

Supplementary Material

Table S1. Resistance profile of the pathogenic strains *Escherichia coli* O1/O18 and *Salmonella* serotype Enteritidis, tested with agar diffusion method. R = resistant, S = sensitive.

Antibiotics	Concentration	<i>E. coli</i> O1/O18	<i>S. Enteritidis</i>
Amoxicillin	25 µg	R	S
Ampicillin	25 µg	R	S
Bacitracin	10 units	R	R
Cefacetril	30 µg	S	S
Cefalexin	30 µg	S	S
Chloramphenicol	30 µg	S	S
Ciprofloxacin	5 µg	S	S
Clindamycin	10 µg	R	R
Doxycyclin	30 µg	S	S
Erythromycin	30 µg	S	S
Framycetin	100 µg	S	S
Fusidinsäure	10 µg	R	R
Gentamycin	30 µg	S	S
Kanamycin	30 µg	S	S
Lincomycin	15 µg	R	R
Metronidazol	5 µg	R	R
Ofloxacin	5 µg	S	S
Oxacillin	5 µg	R	R
Rifampicin	30 µg	S	S
Streptomycin	25 µg	R	S
Sulfamethoxazol	25 µg	R	R
Sulfamethoxazol/Trim.	25 µg	R	S
Tetracyclin	30 µg	S	S
Trimethoprim	5 µg	R	S
Vancomycin	5 µg	R	R
Tylosin	30 µg	R	R
Marbofloxacin	5 µg	S	S
Piperacillin	75 µg	S	S

Cefotaxime	5 µg	S	S
Amoxicillin	25 µg	R	S
Ampicillin	25 µg	R	R
Bacitracin	10 units	R	S
Cefacetril	30 µg	S	S
Cefalexin	30 µg	S	R
Chloramphenicol	30 µg	S	S
Ciprofloxacin	5 µg	S	S
Nystatin	100 units	R	
Colistin	25 µg		S

Table S2. Relative abundance of the most dominant bacterial genera in caecal samples of 25-week-old broiler breeders in different flocks (n = 5).

Genus	Broiler breeder flock			SEM	p-value*
	A	B	C		
<i>Bacteroides</i>	17.41	17.21	17.44	2.62	0.966
<i>Lactobacillus</i>	14.4	17.64	12.00	2.51	0.765
Unknown <i>Lachnospiraceae</i>	12.53	12.81	14.94	1.93	0.753
<i>Streptococcus</i>	7.53	12.96	1.94	2.90	0.236
<i>Rikenellaceae RC9 gut group</i>	6.00	2.96	2.12	0.73	0.071
<i>Blautia</i>	5.02	5.20	5.43	0.35	0.954
<i>Subdoligranulum</i>	4.14	8.30	7.52	1.34	0.212
Unknown <i>Bacteroidales</i>	3.07 ^b	4.19 ^b	0.44 ^a	0.86	0.035
<i>Lachnoclostridium</i>	2.78	1.43	2.90	0.33	0.072
<i>Romboutsia</i>	2.58	0.92	1.82	0.39	0.207
<i>Ruminococcaceae UCG-014</i>	2.05 ^b	0.51 ^a	1.01 ^{a,b}	0.22	0.014
<i>Ruminococcaceae UCG-015</i>	1.99 ^b	0.71 ^a	1.87 ^b	0.23	0.036
<i>Turicibacter</i>	1.95 ^b	0.16 ^a	0.82 ^{a,b}	0.34	0.032
<i>Christensenellaceae R-7 group</i>	1.88 ^{a,b}	0.75 ^a	2.29 ^b	0.28	0.023
<i>Olsenella</i>	1.61	1.36	2.68	0.63	0.147
<i>Alistipes</i>	1.52	0.65	5.26	1.24	0.263
<i>Enorma</i>	1.30	2.08	2.85	0.49	0.183
<i>Collinsella</i>	0.87	1.09	2.99	0.51	0.41
<i>Parabacteroides</i>	0.67	0.29	2.26	0.44	0.467
<i>Fusicatenibacter</i>	0.54	0.72	3.32	0.59	0.08
<i>Ruminococcaceae UCG-008</i>	0.32	0.13	1.08	0.16	0.252

<i>Fournierella</i>	0.24	0.09	1.45	0.3	0.088
<i>Faecalibacterium</i>	0.24	1.33	0.54	0.31	0.24
<i>Bifidobacterium</i>	0.15	1.21	1.58	0.49	0.925

* = Kruskal-Wallis Test (significant differences are marked in bold, trends in italics)

a,b = different letters indicate significant differences within a row (Mann-Whitney Test)

Table S3. Relative abundance of the most dominant bacterial genera in caecal samples of 50-week-old broiler breeders in different flocks (n = 5).

Genus	Broiler breeder flock			SEM	p-value*
	A	B	C		
Unknown <i>Lachnospiraceae</i>	23.65	23.25	24.85	1.128	0.979
<i>Bacteroides</i>	18.9 ^b	12.14 ^b	1.58 ^a	2.553	0.012
<i>Lactobacillus</i>	8.58	8.12	1.33	2.395	0.147
<i>Subdoligranulum</i>	4.97	4.18	7.08	0.497	0.17
<i>Blautia</i>	4.61 ^{a,b}	6.34 ^b	1.91 ^a	0.58	0.02
<i>Akkermansia</i>	3.75	4.42	4.24	1.746	0.888
<i>Lachnoclostridium</i>	3.07	2.83	1.94	0.21	0.179
<i>Romboutsia</i>	2.64	1.54	1.47	0.431	0.463
<i>Turicibacter</i>	2.59	0.69	0.72	0.479	0.052
Unknown <i>Bacteroidales</i>	2.37	2.2	0.73	0.371	0.082
<i>Fusicatenibacter</i>	2.23	1.87	3.71	0.289	0.177
<i>Ruminococcaceae UCG-005</i>	2	2.38	2.75	0.321	0.579
<i>Christensenellaceae R-7 group</i>	1.74 ^a	1.44 ^a	7.03 ^b	0.731	0.027
<i>Streptococcus</i>	1.4	1.66	4.11	0.656	0.619
<i>Megamonas</i>	1.35	7.7	0.05	2.443	0.158
<i>Rikenellaceae RC9 gut group</i>	1.22	0.77	1.36	0.234	0.351
<i>Olsenella</i>	1.2	3.91	2.43	0.524	0.074
<i>Marvinbryantia</i>	1.14	0.87	1.3	0.149	0.437
<i>Prevotellaceae Ga6A1 group</i>	1.03	0.44	0.13	0.246	0.36
<i>Flavonifractor</i>	0.87	0.46	1.71	0.197	0.36
<i>Sellimonas</i>	0.82 ^{a,b}	1.42 ^b	0.29 ^a	0.126	0.001
<i>Enorma</i>	0.8	2.67	2.02	0.422	0.114
<i>Faecalibacterium</i>	0.63	2.08	1.39	0.284	0.168
<i>Collinsella</i>	0.56	n.d.	2.48	0.525	0.05
<i>Parabacteroides</i>	0.45	0.55	0.25	0.053	0.07
<i>Bifidobacterium</i>	0.41	8.09	1.12	1.603	0.053
<i>Fournierella</i>	0.34	0.13	1.35	0.367	0.585
<i>Alistipes</i>	0.23 ^b	2.06 ^b	0.06 ^a	0.445	0.044

<i>Unknown Eggerthellaceae</i>	0.22	0.15 ^a	1.13 ^b	0.113	0.035
<i>Tyzzerella</i>	0.21	0.54	3.12	0.452	<i>0.063</i>

* = Kruskal-Wallis Test (significant differences are marked in bold, trends in italics)

^{a,b} = different letters indicate significant differences within a row (Mann-Whitney Test)

n.d. = not detected

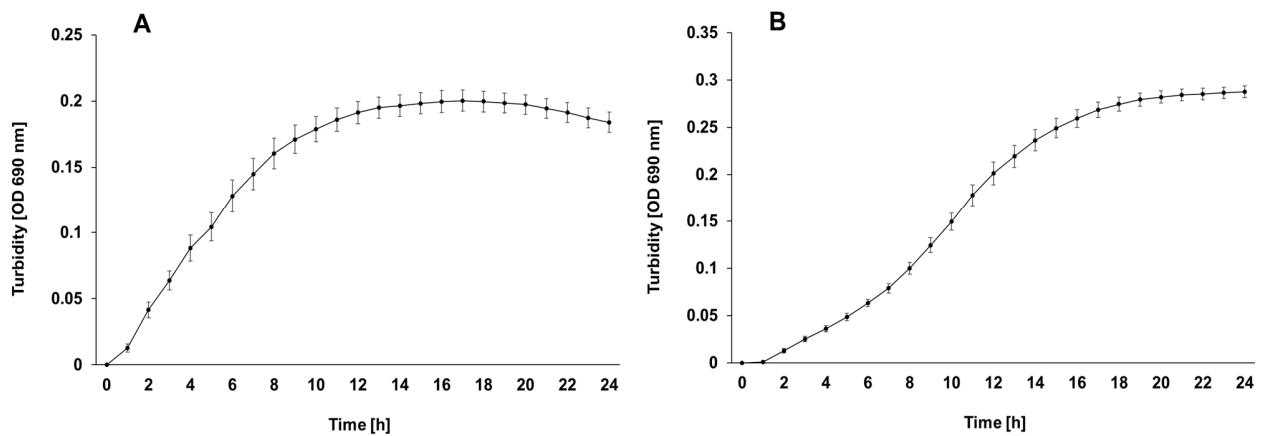


Figure S1. Mean control growth curves of the pathogenic strains *Escherichia coli* O1/O18 (A) and *Salmonella* Enteritidis (B) after incubation in chicken caecal slurries ($n = 30$), error bars indicate the SEM.