^{ab}	3.9^{ab}	0.83	0.005	0.28	0.01
Cecum								
P_*Proteobacteria*	3.79^{b}	$4.44^{a,b}$	7.50^{a}	$5.60^{a,b}$	2.832	0.009	0.003	0.95
G_*Bacteroides*	1.27^{b}	1.57^{b}	6.77^{a}	1.58^{b}	0.715	<0.001	0.006	0.04
G_*Flavonifractor*	0.09^{b}	$0.23^{a,b}$	0.34^{a}	0.10^{b}	0.052	0.002	0.27	0.66
Fructose and mannose metabolism	1.72^{b}	1.79^{b}	2.20^{a}	1.74^{b}	1.607	<0.001	0.002	0.006
Folate biosynthesis	0.57^{b}	0.61^{b}	0.67^{a}	0.56^{b}	0.533	<0.001	0.17	0.11
D-alanine metabolism	0.29^{a}	0.28^{a}	0.27^{b}	0.29^{a}	0.251	<0.001	<0.001	0.009
Phenylalanine, tyrosine and tryptophan biosynthesis	$1.29^{a,b}$	$1.36^{a,b}$	1.41^{a}	1.22^{b}	1.150	0.005	0.83	0.14
Streptomycin biosynthesis	$0.43^{a,b}$	$0.45^{a,b}$	0.49^{a}	0.40^{b}	0.373	0.004	0.86	0.08
Galactose metabolism	0.83^{b}	$0.89^{a,b}$	1.10^{a}	$0.82^{a,b}$	0.732	<0.001	0.07	0.05
N-glycan biosynthesis	0.028^{b}	$0.034^{a,b}$	0.041^{a}	0.028^{b}	0.0241	0.001	0.25	0.20

Sow treatment	**Control**[2]		**FMTp**[3]		**S.E.M.**	**P-value**		
Offspring treatment	**Control**[4]	**Inulin**[5]	**Control**	**Inulin**		**Interaction**	**Sow**	**Offspring**
Butyric acid (µmol/g digesta)	9.5^{a}	9.8^{a}	6.9^{b}	1.5^{c}	1.02	<0.001	<0.001	0.01
Valeric acid (µmol/g digesta)	6.1^{b}	8.9^{a}	6.6^{b}	4.7^{c}	0.92	0.01	0.04	0.89
Isovaleric acid (µmol/g digesta)	2.4^{b}	2.9^{b}	5.3^{a}	1.4^{c}	0.54	<0.001	0.83	0.003
Colon								
P_*Lentisphaerae*	$0.18^{a,b}$	0.42^{a}	0.25^{a}	0.06^{b}	0.028	0.005	0.15	0.51
Steroid hormone biosynthesis	0.04^{b}	$0.05^{a,b}$	0.09^{a}	$0.05^{a,b}$	0.029	0.007	0.04	0.09
Retinol metabolism	0.027^{b}	$0.037^{a,b}$	0.047^{a}	$0.029^{a,b}$	0.0213	0.003	0.47	0.15
Glycine, serine and threonine metabolism	1.91^{a}	$1.88^{a,b}$	1.83^{b}	1.92^{a}	1.794	0.003	0.17	0.09
Glycosphingolipid biosynthesis-lacto and neolacto series	0.0005^{b}	$0.0008^{a,b}$	0.0011^{a}	0.0003^{c}	0.00029	<0.001	0.49	0.08
Isobutyric acid (µmol/g digesta)	4.4^{b}	3.9^{b}	13.6^{a}	6.5^{b}	2.14	0.02	0.01	0.15

[1] Least square means and pooled standard error of the mean are presented. Sows: [2] Control (n=11) and [3] FMT procedure (FMTP; n=11); Piglets: [4] Control (n=16), [5] Inulin (n=16) for the first 6 weeks post-weaning. P_ indicates phylum; G_ indicates genus, [6] Also reflects relative abundance at phylum level (i.e. *Chlamydiae*). Compositional and predicted functional differences are depicted as median relative abundance values. [7] RFI: residual feed intake measured between day 35 and 140 of age.

[a,b,c] Within each row, values that do not share a common superscript are significantly different ($P \leq 0.05$).

Table S2. Effect of fecal microbiota transplantation (FMT) in sows and/or dietary supplementation of offspring with inulin for 42 days post-weaning on number of operational taxonomic units in the offspring feces and digesta

Timepoint/ intestinal site	**Control sow**		**FMTp sow**		**Control sow**	**FMTp sow**	**Control offspring**	**Inulin offspring**
	Control offspring	**Inulin offspring**	**Control offspring**	**Inulin offspring**				
Day 28 (Weaning)	301	294	346	304	406	440	448	410
Day 50	148	180	221	148	226	266	266	232
Day 65	29	23	20	32	42	47	45	44
Day 100	387	302	337	336	438	417	446	400
Day 130	335	375	297	358	460	431	421	467
Ileum	43	27	31	36	44	45	48	38
Cecum	165	129	229	179	217	275	275	220
Colon	227	230	247	194	321	322	336	304

Table S3. Composition and chemical analysis of all diets used in the study (on an as-fed basis; g/Kg)

Diet Type	Starter		Link		Weaner		Finisher	Sow	
	Control	Inulin	Control	Inulin	Control	Inulin		Pregnant	Lactation
Barley	0.0	0.0	0.0	0.0	24.8	25.3	38.5	89.7	34.9
Wheat	22.2	19.1	39.9	36.9	43.1	36.9	40.4	0.0	43.2
Maize	8.0	8.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Soya	16.9	19.7	22.9	24.7	20.0	21.4	17.5	7.0	15.0
Full fat soya	10.0	7.0	7.0	5.0	5.0	5.0	0.0	0.0	0.0
Inulin	0.0	2.0	0.0	2.0	0.0	3.0	0.0	0.0	0.0
Lactofeed 70[1]	20.0	20.0	20.0	20.0	0.0	0.0	0.0	0.0	0.0
Skim milk powder	12.5	12.5	5.0	5.0	0.0	0.0	0.0	0.0	0.0
Soya oil	7.5	8.8	2.5	3.6	4.0	5.3	10.0	10.0	40.0
Lysine HCl (78.8)	0.5	0.4	0.4	0.4	0.5	0.43	4.0	1.0	3.5
DL-Methionine	0.3	0.4	0.2	0.3	0.2	0.2	1.0	1.0	1.0
L-Threonine (98)	0.2	0.2	0.2	0.02	0.2	0.2	1.5	0.0	1.0
L-Tryptophan	0.09	0.09	0.05	0.06	0.02	0.02	0.0	0.0	0.0
Vitamin and mineral mix	0.3	0.3	0.3	0.3	0.3	0.3	1.0	1.5	1.5
Natuphos 5000 FTU/g[5]	0.01	0.01	0.01	0.01	0.01	0.01	0.1	0.1	0.1

Diet Type	Starter		Link		Weaner		Finisher	Sow	
	Control	Inulin	Control	Inulin	Control	Inulin		Pregnant	Lactation
Salt feed grade	0.3	0.3	0.3	0.3	0.3	0.3	3.0	4.0	4.0
Dicalcium phosphate	0.1	0.1	0.1	0.1	0.6	0.6	2.0	5.0	5.0
Limestone flour	1.1	1.1	1.1	1.1	0.9	0.9	13.0	11.0	12.0
Chemical analysis (g/Kg DM)									
Crude protein	235.9	252.8	211.0	205.4	195.7	172.1	161	119	148
Crude fibre	19.8	23.4	34.8	37.5	38.9	31.7	24	32	25
Crude ash	66.2	63.5	48.3	45.4	44.6	49.8	41	37	41
Ether extract	114.7	57.9	70.7	27.2	33.2	63.4	27	29	63
DE MJ/kg[6]	17.9	17.0	16.9	16.0	15.9	16.3	16.3	15.6	16.8
NE (IFIP)[7]	11.43	10.25	10.55	9.78	9.50	10.45	9.8	9.5	10.5
Amino acids (g/Kg)									
Lysine	16.2	15.0	13.0	11.1	6.4	9.9	11.50	6.50	9.90
Methionine	6.8	5.7	4.5	3.6	2.1	3.4	3.70	2.00	3.40
Meth + Cyst	9.7	9.0	7.9	6.8	4.7	6.4	7.40	5.00	6.80
Threonine	10.5	9.8	8.7	7.5	4.5	6.5	7.90	4.60	6.70
Tryptophan	3.6	3.3	2.6	2.2	1.6	2.0	1.50	1.20	1.40

[1] Lactofeed 70 contains 70% lactose, 11.5% protein, 0.5% oil, 7.5% ash and 0.5% fibre (Volac, Cambridge, UK).

[2] Premix provided per Kg of complete diet: Copper sulphate $7H_2O$, 62 g; Ferrous sulphate monohydrate, 450 g; Manganese oxide, 60 g; Zinc oxide, 150 g; Potassium iodate, 1 g; Sodium selenite, 0.6 g; Cu, 155 mg; Fe, 90 mg; Mn, 47 mg; Zn, 120 mg, I, 0.6 mg; Se, 0.3 mg; vitamin A, 6000 IU; vitamin $D_{3,}$ 1000 IU; vitamin E, 100 IU; vitamin K, 4 mg; vitamin $B_{12,}$ 15 µg; riboflavin, 2 mg; nicotinic acid, 12 mg; pantothenic acid, 10 mg; choline chloride, 250 mg; vitamin $B_{1,}$ 2 mg; vitamin $B_{6,}$ 3 mg; Endox, 60 g.

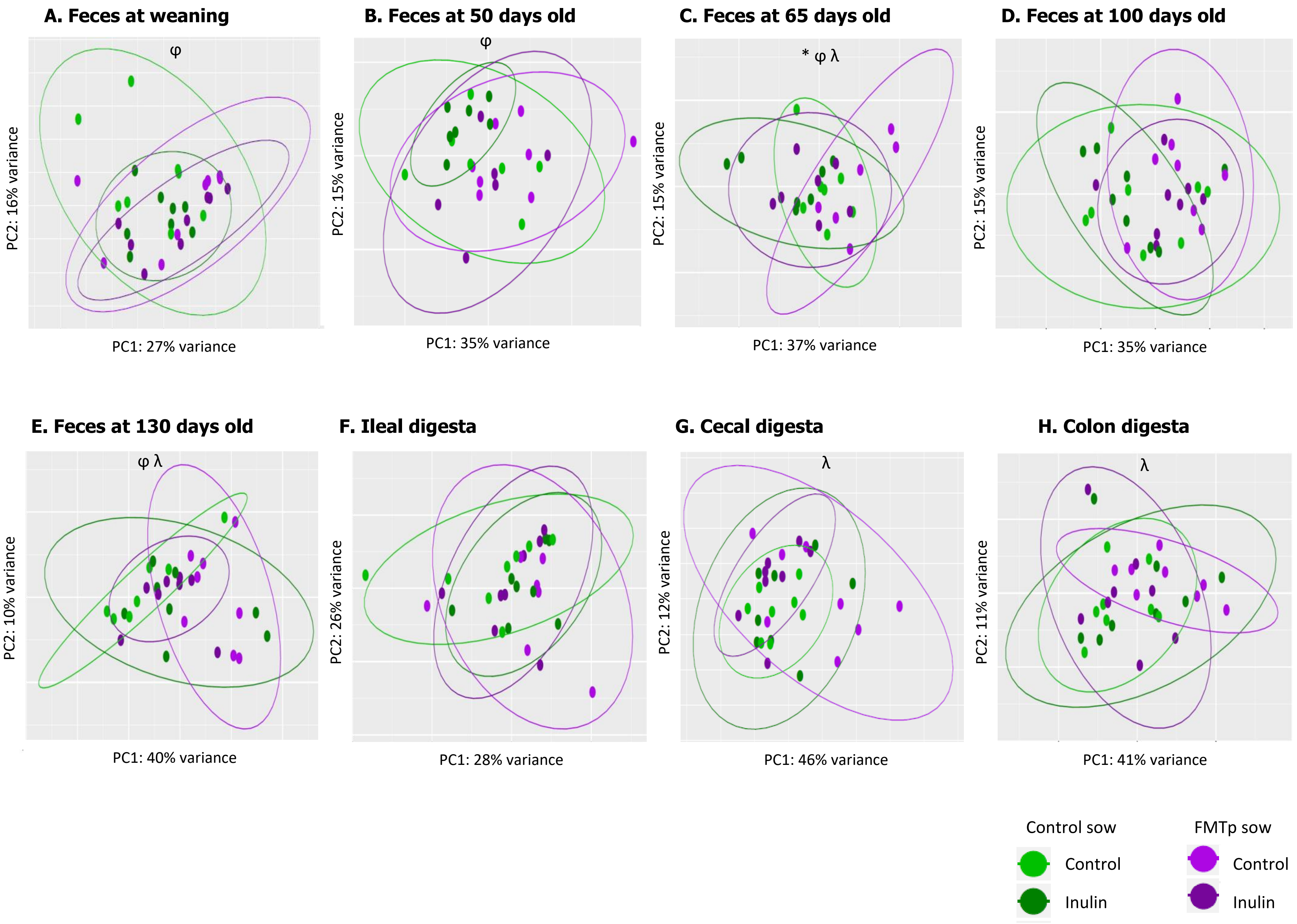
[3] Premix provided per Kg of complete diet: Copper sulphate $7H_2O$, 60 g; Ferrous sulphate monohydrate, 120 g; Manganese oxide, 40 g; Zinc oxide, 100 g; Potassium iodate, 0.5 g; Sodium selenite, 0.4 g; Cu, 15 mg; Fe, 24 mg; Mn, 31 mg; Zn, 80 mg, I, 0.3 mg; Se, 0.2 mg; vitamin A, 2000 IU; vitamin $D_{3,}$ 500 IU; vitamin E, 40 IU; vitamin K, 4 mg; vitamin $B_{12,}$ 15 µg; riboflavin, 2 mg; nicotinic acid, 12 mg; pantothenic acid, 10 mg; vitamin $B_{1,}$ 2 mg; vitamin $B_{6,}$ 3 mg.

[4] Premix provided per Kg of complete diet: Copper sulphate $7H_2O$, 60 g; Ferrous sulphate monohydrate, 200 g; Manganese oxide, 80 g; Zinc oxide, 100 g; Potassium iodate, 1 g; Sodium selenite, 0.4 g; Cu, 15 mg; Fe, 70 mg; Mn, 62 mg; Zn, 80 mg, I, 0.6 mg; Se, 0.2 mg; vitamin A, 1000 IU; vitamin $D_{3,}$ 1000 IU; vitamin E, 100 IU; vitamin K, 2 mg; vitamin $B_{12,}$ 15 µg; riboflavin, 5 mg; nicotinic acid, 12 mg; pantothenic acid, 10 mg; choline chloride, 500 mg; Biotin, 200 mg; Folic acid, 5 g; vitamin $B_{1,}$ 2 mg; vitamin $B_{6,}$ 3 mg.

[5] Phytase: Natuphos – BASF; 5000 FTU/gm equal to 500 FTU per Kg finished feed.

[6] Digestible energy is megajoules per kilogram of dry matter (DE= 4168-9.1*ASH +1.9*CP+3.9*EE-3.6*NDF)

[7] Calculated values


A. Feces at weaning

B. Feces at 50 days old

C. Feces at 65 days old

D. Feces at 100 days old

E. Feces at 130 days old

F. Ileal digesta

G. Cecal digesta

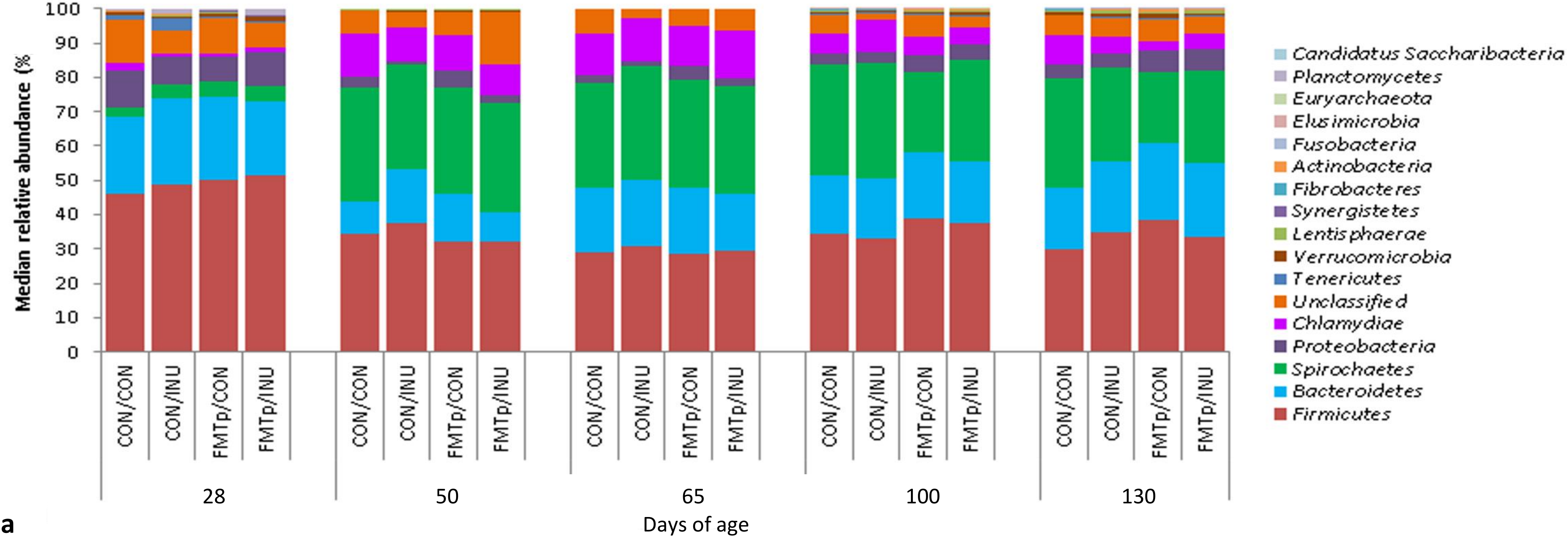
H. Colon digesta

Fig S1. Microbial diversity variation due to fecal microbiota transplantation (FMT) in sows and/or dietary supplementation of offspring with inulin for 42 days post-weaning in the offspring feces at A. 28, B. 50, C. 65, D. 100 and E. 130 days of age and in the offspring F. ileum, G. cecum and H. colon, represented by principal component analyses (PCA; genus-level).

The amount of variance is depicted by the percentages on each axis. *Indicates significant differences at sow x offspring treatment level ($P\leq0.05$); φ indicates sow treatment effect ($P\leq0.05$); λ indicates offspring treatment effect ($P\leq0.05$).

Data from 32 pigs: Sow treatment level control n=16; FMT procedure (FMTp) n=16; Offspring treatment level control n=16; Inulin n=16

A. Feces



B. Digesta

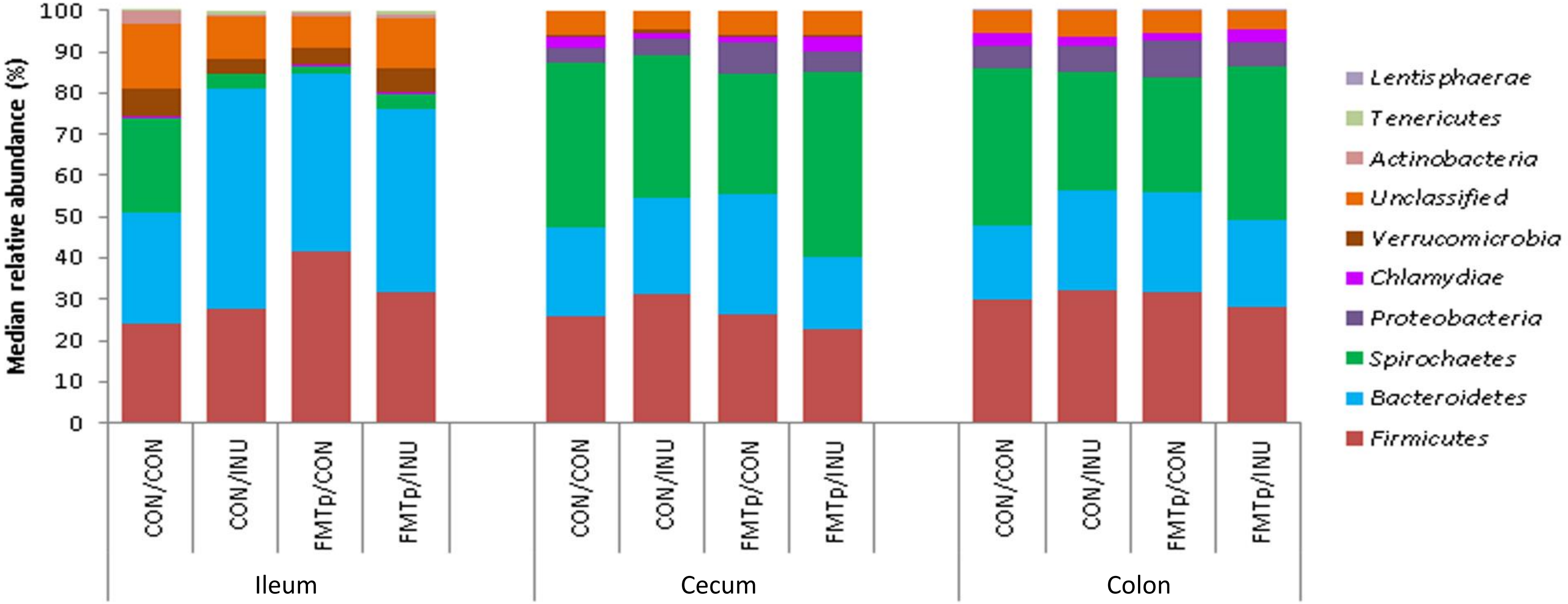


Fig S2. Effect of fecal microbiota transplantation (FMT) in sows and/or dietary supplementation of offspring with inulin for 42 days post-weaning on microbial composition at the phylum level in offspring in A. feces at 28, 50, 65, 100 and 130 days of age, and B. digesta from ileum, cecum and colon

Data from 32 pigs: Sow treatment level: control (CON) n=16; FMT procedure (FMTp) n=16; Offspring treatment level: Control (CON) n=16; Inulin (INU) n=16.

Bars represent mean relative abundance of phyla detected for each of the treatments.

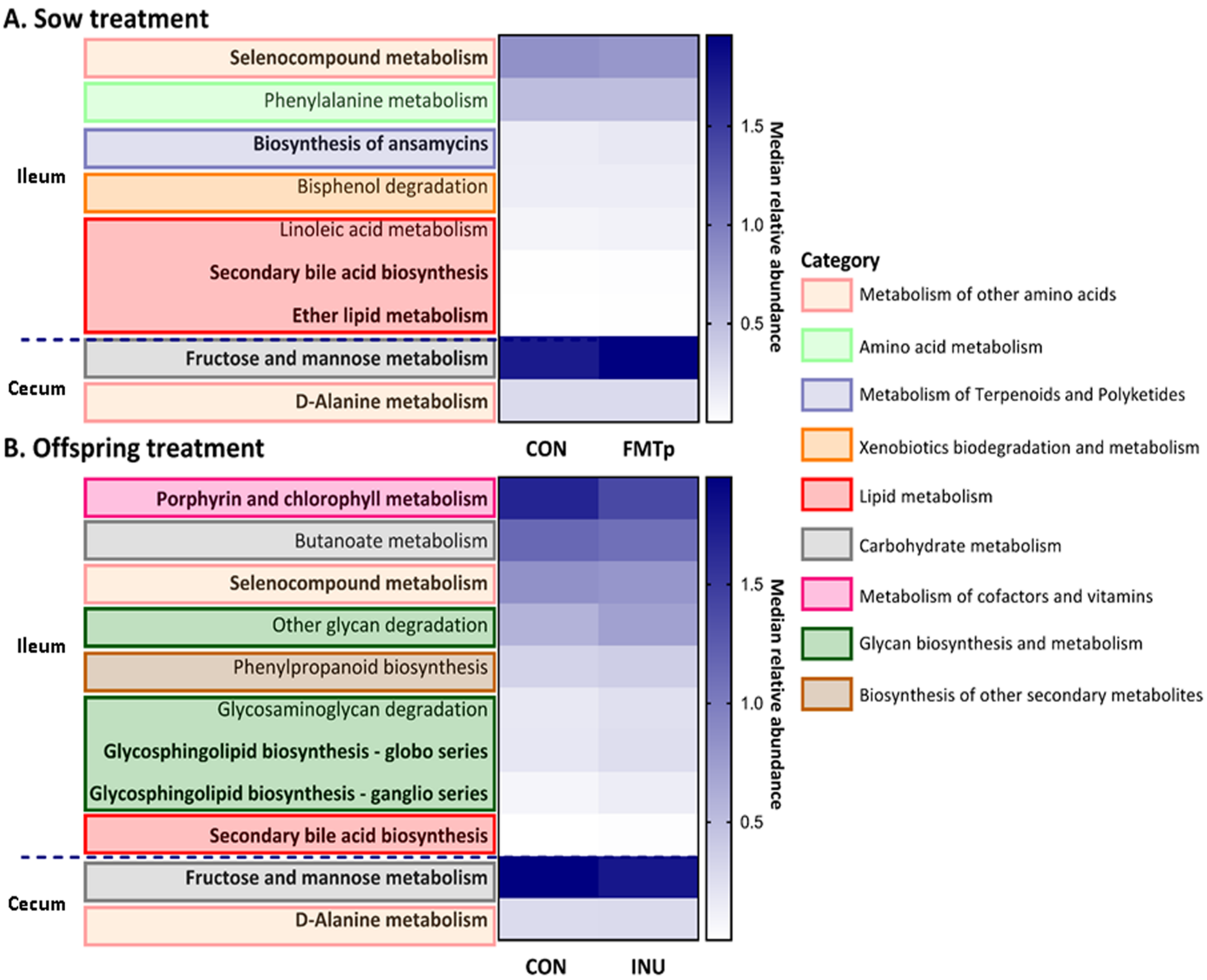

A. Sow treatment
Ileum
Selenocompound metabolism
Phenylalanine metabolism
Biosynthesis of ansamycins
Bisphenol degradation
Linoleic acid metabolism
Secondary bile acid biosynthesis
Ether lipid metabolism
Cecum
Fructose and mannose metabolism
D-Alanine metabolism
CON
FMTp
1.5
1.0
0.5
Median relative abundance
B. Offspring treatment
Ileum
Porphyrin and chlorophyll metabolism
Butanoate metabolism
Selenocompound metabolism
Other glycan degradation
Phenylpropanoid biosynthesis
Glycosaminoglycan degradation
Glycosphingolipid biosynthesis - globo series
Glycosphingolipid biosynthesis - ganglio series
Secondary bile acid biosynthesis
Cecum
Fructose and mannose metabolism
D-Alanine metabolism
CON
INU
1.5
1.0
0.5
Median relative abundance
Category
Metabolism of other amino acids
Amino acid metabolism
Metabolism of Terpenoids and Polyketides
Xenobiotics biodegradation and metabolism
Lipid metabolism
Carbohydrate metabolism
Metabolism of cofactors and vitamins
Glycan biosynthesis and metabolism
Biosynthesis of other secondary metabolites

Fig. S3. Effect of fecal microbiota transplantation (FMT) in sows and/or dietary supplementation of offspring with inulin for 42 days post-weaning on predicted functional pathways for offspring fecal and intestinal microbiota at A. sow and B. offspring treatment level

Data from 32 pigs: Sow treatment level: control (CON) n=16; FMT procedure (FMTp) n=16; Offspring treatment level: Control (CON) n=16; Inulin (INU) n=16.

Pathways are from the KEGG database and level 3 pathways are presented. Median relative abundance for pathways differing between offspring, due to a sow or offspring treatment effect are represented in the heat maps.

Predicted bacterial pathways in bold depict those also affected by a sow x offspring treatment interaction. Additional sow treatment x offspring treatment interactions not shown in either panel A or B are shown in Table S1.

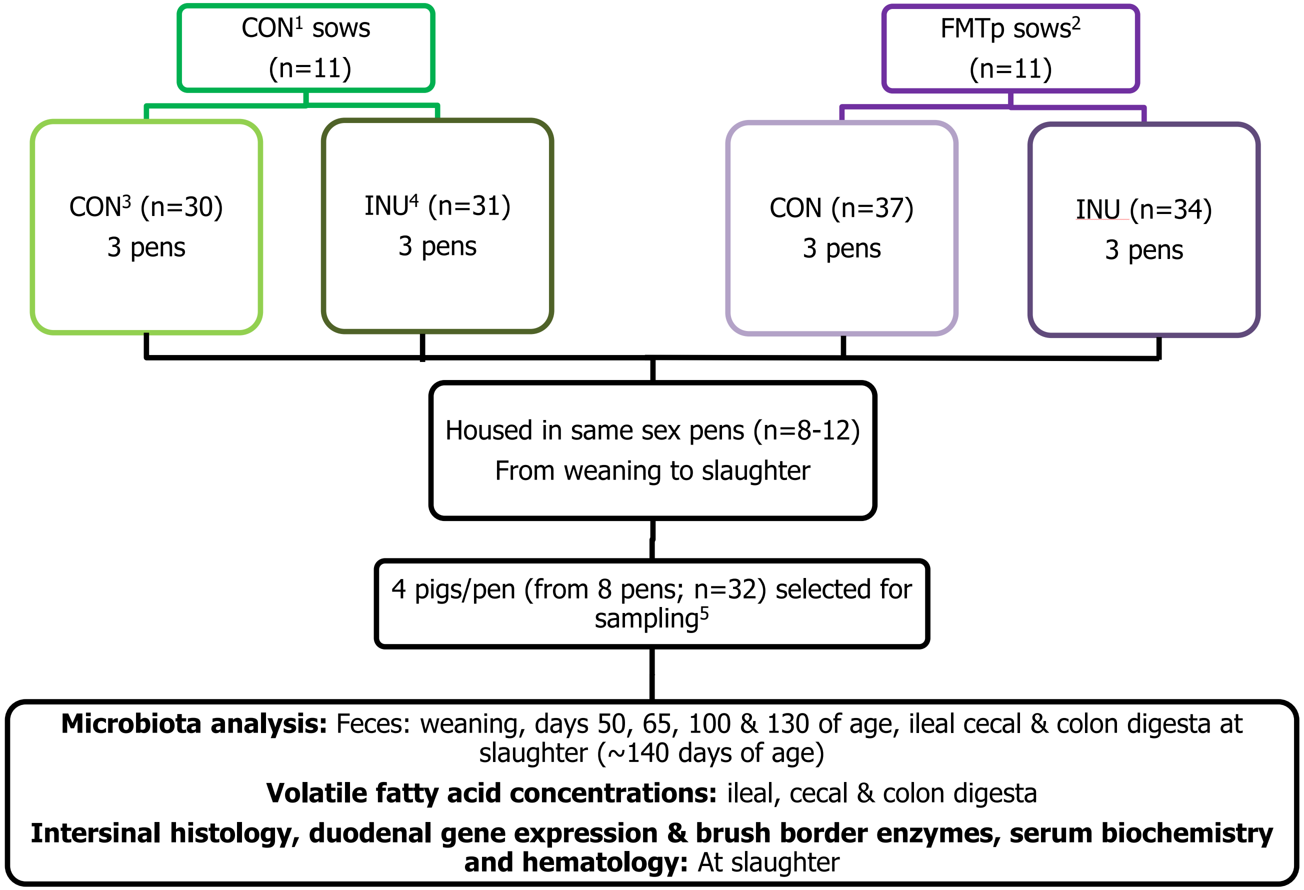

CON¹ sows (n=11)
FMTp sows² (n=11)
CON³ (n=30) 3 pens
INU⁴ (n=31) 3 pens
CON (n=37) 3 pens
INU (n=34) 3 pens
Housed in same sex pens (n=8-12) From weaning to slaughter
4 pigs/pen (from 8 pens; n=32) selected for sampling⁵
Microbiota analysis: Feces: weaning, days 50, 65, 100 & 130 of age, ileal cecal & colon digesta at slaughter (~140 days of age)
Volatile fatty acid concentrations: ileal, cecal & colon digesta
Intersinal histology, duodenal gene expression & brush border enzymes, serum biochemistry and hematology: At slaughter

Fig S4. Schematic depicting sow treatments, offspring treatments and sample collection.

Sows: [1]CON: control; [2]Fecal microbiota transplantation procedure (FMTp), and were given a 1-week course of antibiotics from day 60 of gestation to kill off as much of the resident microbiota as possible, followed by a purgative and fasting for 36 h to empty the gastrointestinal tract. On days 70 and 100 of gestation, each sow was given 200 mL of thawed inoculum via gastric intubation as well as an anti-acid to prevent inactivation of the inoculum by gastric acid.

Piglets: [3]CON: control or [4]INU: inulin for the first 6 weeks post-weaning (2% for the first 3 weeks, and 3% for the next 3 weeks). Thereafter, all pigs were fed the same finisher diet until slaughter at 140 days of age.

[5]32 pigs selected; Sow treatment level: CON: n=16; FMTp: n=16; Pig treatment level: CON: n=16; INU: n=16.