Table S8. Effects of Virginiamycin and organic acids supplementation on the relative abundance (%) of the predominant microbiota at the species classification in the cecal digesta of broilers at the age of 21 days.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Taxonomy | | | | Groups 1 | | | | | SEM | *P* value |
| Phyla classification | Family classification | Genus classification | Species classification | NC | PC | DOA | WOA | MOA |
| Bacteroidetes | Bacteroidaceae | Bacteroides | Bacteroides\_dorei | 0.0005 a | 0.0011 a | 0 a | 0.0049 b\*# | 0 a | 0.0006 | 0.036 |
| Bacteroides\_coprocola | 0 a | 0 a | 0 a | 0.00054 b\*# | 0 a | 0.00011 | 0.426 |
| Bacteroides\_coprophilus | 0 a | 0 a | 0 a | 0.00108 b\*# | 0 a | 0.00015 | 0.068 |
| Bacteroides\_fragilis | 0.0003 a | 0.0014 a | 0.0008 a | 0.0019 a | 0.0011 a | 0.0005 | 0.862 |
| Bacteroides\_intestinalis | 0 a | 0 a | 0.00027 ab | 0.00108 b\*# | 0 a | 0.00018 | 0.224 |
| Bacteroides\_plebeius | 0.0005 ab | 0 a | 0 a | 0.0030 b# | 0 a | 0.0004 | 0.130 |
| Chitinophagaceae | Chitinophaga | bacterium\_CYSHGTNA05-1 | 0.00054 a | 0 a | 0.00054 a | 0 a | 0 a | 0.00015 | 0.567 |
| Porphyromonadaceae | Barnesiella | Barnesiella\_viscericola | 0 a | 0 a | 0.00027 a | 0.00027 a | 0 a | 0.00008 | 0.567 |
| Parabacteroides | Parabacteroides\_distasonis | 0 a | 0 a | 0 a | 0.00081 a | 0 a | 0.00016 | 0.426 |
| Parabacteroides\_merdae | 0.00054 a | 0 a | 0 a | 0.00081 a | 0 a | 0.00014 | 0.177 |
| Rikenellaceae | Alistipes | Faecalibacterium\_prausnitzii | 0 a | 0 a | 0 a | 0.00027 b\*# | 0 a | 0.00005 | 0.426 |
| Firmicutes | Aerococcaceae | Aerococcus | Aerococcus\_viridans | 0.00081 a | 0 a | 0 a | 0.00108 a | 0 a | 0.00027 | 0.561 |
| Christensenellaceae | Christensenellaceae\_R-7\_group | bacterium\_YE57 | 0.0076 a | 0.0022 a | 0.0027 a | 0.0051 a | 0.0019 a | 0.0011 | 0.418 |
| Clostridiaceae\_1 | Clostridium\_sensu\_stricto\_1 | Clostridium\_butyricum | 0 a | 0 a | 0 a | 0.00189 b\*# | 0.00081 ab | 0.00026 | 0.075 |
| Clostridium\_perfringens | 0.0068 a | 0 a | 0.0024 a | 0.0014 a | 0 a | 0.0012 | 0.339 |
| Enterococcaceae | Anaerofustis | Anaerofustis\_stercorihominis | 0 a | 0.0019 ab | 0.0046 a | 0.0176 b\*# | 0.0003 a | 0.0023 | 0.080 |
| Enterococcus | Enterococcus\_durans | 0.14 a | 0.42 a | 0.19 a | 0.13 a | 0.47 a | 0.06 | 0.206 |
| Erysipelotrichaceae | Erysipelatoclostridium | bacterium\_ic1391 | 0.43 a | 0.95 a | 1.01 a | 0.70 a | 0.45 a | 0.15 | 0.634 |
| [Clostridium]\_spiroforme | 1.06 b | 0.42 ab | 0.35 a# | 0.50 ab | 0.49 ab | 0.11 | 0.223 |
| unidentified\_Erysipelotrichaceae | Clostridiales\_bacterium\_60-7e | 0.11 a | 0.23 a | 0.20 a | 0.26 a | 0.36 a | 0.05 | 0.567 |
| Clostridiales\_bacterium\_10-3b | 0.044 a | 0.075 a | 0.048 a | 0.101 ab | 0.183 b\*# | 0.018 | 0.080 |
| Lachnospiraceae | Anaerosporobacter | Clostridiales\_bacterium\_77-5d | 0 a | 0.00108 a | 0.00081 a | 0.00054 a | 0.00027 a | 0.00025 | 0.702 |
| Anaerostipes | Anaerostipes\_butyraticus | 0.12 a | 0.43 b\* | 0.06 a ## | 0.16 ab | 0.20 ab | 0.05 | 0.116 |
| Blautia | Blautia\_glucerasea | 0.4 a | 0.5 a | 2.6 b \*# | 0.2 a | 0.3 a | 0.3 | 0.051 |
| Coprococcus\_1 | intestinal\_bacterium\_CG19-1 | 0.0014 a | 0.0005 a | 0.0022 a | 0 a | 0 a | 0.0005 | 0.559 |
| Dorea | Dorea\_longicatena | 0 a | 0 a | 0.00027 ab | 0.00135 b \*# | 0 a | 0.00020 | 0.121 |
| Lachnoclostridium | Clostridium\_sp.\_BR31 | 0.22 a | 0.15 a | 0.27 a | 0.28 a | 0.32 a | 0.03 | 0.492 |
| [Ruminococcus]\_gauvreauii\_group | bacterium\_ic1294 | 0.032 ab | 0.038 ab | 0.052 b | 0.009 a | 0.052 b | 0.007 | 0.345 |
| bacterium\_ic1296 | 0.292 b | 0.092 a\* | 0.218 ab | 0.232 ab | 0.267 b# | 0.028 | 0.171 |
| Sellimonas | bacterium\_P1C11 | 0.33 b | 0.10 a\* | 0.15 ab | 0.25 ab | 0.26 ab | 0.03 | 0.131 |
| Lactobacillaceae | Lactobacillus | Lactobacillus\_agilis | 2.7 ab | 0.2 a | 8.3 c \*## | 0.3 a | 2.6 b | 1.0 | 0.048 |
| Lactobacillus\_crustorum | 0.0016 ab | 0.0022 ab | 0.0095 b | 0 a | 0 a | 0.0019 | 0.497 |
| Lactobacillus\_equicursoris | 0.070 b | 0 a\* | 0 a\* | 0 a\* | 0.002 a\* | 0.012 | 0.215 |
| Lactobacillus\_gasseri | 1.33 a | 12.32 b \*\* | 0.60 a ## | 0.17 a ## | 0.42 a ## | 1.28 | 0.003 |
| Lactobacillus\_mucosae | 0 a | 0.00054 b\* | 0 a # | 0 a # | 0 a # | 0.00011 | 0.426 |
| Lactobacillus\_pontis | 0.0030 a | 0.0035 a | 0.0043 ab | 0.0032 a | 0.0081 b\* | 0.0009 | 0.367 |
| Lactobacillus\_salivarius | 10.29 b | 5.14 ab | 3.94 a \* | 1.99 a \* | 5.11 ab | 1.21 | 0.283 |
| Peptococcaceae | Desulfotomaculum | Desulfotomaculum\_ruminis | 0.00081 a | 0 a | 0.00081 a | 0 a | 0 a | 0.00023 | 0.567 |
| Ruminococcaceae | Butyricicoccus | Butyricicoccus\_pullicaecorum | 0 a | 0 a | 0.00135 b \*# | 0 a | 0.00054 ab | 0.00022 | 0.195 |
| Candidatus\_Soleaferrea | Ruminococcaceae\_bacterium\_GD6 | 0.0003 a | 0.0008 a | 0.0005 a | 0.0008 a | 0.0011 a | 0.0003 | 0.948 |
| Faecalibacterium | bacterium\_ic1379 | 0.008 a | 0.040 a | 0.009 a | 0.102 b \*# | 0.004 a | 0.011 | 0.020 |
| Ruminiclostridium\_5 | [Clostridium]\_leptum | 0.00162 b | 0.00054 ab | 0 a \* | 0 a \* | 0.00027 a \* | 0.00021 | 0.065 |
| Ruminococcaceae\_UCG-014 | [Clostridium]\_papyrosolvens | 0.01 a | 0.20 b \* | 0.01 a # | 0.06 ab | 0.01 a # | 0.04 | 0.493 |
| unidentified\_Ruminococcaceae | Ruminococcaceae\_bacterium\_668 | 0.0035 a | 0 a | 0.0054 a | 0.0062 a | 0.0049 a | 0.0013 | 0.632 |
| Ruminococcaceae\_bacterium\_AM2 | 0.198 b | 0.016 a \*\* | 0.080 ab | 0.042 a \* | 0.058 a \* | 0.021 | 0.057 |
| Ruminococcus\_sp.\_16442 | 0.044 b | 0.019 a \* | 0.011 a \*\* | 0.027 ab | 0.021 a \* | 0.004 | 0.038 |
| Streptococcaceae | Streptococcus | Streptococcus\_gallolyticus\_subsp.\_macedonicus | 2.5 c | 0 a \* | 1.6 bc | 0.1 ab \* | 0 ab \* | 0.4 | 0.112 |
| Streptococcus\_pluranimalium | 0.00108 b | 0.00054 ab | 0.00027 ab | 0 a \* | 0 a \* | 0.00019 | 0.324 |
| Lactococcus | Lactococcus\_garvieae | 0.0076 b | 0 a \* | 0.0016 ab | 0.0005 a \* | 0 a \* | 0.0011 | 0.134 |
| Veillonellaceae | Megasphaera | Megasphaera\_elsdenii | 0.00162 b | 0.00054 ab | 0 a \* | 0.00027 ab | 0 a \* | 0.00025 | 0.206 |
| Veillonella | Veillonella\_ratti | 0 a | 0 a | 0 a | 0.00135 b \*# | 0 a | 0.00027 | 0.426 |
| Proteobacteria | Burkholderiaceae | Burkholderia-Paraburkholderia | Burkholderia\_sp.\_CCGE1003 | 0.0030 a | 0.0014 a | 0.0100 b \*\*## | 0.0003 a | 0.0003 a | 0.0010 | 0.005 |
| Burkholderia\_symbiont\_of\_Cavelerius\_saccharivorus | 0.00081 b | 0.00027 a \* | 0.00217 c \*# | 0 ab | 0 ab | 0.00027 | 0.037 |
| Comamonadaceae | Delftia | Delftia\_tsuruhatensis | 0.00081 a | 0.00108 a | 0.00054 a | 0.00081 a | 0.00108 a | 0.00027 | 0.971 |
| Enterobacteriaceae | Escherichia-Shigella | Escherichia\_coli | 2.8 a | 6.5 b \* | 5.0 b \* | 0.9 a ## | 0.7 a ## | 0.7 | 0.007 |
| Proteus | Proteus\_mirabilis | 0 a | 0.003 a | 0.011 a | 0.012 a | 0 a | 0.003 | 0.636 |
| Orbaceae | Gilliamella | Serratia\_symbiotica | 0 a | 0 a | 0 a | 0.00027 b \*# | 0 a | 0.00005 | 0.426 |
| Moraxellaceae | Psychrobacter | Psychrobacter\_meningitidis | 0 a | 0 a | 0.00081 b \*# | 0 a | 0 a | 0.00016 | 0.426 |
| Xanthomonadaceae | Stenotrophomonas | [Pseudomonas]\_geniculata | 0.00054 a | 0 a | 0 a | 0.00027 a | 0.00054 a | 0.00014 | 0.563 |
| Acidobacteria | Acidobacteriaceae\_(Subgroup\_1) | unidentified\_Acidobacteriac | bacterium\_Ellin326 | 0 a | 0 a | 0.00162 b \*# | 0.00027 a | 0.00054 a | 0.00022 | 0.108 |
| Coriobacteriaceae | Gordonibacter | Gordonibacter\_urolithinfaciens | 0.008 a | 0.052 a | 0.005 a | 0.011 a | 0.045 a | 0.009 | 0.325 |
| Gordonibacter\_pamelaeae | 0.006 a | 0.022 ab | 0.007 a | 0.030 b \* | 0.025 ab | 0.004 | 0.140 |
| unidentified\_Acidimicrobiales | unidentified\_Acidimicrobiales | actinobacterium\_YJF2-33 | 0 a | 0 a | 0.00027 b \*# | 0 a | 0 a | 0.00005 | 0.426 |
| unidentified\_Subgroup\_2 | unidentified\_Subgroup\_2 | bacterium\_Ellin7505 | 0.00162 b | 0.00054 ab | 0.00027 ab | 0 a \* | 0 a \* | 0.00026 | 0.256 |
| Verrucomicrobia | Verrucomicrobiaceae | Akkermansia | Akkermansia\_muciniphila | 0.0003 a | 0 a | 0 a | 0.0041 b \*# | 0.0016 ab | 0.0005 | 0.073 |
| unidentified\_OPB35\_soil\_group | unidentified\_OPB35\_soil\_group | bacterium\_Ellin5102 | 0.00054 ab | 0 a | 0.00081 b # | 0 a | 0.00054 ab | 0.00017 | 0.469 |
| bacterium\_Ellin516 | 0.00027 b | 0 a \* | 0 a \* | 0 a \* | 0 a \* | 0.00005 | 0.426 |
| Others | | | | 76.9 ab | 72.1 a | 75.2 a | 93.4 c \*\*## | 87.6 b ## | 2.2 | 0.002 |

Notes: Superscript 1: NC = negative control, basal diet and basal drinking water with no antibiotic supplementation; PC = positive control, antibiotics supplementation; DOA = NC plus diet-administered OA supplementation; WOA = NC plus water-administered OA supplementation; MOA = NC plus diet-administered and water-administered OA supplementation. Values are expressed as means with pooled SEM values. P value is expressed combined significance. In the same line, values with different letters are significantly different for all possible combinations of these different groups (*P* < 0.05 or *P* < 0.01), n = 8. In the same line, superscript \* indicates significant difference between PC, DOA, WOA or MOA group and NC group at the level of 0.05, and superscript \*\* indicates significantly different between PC, DOA, WOA or MOA group and NC group at the level of 0.01; superscript # indicates significant difference between DOA, WOA or MOA group and NC group at the level of 0.05, and superscript ## indicates significantly different between DOA, WOA or MOA group and NC group at the level of 0.01.