

Fecal microbiota transplantation from warthog to pig confirms the influence of the gut microbiota on African swine fever susceptibility

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Supplementary Table S1. Number of sequences per sample obtained after filtering used for this study.

Sample ID (#animal_dpft)	Sequence Count
13D15	1,425
1D15	39,774
3D15	34,841
4D15	11,643
6D15	48,778
9D15	62,010
16D15	44,153
18D15	51,097
22D15	55,039
24D15	23,711
25D15	26,415
28D15	30,556
29D15	43,867
30D15	36,541
36D15	27,450
37D15	23,849
41D15	53,813
43D15	67,027
44D15	29,913
46D15	19,050

Sample ID (pools)	Sequence Count
pWF	81,614
pPF	53,689

Sample ID (#animal_dpft)	Sequence Count
13D0	47,310
16D0	50,364
18D0	24,635
22D0	39,719
24D0	45,343
37D0	38,801
41D0	46,035
43D0	43,323
44D0	30,032
46D0	38,076

Supplementary Table S1. Number of sequences per sample obtained after filtering used for this study (cont.).

Sample ID (#animal_dpft)	Sequence Count
13D8	25,989
16D8	44,081
18D8	32,428
22D8	40,595
24D8	15,640
37D8	19,232
41D8	38168
43D8	16,850
44D8	10,054
46D8	26,878

Supplementary Table S2. Relative abundance (%) of taxa assigned at different levels (Phyla, Family and Genera) for each animal sample and mean relative abundance (%) for each group of animals.

Kingdom	Phyla	PF_15.dppt							WF_15.dppt							AMF_15.dppt							PBS_15.dppt						
		16	18	22	24	AVERAGE	25	28	29	30	36	AVERAGE	37	41	43	44	46	AVERAGE	1	3	4	9	11	AVERAGE					
Bacteria	Actinobacteria	0.000	0.149	0.220	0.169	0.134	0.000	0.000	0.217	0.000	0.204	0.084	0.117	0.000	0.179	0.057	0.037	0.078	0.000	0.000	0.000	0.000	0.000	0.103					
Bacteria	Bacteroidetes	18.590	17.825	24.712	29.147	22.568	26.163	15.038	30.996	17.952	21.322	22.294	26.399	15.649	20.486	41.484	29.291	26.662	16.138	12.282	12.282	19.267	14.780	16.570					
Bacteria	Chloroflexi	0.000	0.168	0.000	0.000	0.000	0.000	0.383	0.000	0.000	0.531	0.181	0.583	0.106	0.704	0.704	1.475	0.503	0.000	0.000	0.000	0.000	0.116						
Bacteria	Cyanobacteria	0.283	0.618	0.325	0.198	0.358	0.000	0.000	0.532	0.501	0.197	0.274	0.021	0.136	0.275	0.000	0.016	0.106	0.000	0.000	0.000	0.000	0.000	0.067					
Bacteria	Deltaproteobacteria	0.116	0.061	0.000	0.017	0.048	0.029	0.000	0.000	0.000	0.342	0.094	0.109	0.098	0.136	0.097	0.000	0.088	0.000	0.000	0.000	0.000	0.000	0.284					
Bacteria	Eusimicrobia	0.000	0.029	0.000	0.000	0.019	0.011	0.000	0.000	0.000	0.120	0.041	0.000	0.000	0.000	0.007	0.315	0.064	0.000	0.000	0.000	0.000	0.000	0.063					
Archaea	Euryarchaeota	0.000	0.000	0.124	0.257	0.095	0.000	0.000	0.000	0.000	0.058	0.012	0.294	0.000	0.069	0.057	0.278	0.139	0.000	0.000	0.000	0.000	0.000	0.007					
Bacteria	Firmicutes	69.123	70.624	55.619	50.673	61.510	61.064	83.178	60.932	49.646	63.333	63.631	52.891	70.446	66.267	48.130	54.908	58.528	65.309	76.226	76.226	52.015	57.191	64.754					
Bacteria	Fusobacteria	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000					
Bacteria	Lentisphaerae	0.358	0.131	0.104	0.000	0.148	1.049	0.000	0.506	0.213	0.244	0.402	0.084	0.210	0.149	0.000	0.110	0.111	0.000	0.000	0.000	0.000	0.000	0.147					
Bacteria	OD1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000					
Bacteria	Planctomycetes	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000					
Bacteria	Proteobacteria	1.649	0.742	2.353	1.101	1.461	0.216	0.507	1.040	2.230	2.200	1.239	3.489	0.433	1.599	1.464	0.766	1.550	0.832	0.000	0.000	0.000	0.000	0.000					
Bacteria	Spirochaetes	1.619	0.613	1.446	2.029	1.427	0.541	0.000	0.513	0.364	0.066	0.297	2.252	1.646	1.513	1.936	2.835	2.036	0.000	0.000	0.000	0.000	0.000	0.000					
Bacteria	Synergistetes	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000					
Bacteria	Tenericutes	0.000	0.086	0.233	1.485	0.451	0.053	0.000	0.000	0.000	0.109	0.032	1.413	0.299	0.179	0.114	0.115	0.424	0.000	0.000	0.000	0.000	0.000	0.000					
Bacteria	TM7	0.231	0.646	0.603	0.789	0.567	0.000	0.000	0.000	0.000	0.761	0.152	1.135	0.983	0.315	0.528	0.667	0.526	0.644	0.373	0.000	0.000	0.000	0.036					
Bacteria	Unclassified	7.698	7.910	13.470	13.466	10.636	10.774	0.772	4.938	28.965	10.226	11.135	11.497	8.375	8.153	5.770	8.934	8.546	12.222	11.492	11.492	22.112	25.472	15.823					
Bacteria	Unclassified	0.152	0.110	0.420	0.333	0.254	0.000	0.000	0.210	0.057	0.295	0.112	0.021	0.544	0.136	0.154	0.000	0.171	0.181	0.772	0.000	0.139	0.077	0.234					
Bacteria	Verrucomicrobia	0.181	0.258	0.342	0.236	0.254	0.000	0.000	0.000	0.000	0.000	0.000	0.692	0.795	0.336	0.000	0.000	0.365	0.000	0.000	0.000	0.000	0.034	0.014					

Supplementary Table S3. Crypt depth and villi height in ileum and colon after FMT

Crypt depth and villi height in ileum by group (μm)								
	PBS group		PF group		WF group		AWF group	
	mean	SEM	mean	SEM	mean	SEM	mean	SEM
Villi Height	344.250	17.115	334.333	10.793	336.200	8.861	334.333	12.426
Crypt Depth	217.750	7.574	221.667	12.309	223.400	7.807	224.000	10.368
V/C	1.649	0.111	1.662	0.111	1.603	0.073	1.580	0.087

V/C: Villi height/Crypt Depth ratio

Crypt depth in colon by group (μm)								
	PBS group*		PF group *		WF group		AWF group	
	mean	SEM	mean	SEM	mean	SEM	mean	SEM
Crypt Depth	495	7.425	466.000	14.016	489.000	6.222	474.667	13.128

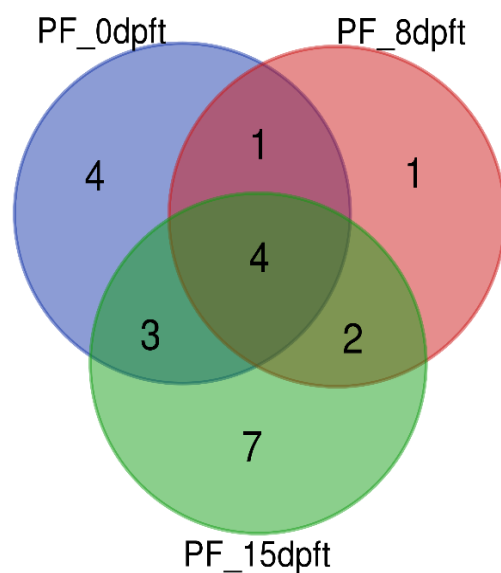
* *P* value (0.01-0.05)

Supplementary Table S4. Score for clinical signs recorded throughout the study

Score	Body condition		Behavior	Digestive signs	Respiratory signs	Other signs
	Vertebra	Ribs	Signs	Signs	Signs	Dermatitis, testicular tummeffaction, lameness
0	Non visible	Non visible	Active, alert, plays	Perianal skin clean	Non apparent	Non apparent
1	Visible in the dorsum	Non visible	Sadness, quite	Perianal skin dirty	Mild dispnea	Mild
2	Prominent	Visible	Mild depression, alert	Hind limbs dirty	Evident dyspnea	Moderate
3	Very marked	Individually	Depression, stillness, postration	Red/blotchy skin lesions in the back	panting, difficult breathing	Severe

Supplementary Table S5. Core taxa list from different sampling times in PF and AWF groups and Venn diagrams representing the shared taxa.

Groups	total	family	Genera
PF_0dpft PF_8 dpft PF_15dpft	4	<i>Ruminococcaceae</i>	<i>Clostridium</i>
		<i>Prevotellaceae</i>	<i>Prevotella</i>
		<i>Ruminococcaceae</i>	<i>Sporobacter</i>
		<i>Ruminococcaceae</i>	<i>Papillibacter</i>
PF_0dpft PF_8dpft	1	[<i>Barnesiellaceae</i>]	<i>Barnesiella</i>
PF_0dpft PF_15dpft	3	<i>Veillonellaceae</i>	<i>Succinispira</i>
		<i>Clostridiaceae</i>	<i>Clostridium</i>
		<i>Ruminococcaceae</i>	<i>Butyricoccus</i>
PF_15dpft PF_8dpft	2	<i>Erysipelotrichaceae</i>	<i>gut</i>
		<i>Paraprevotellaceae</i>	<i>Paraprevotella</i>
PF_0dpft	4	<i>Desulfovibrionaceae</i>	<i>Desulfovibrio</i>
		<i>Ruminococcaceae</i>	<i>Bacteroides</i>
		<i>Lachnospiraceae</i>	<i>Roseburia</i>
		<i>Lachnospiraceae</i>	<i>Ruminococcus</i>
PF_8dpft	1	<i>Erysipelotrichaceae</i>	<i>Anaerorhabdus</i>
PF_15dpft	7	<i>Spirochaetaceae</i>	<i>Treponema</i>
		<i>Ruminococcaceae</i>	<i>Faecalibacterium</i>
		<i>Veillonellaceae</i>	<i>Selenomonas</i>
		<i>Pasteurellaceae</i>	<i>Actinobacillus</i>
		<i>Lachnospiraceae</i>	<i>Clostridium</i>
		<i>Campylobacteraceae</i>	<i>Campylobacter</i>
		<i>Erysipelotrichaceae</i>	<i>Asteroleplasma</i>



Supplementary Table S5. Core taxa list from different sampling times in PF and AWF groups and Venn diagrams representing the shared taxa (cont.).

Groups	total	Family	Genera
AWF_0 dpft AWF_8 dpft AWF_15 dpft	6	<i>Ruminococcaceae</i>	<i>Clostridium</i>
		<i>Prevotellaceae</i>	<i>Prevotella</i>
		<i>[Barnesiellaceae]</i>	<i>Barnesiella</i>
		<i>Erysipelotrichaceae</i>	<i>gut</i>
		<i>Ruminococcaceae</i>	<i>Sporobacter</i>
		<i>Paraprevotellaceae</i>	<i>Paraprevotella</i>
AWF_0 dpft AWF_8 dpft	1	<i>Veillonellaceae</i>	<i>Succinispira</i>
AWF_0 dpft AWF_15 dpft	3	<i>Erysipelotrichaceae</i>	<i>Anaerorhabdus</i>
		<i>Clostridiaceae</i>	<i>Clostridium</i>
		<i>Ruminococcaceae</i>	<i>Papillibacter</i>
AWF_8 dpft AWF_15 dpft	2	<i>Ruminococcaceae</i>	<i>Faecalibacterium</i>
		<i>Erysipelotrichaceae</i>	<i>Asteroleplasma</i>
AWF_0dpft	3	<i>Peptostreptococcaceae</i>	<i>Clostridium</i>
		<i>Ruminococcaceae</i>	<i>Butyricoccus</i>
		<i>Lachnospiraceae</i>	<i>Defluviitalea</i>
AWF_8dpft	2	<i>Ruminococcaceae</i>	<i>Gemmiger</i>
		<i>Lachnospiraceae</i>	<i>Clostridium</i>
AWF_15dpft	4	<i>Desulfovibrionaceae</i>	<i>Desulfovibrio</i>
		<i>Spirochaetaceae</i>	<i>Treponema</i>
		<i>Veillonellaceae</i>	<i>Selenomonas</i>
		<i>Lachnospiraceae</i>	<i>Roseburia</i>



Supplementary Table S6. Average haematology parameters in pigs at 4 dpft and 15 dpft.

	4 dpft				15 dpft				Reference
	PBS	PF	WF	AWF	PBS	PF	WF	AWF	
WBC (x10E3)	21.46	22.89	24.22	23.25	24.93*	31.8	34.12*	29.8	11.0 - 22.0
RBC (x10E6)	5.93	5.79	5.92	5.64	6.45	5.99	6.17	5.84	6.8 -12.9
LYM (x10E3)	7.9	7.6	7.88	8.98	9.58	9.71	10.36	10.75	4.3 - 13.0
% LYM	43.27	40.1	37.25	39.88	40.91	33.41	34.53	37	
MONO (x10E3)	0.73	0.84	0.98	0.88	1.09	1.22	0.95	0.92	0.2 - 2.2
% MONO	3.7	3.84	4.54	3.93	4.54	3.83	3.13	3.15	
EOS (x10E3)	0.7	0.28	0.36	0.31	0.5	0.59	0.6	0.51	0.05 - 2.4
% EOS	3.88	1.38	1.48	1.34	2.06	1.93	1.78	1.76	
NEU (x10E3)	11.91	13.93	14.84	12.82	13.52*	20.06	22.00*	17.38	3.1 - 10.5
%NEU	48.14	53.48	56	53.68	51.47	60	59.85	57.26	
BASO (x10E3)	0.04	0.05	0.04	0.05	0.07	0.06	0.06	0.05	
% BASO	0.22	0.22	0.19	0.21	0.28	0.21	0.21	0.17	

**P* value < 0.05

PBS: non-transplanted group; PF: pig feces group; WF: warthog feces group; AWF: antibiotic + warthog feces group.