**SUPPLEMENTARY MATERIAL**

**Presence of adult companion goats favors the rumen microbial and functional development in artificially reared kids**

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**Supplementary Table S1.** Chemical composition (in % DM) of the feeds.

|  |  |  |  |
| --- | --- | --- | --- |
|  | Milk replacer1 | Starter concentrate2 | Oatshay |
| Organic matter | 92.8 | 93.1 | 90.2 |
| Crude protein | 24.0 | 12.9 | 8.1 |
| Ether extract | 22.0 | 3.2 | 2.2 |
| Neutral-detergent fiber |  | 22.9 | 50.9 |
| Acid-detergent fiber |  | 9.12 | 32.6 |

1 Declared composition

2 Ingredient list: wheat bran, barley, corn, wheat, sunflower seed flour, soybean flour, CaCO3, NaCl, vitamin mineral premix and NaCO3.

**Supplementary Table S2.** Description of the of the rumen protozoal community in the two adult companions (*n*=8).

|  |  |
| --- | --- |
|  | Adults1 |
| Protozoal counts, log10 cells/mL | 5.81 |
| Subf. *Entodiniinae*, % | 75.2 |
| Subf. *Diplodiniinae*, % | 5.06 |
| *Ophryoscolex* spp., % | 10.6 |
| *Isotricha* spp., % | 2.33 |
| *Dasytricha* spp., % | 6.80 |

1Average between the two adult companions.

**Supplementary Table S3.** Diversity indexes and abundances of rumen bacterial taxa in the rumen of goat kids reared in absence (CTL) or presence of adult companions (CMP) at 7 weeks of age (n =8).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Treatments |  |  |  |
|  | CTL | CMP | Adults1 | SEM | *P*-value2 |
| Richness | 216 | 348 | 446 | 20.3 | <0.001 |
| Shannon | 3.910 | 4.670 | 5.290 | 0.135 | <0.001 |
| Evenness | 0.728 | 0.798 | 0.871 | 0.015 | 0.016 |
| Simpson | 0.949 | 0.973 | 0.999 | 0.006 | 0.051 |
| Good’s coverage | 0.991 | 0.994 | 0.999 | 0.002 | 0.502 |
| **Abundance** (%) |  |  |  |  |  |
| *p\_Actinobacteria, f\_Coriobacteriaceae, g\_Olsenella* | 0.124 | 0.036 | 0.823 | 0.025 | 0.079 |
| *p\_Bacteroidetes* | 64.20 | 71.50 | 62.60 | 1.960 | 0.093 |
| *f\_Barnesiellaceae, g\_Barnesiella* | 3.960 | 0.579 | 0.639 | 1.040 | 0.115 |
| *f\_Paraprevotellaceae* | 3.230 | 5.770 | 2.400 | 0.704 | 0.059 |
| *g\_CF231* | 0.346 | 0.621 | 1.290 | 0.090 | 0.195 |
| *g\_YRC22* | 0.136 | 0.029 | 0.064 | 0.058 | 0.643 |
| *f\_Bacteroidaceae, g\_BF311* | 0.179 | 0.615 | 1.57 | 0.108 | 0.027 |
| *f\_Porphyromonadaceae* | 0.117 | 0.016 | 0.113 | 0.031 | 0.130 |
| *f\_Prevotellaceae, g\_Prevotella* | 35.30 | 38.70 | 19.90 | 2.370 | 0.753 |
| *f\_RF16* | 0.034 | 0.282 | 0.049 | 0.107 | 0.125 |
| *f\_Sphingobacteriaceae, g\_Pedobacter* | 0.349 | 0.154 | 0.049 | 0.119 | 0.746 |
| *p\_Chloroflexi* | 0.010 | 0.021 | 0.042 | 0.120 | 0.334 |
| *p\_Cyanobacteria* | 0.015 | 0.081 | 0.054 | 0.164 | 0.021 |
| *p\_Elusimicrobia* | 0.162 | 0.393 | 0.108 | 0.078 | 0.290 |
| *f\_Elusimicrobiaceae* | 0.154 | 0.205 | 0.049 | 0.054 | 0.742 |
| *p\_Fibrobacteres, g\_Fibrobacter* | 2.180 | 2.230 | 8.590 | 0.451 | 0.916 |
| *p\_Firmicutes* | 16.60 | 13.70 | 21.40 | 0.837 | 0.059 |
| *f\_Clostridiaceae* | 0.167 | 0.121 | 0.196 | 0.037 | 0.916 |
| *g\_Clostridium* | 0.383 | 0.245 | 0.771 | 0.052 | 0.248 |
| *f\_Lachnospiraceae* | 3.240 | 1.640 | 4.340 | 0.537 | 0.345 |
| *g\_Lactonifactor* | 1.160 | 0.232 | 0.277 | 0.403 | 0.318 |
| *f\_Ruminococcaceae* | 7.310 | 5.090 | 5.710 | 0.705 | 0.093 |
| *g\_Ruminococcus* | 0.390 | 0.432 | 0.766 | 0.073 | 0.753 |
| *g\_Papillibacter* | 0.299 | 0.057 | 0.044 | 0.0667 | 0.125 |
| *g\_Sporobacter* | 0.301 | 0.086 | 0.213 | 0.075 | 0.267 |
| *f\_Veillonellaceae* | 0.677 | 1.398 | 1.210 | 0.184 | 0.027 |
| *g\_Selenomonas* | 0.139 | 0.325 | 0.147 | 0.068 | 0.035 |
| *g\_Succinispira* | 0.009 | 0.685 | 0.850 | 0.142 | 0.001 |
| *f\_Erysipelotrichaceae* | 1.030 | 1.470 | 0.747 | 0.269 | 0.046 |
| *g\_Bulleidia* | 0 | 0.121 | 0.054 | 0.036 | 0.004 |
| *p\_Lentisphaerae* | 0.207 | 0.242 | 0.306 | 0.044 | 0.834 |
| *f\_Victivallaceae* | 0.204 | 0.242 | 0.267 | 0.044 | 0.834 |
| *g\_Victivallis* | 0.063 | 0.065 | 0.054 | 0.016 | 0.832 |
| *p\_Proteobacteria* | 4.240 | 2.230 | 0.857 | 1.040 | 0.338 |
| *f\_Neisseriaceae* | 0.052 | 0.045 | 0 | 0.009 | 0.431 |
| *f\_Rhodocyclaceae* | 0.214 | 0.051 | 0.024 | 0.048 | 0.059 |
| *g\_Georgfuchsia* | 0.209 | 0.046 | 0 | 0.048 | 0.046 |
| *f\_Desulfovibrionaceae* | 0.439 | 0.237 | 0.443 | 0.057 | 0.036 |
| *f\_Succinivibrionaceae* | 0.581 | 0.480 | 0.323 | 0.196 | 0.529 |
| *g\_Succinivibrio* | 0.277 | 0.040 | 0.147 | 0.108 | 0.324 |
| *p\_Spirochaetes* | 6.570 | 2.090 | 0.695 | 1.220 | 0.021 |
| *f\_Sphaerochaetaceae, g\_Sphaerochaeta* | 0.026 | 0.059 | 0 | 0.019 | 0.666 |
| *f\_Spirochaetaceae* | 5.050 | 1.250 | 0.409 | 1.020 | 0.021 |
| *g\_Spirochaeta* | 0.020 | 0.551 | 0.127 | 0.012 | 0.062 |
| *g\_Treponema* | 2.040 | 0.582 | 0.152 | 0.389 | 0.036 |
| *p\_SR1* | 0 | 0.114 | 0.260 | 0.038 | 0.001 |
| *p\_Synergistetes* | 0.072 | 0.187 | 0.176 | 0.034 | 0.059 |
| *f\_Dethiosulfovibrionaceae* | 0.067 | 0.181 | 0.166 | 0.035 | 0.093 |
| *g\_Dethiosulfovibrio* | 0.007 | 1.200 | 0.716 | 0.035 | 0.004 |
| *p\_Tenericutes* | 0.042 | 0.097 | 0.105 | 0.022 | 0.088 |
| *p\_TM7, f\_F16* | 0.080 | 0.231 | 0.037 | 0.037 | 0.021 |
| *p\_Verrucomicrobia* | 1.280 | 3.350 | 0.764 | 0.620 | 0.074 |
| *f\_R4\_41B* | 0.683 | 0.395 | 0.071 | 0.145 | 0.207 |
| *f\_RFP12* | 0.585 | 2.95 | 0.597 | 0.577 | 0.016 |

1Description of the rumen bacterial community in the two adult companions.

2*P*-values for the differences between CTL and CMP kids. Only taxa with an average abundance > 0.05% are shown. *p*=phylum; *f*=family; *g*=genus

**Supplementary Table S4.** Diversity indexes of the methanogen community in the rumen of goat kids reared in absence (CTL) or presence of adult companions (CMP) at 7 weeks of age (n=8).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Treatments |  |  |  |
|  | CTL | CMP | Adults1 | SEM | *P*-value2 |
| Richness | 17.6 | 21.1 | 18.5 | 2.080 | 0.439 |
| Shannon | 2.18 | 2.48 | 2.38 | 0.124 | 0.190 |
| Evenness | 0.77 | 0.83 | 0.82 | 0.021 | 0.064 |
| Simpson | 0.80 | 0.87 | 0.87 | 0.023 | 0.103 |
| Good’s coverage | 0.741 | 0.642 | 24.4 | 0.0292 | 0.237 |

1Description of the rumen bacterial community in the adult companions.

2*P*-values for the differences between CTL and CMP kids. Only taxa with an average.

**Supplementary Table S5.** Correlations between the rumen microbiota and rumen fermentation and physiological parameters (only Spearman correlations with *ρ* > 0.4 and *P* < 0.01 are shown).

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Correlations | Acetate | Propionate | Isobutyrate | Butyrate | Isovalerate | Valerate | VFA | BW | ADG-pre-weaning | ADG-post-weaning | Blood BHB | Blood glucose | Blood urea | Blood proteins | BHB/Glucose |
| Bacterial concentration |  |  |  | 0,45 | -0,40 |  | 0,45 |  |  |  | 0,85 | 0,57 |  | 0,43 | 0,65 |
| Bacterial ASV |  |  | -0,40 |  |  | -0,45 | 0,41 |  |  |  |  | -0,49 | 0,55 |  | 0,42 |
|  p\_\_Cyanobacteria |  |  |  |  |  |  |  |  |  |  |  |  | 0,45 |  |  |
|  p\_\_Fibrobacteres |  |  |  |  |  |  |  | 0,47 | 0,47 |  | 0,40 |  |  |  |  |
|  p\_\_Firmicutes |  |  |  |  |  |  |  |  |  |  |  |  |  | -0,41 |  |
|  p\_\_Spirochaetes |  |  |  |  |  |  |  |  | -0,44 |  | -0,40 | 0,50 | -0,67 |  | -0,50 |
|  p\_\_SR1 |  |  |  |  |  | -0,40 |  |  |  |  | 0,53 | -0,59 | 0,62 |  | 0,61 |
|  p\_\_Synergistetes |  |  | -0,41 |  |  |  |  |  |  |  |  |  |  |  |  |
|  p\_\_TM7 |  | 0,43 | -0,44 |  |  |  |  |  |  |  |  | -0,47 |  |  | 0,52 |
|  p\_\_Verrucomicrobia |  |  |  |  |  |  |  |  |  |  |  |  | 0,42 |  |  |
|  f\_\_[Barnesiellaceae] |  |  |  |  |  |  |  |  |  |  |  |  | -0,42 |  |  |
|  f\_\_Ruminococcaceae |  |  |  |  |  |  |  |  |  |  |  |  | -0,58 |  |  |
|  f\_\_Erysipelotrichaceae |  |  |  |  |  |  |  |  |  |  |  |  | 0,50 |  |  |
|  f\_\_Rhodocyclaceae |  |  |  |  |  |  |  |  |  |  | -0,43 | 0,43 |  |  | -0,50 |
|  f\_\_Succinivibrionaceae |  |  |  |  |  |  |  |  |  |  |  |  | 0,40 |  |  |
|  f\_\_Spirochaetaceae |  |  |  |  |  |  |  |  | -0,41 |  | -0,43 | 0,56 | -0,67 |  | -0,53 |
|  f\_\_Dethiosulfovibrionaceae |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  f\_\_F16 |  | 0,43 | -0,44 |  |  |  |  |  |  |  | 0,53 | -0,47 |  |  | 0,52 |
|  f\_\_R4-41B |  | -0,41 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Methanogens concentration | -0,56 | 0,52 |  | 0,53 |  |  | 0,40 | 0,93 |  |  | 0,85 | 0,48 | 0,69 | 0,69 | 0,63 |
|  g\_\_Methanobrevibacter |  |  |  |  |  |  |  |  |  |  | -0,74 | 0,74 | -0,45 | 0,40 | -0,79 |
|  g\_\_Group12 |  |  | 0,44 |  |  | 0,46 | -0,45 |  |  |  |  |  | -0,58 |  |  |
|  g\_\_Group9 |  |  |  |  |  |  |  |  |  |  |  |  | 0,67 |  |  |
|  g\_\_Methanomicrobium |  |  |  |  |  |  |  |  |  | -0,52 | 0,40 |  | 0,50 |  |  |
| Protozoal concentration | -0,60 |  |  | 0,55 |  |  |  | 0,57 |  |  |  |  | 0,78 | 0,99 |  |
| Protozoa (optical count) | -0,55 |  |  | 0,43 |  |  |  | 0,64 |  |  |  |  | 0,57 | 0,81 |  |
| Entodinium | -0,44 |  |  |  |  |  |  | 0,54 |  |  | 0,45 |  | 0,75 | 0,95 |  |
| Diplodiniinae | -0,40 |  |  |  |  |  |  | 0,68 |  |  |  | 0,46 | 0,91 | 0,99 |  |
| Ophryoscolex |  |  |  |  |  |  |  | 0,65 |  |  |  |  |  | 0,51 |  |
| Isotricha |  |  |  |  |  |  |  |  |  |  | 0,42 | 0,59 | 0,71 |  | 0,40 |
| Dasytricha |  |  |  |  |  |  |  | 0,87 |  |  | 0,60 |  |  |  |  |
| Anaerobic fungal concentration | 0,43 |  |  |  |  |  |  | 0,40 |  |  | 0,90 | 0,77 |  |  | 0,85 |