Table S9. 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 42 days.

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| --- | --- | --- | --- |
| Taxonomy | Groups 1 | SEM | *P* value |
| Phyla classification | Family classification | Genus classification | Species classification | NC | PC | DOA | WOA | MOA |
| Bacteroidetes | Bacteroidaceae | Bacteroides | Bacteroides\_fragilis | 0.00037 a | 0.00037 a | 0.00112 a | 0 a | 0.00112 a | 0.00024 | 0.498 |
| Porphyromonadaceae | Barnesiella | Barnesiella\_viscericola | 5.01 a | 4.80 a | 5.08 a | 4.55 a | 5.26 a | 0.19 | 0.828 |
| Firmicutes | Bacillaceae | Bacillus | Bacillus\_alcalophilus | 0 a | 0 a | 0 a | 0 a | 0.00074 a | 0.00015 | 0.426 |
| Aerococcaceae | Aerococcus | Aerococcus\_viridans | 0 a | 0.00149 b \* | 0.00037 ab | 0.00074 ab | 0 a # | 0.00023 | 0.054 |
| Enterococcaceae | Enterococcus | Enterococcus\_durans | 0.077 ab | 0.121 b | 0.041 a # | 0.023 a # | 0.013 a ## | 0.013 | 0.605 |
| Lactobacillaceae | Lactobacillus | Lactobacillus\_agilis | 1.08 a | 0.24 a | 0.80 a | 0.86 a | 0.44 a | 0.18 | 0.605 |
| Lactobacillus\_crustorum | 0.005 a | 0.007 a | 0.006 a | 0.001 a | 0 a | 0.002 | 0.553 |
| Lactobacillus\_gasseri | 0.20 a | 1.98 b \*\* | 0.07 a ## | 0.07 a ## | 0.06 a ## | 0.20 | 0.002 |
| Lactobacillus\_mucosae | 0.0011 a | 0 a | 0.0015 a | 0 a | 0 a | 0.0003 | 0.244 |
| Lactobacillus\_pontis | 0.1 a | 0 a | 3.9 a | 0 a | 0.1 a | 0.8 | 0.438 |
| Lactobacillus\_salivarius | 1.19 ab | 2.74 b | 0.60 a ## | 1.13 a # | 0.80 a # | 0.27 | 0.090 |
| Lactobacillus\_vaginalis | 0.009 a | 0.020 a | 0.064 a | 0.013 a | 0.014 a | 0.011 | 0.547 |
| Lactococcus\_garvieae | 0.0037 a | 0.0022 a | 0.0037 a | 0 a | 0 a | 0.0010 | 0.630 |
| Streptococcaceae | Streptococcus | Streptococcus\_gallolyticus\_subsp.\_macedonicus | 0.6 b | 0 a \* | 2.6 b # | 0.7 b # | 0.1 b ## | 0.4 | 0.197 |
| Christensenellaceae | Christensenellaceae\_R-7\_group | bacterium\_YE57 | 0.0007 a | 0.0030 a | 0.0007 a | 0.0022 a | 0.0026 a | 0.0004 | 0.205 |
| Eubacteriaceae | Eubacterium | Eubacterium\_limosum | 0 a | 0 a | 0 a | 0 a | 0.0078 a | 0.0016 | 0.426 |
| Lachnospiraceae | [Ruminococcus]\_gauvreauii\_group | bacterium\_ic1296 | 0.046 b | 0.039 b | 0.039 ab | 0.061 b | 0.017 a \* ##  | 0.005 | 0.042 |
| [Ruminococcus]\_torques\_group | bacterium\_ic1294 | 0.00074 a | 0.00074 a | 0.00037 a | 0 a | 0 a | 0.00019 | 0.563 |
| Anaerosporobacter | Clostridiales\_bacterium\_77-5d | 0 a | 0 a | 0.25 a | 0 a | 0 a | 0.05 | 0.423 |
| Anaerostipes | Anaerostipes\_butyraticus | 0.014 a | 0.034 a | 0.026 a | 0.063 a | 0.040 a | 0.009 | 0.579 |
| Blautia | Blautia\_glucerasea | 0.93 ab | 1.34 ab | 1.26 ab | 1.17 b | 0.24 a | 0.24 | 0.609 |
| Lachnoclostridium | Clostridium\_sp.\_BR31 | 0.078 a | 0.083 a | 0.088 a | 0.091 a | 0.073 a | 0.009 | 0.976 |
| Roseburia | Clostridia\_bacterium\_UC5.1-2E3 | 0.098 a | 0.028 a | 0.027 a | 0.029 a | 0.139 a | 0.021 | 0.322 |
| Sellimonas | bacterium\_P1C11 | 0.122 a | 0.105 a | 0.117 a | 0.135 a | 0.078 a | 0.016 | 0.869 |
| Peptococcaceae | Desulfotomaculum | Desulfotomaculum\_ruminis | 0.00074 ab | 0 a | 0.00149 b # | 0 a | 0 a | 0.00022 | 0.125 |
| Ruminococcaceae | Anaerotruncus | Anaerotruncus\_colihominis | 0.0026 a | 0.0041 a | 0.0037 a | 0.0063 ab | 0.0108 b \*# | 0.0011 | 0.141 |
| Butyricicoccus | Butyricicoccus\_pullicaecorum | 0.094 b | 0.035 a \* | 0.039 a \* | 0.049 ab | 0.038 a \* | 0.009 | 0.224 |
| Candidatus\_Soleaferrea | Ruminococcaceae\_bacterium\_GD6 | 0 a | 0 a | 0.00037 a | 0.00037 a | 0.00223 b \*\* ## | 0.00024 | 0.006 |
| Faecalibacterium | bacterium\_ic1379 | 0.49 b | 0.13 ab | 0.05 a \* | 0.09 ab | 0.32 ab | 0.07 | 0.208 |
| Ruminiclostridium\_9 | Clostridiales\_bacterium\_NK3B98 | 0.0030 a | 0.0037 a | 0.0071 a | 0.0033 a | 0.0045 a | 0.0013 | 0.887 |
| Subdoligranulum | Subdoligranulum\_variabile | 0.00037 a | 0 a | 0 a | 0.00149 b \* ## | 0 a | 0.00019 | 0.038 |
| unidentified\_Ruminococcaceae | Ruminococcaceae\_bacterium\_AM2 | 0.030 a | 0.016 a | 0.066 a | 0.019 a | 0.023 a | 0.009 | 0.413 |
| Ruminococcus\_sp.\_16442 | 0.0052 a | 0.0097 a | 0.0082 a | 0.0104 a | 0.0059 a | 0.0013 | 0.676 |
| Erysipelotrichaceae | Erysipelatoclostridium | [Clostridium]\_spiroforme | 0.101 a | 0.133 a | 0.108 a | 0.071 a | 0.063 a | 0.022 | 0.870 |
| bacterium\_ic1391 | 0.25 a | 0.23 a | 0.10 a | 0.11 a | 0.05 a | 0.05 | 0.647 |
| Faecalitalea | [Eubacterium]\_tortuosum | 0 a | 0.00037 a | 0 a | 0 a | 0 a | 0.00007 | 0.426 |
| unidentified\_Erysipelotrichaceae | Clostridiales\_bacterium\_10-3b | 0.072 a | 0.040 a | 0.026 a | 0.044 a | 0.021 a | 0.010 | 0.513 |
| Veillonellaceae | Megasphaera | Clostridiales\_bacterium\_60-7e | 0.036 ab | 0.028 a | 0.092 ab | 0.196 b # | 0.156 ab | 0.027 | 0.210 |
| Megasphaera\_elsdenii | 0 a | 0 a | 0.00074 a | 0 a | 0 a | 0.00015 | 0.426 |
| Proteobacteria | Bradyrhizobiaceae | Bradyrhizobium | Bradyrhizobium\_elkanii | 0.0019 ab | 0.0048 ab | 0.0063 b | 0 a | 0 a | 0.0009 | 0.055 |
| Burkholderiaceae | Burkholderia-Paraburkholderia | Burkholderia\_symbiont\_of\_Cavelerius\_saccharivorus | 0.00037 a | 0.00074 a | 0.00186 a | 0 a | 0 a | 0.00032 | 0.338 |
| Enterobacteriaceae | Escherichia-Shigella | Escherichia\_coli | 4.7 b | 0.9 a \*\* | 1.0 a \*\* | 0.3 a \*\* | 0.4 a \*\* | 0.5 | 0.014 |
| Proteus | Proteus\_mirabilis | 0.0015 a | 0.0004 a | 0.0033 a | 0.0011 a | 0.0004 a | 0.0006 | 0.583 |
| Acidobacteria | unidentified\_Subgroup\_2 | unidentified\_Subgroup\_2 | bacterium\_Ellin7505 | 0.00037 a | 0.00037 a | 0 a | 0.00037 a | 0 a | 0.00012 | 0.736 |
| Acidobacteriaceae\_(Subgroup\_1) | unidentified\_Acidobacteriaceae\_(Subgroup\_1) | bacterium\_Ellin326 | 0 a | 0 a | 0.00037 a | 0 a | 0.00112 a | 0.00023 | 0.507 |
| unidentified\_Acidimicrobiales | unidentified\_Acidimicrobiales | bacterium\_enrichment\_culture\_clone\_auto73\_4W | 0 a | 0.00037 a | 0 a | 0 a | 0 a | 0.00007 | 0.426 |
| Coriobacteriaceae | Gordonibacter | Gordonibacter\_pamelaeae | 0.004 a | 0.008 ab | 0.004 ab | 0.024 b \* | 0.005 ab | 0.003 | 0.231 |
| Gordonibacter\_urolithinfaciens | 0.0030 ab | 0.0082 ab | 0.0033 ab | 0.0167 b | 0.0019 a | 0.0024 | 0.246 |
| Brevibacteriaceae | Brevibacterium | Brevibacterium\_epidermidis | 0.0048 a | 0.0041 a | 0.0019 a | 0.0019 a | 0.0030 a | 0.0008 | 0.691 |
| Dermabacteraceae | Brachybacterium | Brachybacterium\_paraconglomeratum | 0.0019 a | 0.0030 a | 0.0037 a | 0.0045 a | 0.0011 a | 0.0007 | 0.574 |
| Micrococcaceae | Glutamicibacter | Glutamicibacter\_arilaitensis | 0.0022 a | 0.0015 a | 0.0011 a | 0.0004 a | 0.0004 a | 0.0004 | 0.594 |
| Verrucomicrobia | unidentified\_OPB35\_soil\_group | unidentified\_OPB35\_soil\_group | bacterium\_Ellin5102 | 0.0004 a | 0.0007 a | 0.0022 a | 0.0011 a | 0 a | 0.0004 | 0.417 |
| Verrucomicrobiaceae | Akkermansia | Akkermansia\_muciniphila | 0.14 a | 0 a | 0.01 a | 0 a | 0.20 a | 0.04 | 0.464 |
| Gemmatimonadetes | Gemmatimonadaceae | Gemmatimonas | bacterium\_Ellin5290 | 0 a | 0.00037 a | 0.00037 a | 0 a | 0 a | 0.00010 | 0.567 |
| Others | 84.4 a | 86.9 a | 83.4 a | 90.1 b \* | 91.3 b \* | 1.0 | 0.025 |

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.