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**Supplemental TABLE 1** Fermentation reactions used for calculations of Gibbs energy changes.

|  |  |
| --- | --- |
| Item | Reactions |
| Pathways of glucose fermentation | |
| Reaction 1 | C6H12O6 → 2acetate+ 2 CO2 + 4H2 + 2 H+ |
| Reaction 2  Reaction 3  Reaction 4 | C6H12O6+ 2H2 → 2 propionate + 2H2O+ 2 H+  C6H12O6 → butyrate + H+ + 2 CO2 + 2 H2  C6H12O6 + H2O → acetate + ½ butyrate+ 2 CO2 + 3 H2 + 3/2 H+ |
| Reaction 5 | C6H12O6 → acetate + propionate + CO2 + H2 + 2 H+ |
| Reaction 6 | C6H12O6 → ⅔ acetate + 4/3 propionate + ⅔ CO2 + 2 H+ |
| Pathways of methanogenesis | |
| Reaction 7 | CO2 + 4 H2 → CH4+ 2 H2O |

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**Supplemental TABLE 2** Primers used for qPCR.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Target species | Primer sequences(5'-3') | | Size (bp) | Reference |
| Forward primer | Reverse primer |
| Bacteria | CGGCAACGAGCGCAACCC | CCATTGTAGCACGTGTGTAGCC | 146 | 1 |
| Protozoa | GCTTTCGWTGGTAGTGTATT | CTTGCCCTCYAATCGTWCT | 223 | 2 |
| Fungi | GAGGAAGTAAAAGTCGTAACAAGGTTTC | CAAATTCACAAAGGGTAGGATGATT | 120 | 1 |
| Methanogens | GGATTAGATACCCSGGTAGT | GTTGARTCCAATTAAACCGCA | 192 | 3 |
| *Ruminococcus albus* | CCCTAAAAGCAGTCTTAGTTCG | CCTCCTTGCGGTTAGAACA | 176 | 4 |
| *Ruminococcus flavefaciens* | CGAACGGAGATAATTTGAGTTTACTTAGG | CGGTCTCTGTATGTTATGAGGTATTACC | 132 | 1 |
| *Fibrobacter succinogenes* | GTTCGGAATTACTGGGCGTAAA | CGCCTGCCCCTGAACTATC | 121 | 1 |
| *Selenomonas ruminantium* | CAATAAGCATTCCGCCTGGG | TTCACTCAATGTCAAGCCCTGG | 138 | 2 |
| *Prevotella ruminicola* | GAAAGTCGGATTAATGCTCTATGTTG | CATCCTATAGCGGTAAACCTTTGG | 74 | 2 |
| *Prevotella* spp*.* | GGTTCTGAGAGGAAGGTCCCC | TCCTGCACGCTACTTGGCTG | 121 | 2 |
| *Ruminobacter amylophilus* | CTGGGGAGCTGCCTGAATG | GCATCTGAATGCGACTGGTTG | 102 | 2 |

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**Supplemental TABLE 3**  Select microbial groups, as determined by RT-PCR, in the rumen of growing goats fed diets with 1.45% Mg(OH)2 or 0.6% elemental Mg after 28 d of adaption (n = 10).

|  |  |  |  |
| --- | --- | --- | --- |
| Item | Mg(OH)2 | Elemental Mg | *P*-value |
| Microbial copy numbers, log10 copies/DM rumen contents | | |  |
| Bacteria | 11.7±0.03 | 11.7±0.05 | 0.11 |
| Protozoa | 7.07±0.183 | 7.03±0.115 | 0.81 |
| Fungi | 5.81±0.096 | 5.37±0.114 | 0.001 |
| Methanogens | 9.17±0.051 | 9.34±0.056 | 0.006 |
| Relative abundance, % | | | |
| *F. succinogenes* | 0.205±0.0355 | 0.234±0.0576 | 0.68 |
| *R. albus* | 0.0126±0.0012 | 0.0138±0.0032 | 0.72 |
| *R. flavefaciens* | 0.0326±0.0061 | 0.0558±0.0095 | 0.02 |
| *S. ruminantium* | 0.224±0.0228 | 0.135±0.0254 | 0.008 |
| *R.* *amylophilus* | 0.0017±0.00009 | 0.0019±0.00024 | 0.49 |
| *P.* *ruminicola* | 3.59±0.276 | 3.35±0.226 | 0.48 |
| *Prevotella* spp*.* | 29.9±2.73 | 26.6±1.89 | 0.22 |

Values are means ± SE.

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**Supplemental TABLE 4** Alpha diversity of bacterial communities, as determined by 16S rRNA pyrosequencing, inthe rumen of growing goats fed diets with 1.45% Mg(OH)2 or 0.6% elemental Mg after 28 d of adaption (n = 10).

|  |  |  |  |
| --- | --- | --- | --- |
| Item | Mg(OH)2 | Elemental Mg | *P*-value |
| OUT | 714±34.8 | 758±19.3 | 0.21 |
| Reads | 28888±1194 | 27216±1195 | 0.33 |
| Ace | 837±34.9 | 904±22.3 | 0.04 |
| Chao 1 | 845±37.0 | 915±24.7 | 0.04 |
| Shannon | 4.62±0.141 | 4.76±0.067 | 0.43 |
| Simpson | 0.0405±0.0094 | 0.0275±0.0039 | 0.24 |
| Coverage | 0.994±0.000 | 0.994±0.000 | 0.22 |

Values are means ± SE.

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**Supplemental FIGURE 1**  Relations between ruminal pH and Mg2+ concentration in goats fed diets with 1.45% Mg(OH)2 or 0.6% elemental Mg after 28 d of adaption (n = 10). Rumen contents were sampled at 0, +2.5 and +6 h relative to the commencement of morning feeding. The line in each panel is the best linear regression line. Each point represents 1 goat at 1 particular sampling time, with a total of 30 data points.

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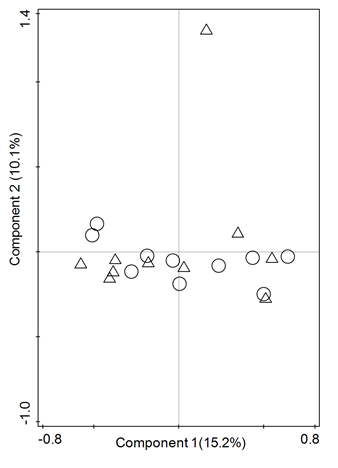
**Supplemental FIGURE 2**  Relationships between dissolved hydrogen (dH2) and dissolved methane (dCH4, A), and CH4 emissions (B) in goats fed diets with 1.45% Mg(OH)2 or 0.6% elemental Mg after 28 d of adaption (n = 10) at + 2.5 h relative to the commencement of morning feeding. The line in each panel is the best linear regression line. Each point represents 1 goat, with a total of 20 data points. OMI, organic matter intake. Δ, Mg (OH)2 treatment; Ο, elemental Mg treatment.

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**Supplemental FIGURE 3**  Relationships between dissolved hydrogen (dH2) and select fermentation end products (A, Total VFAs; B, acetate; C, propionate; D, acetate to propionate ratio; E, RNH2) in goats fed diets with 1.45% Mg(OH)2 or 0.6% elemental Mg after 28 d of adaption (n = 10) at +2.5 h relative to the commencement of morning feeding. Each point represents 1 goat, with a total of 20 data points. RNH2, estimated net H2 production relative to the amount of total volatile fatty acid produced. Δ, Mg (OH)2 treatment; Ο, elemental Mg treatment.

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**Supplemental FIGURE 4**  Principal coordinate analysis (PCoA) of ruminal bacterial OTUs in goats fed diets with 1.45% Mg(OH)2 or 0.6% elemental Mg after 28 d of adaption (n = 10). Shown are the first two principal coordinates explaining the largest amount of variation. Δ, Mg (OH)2 treatment; Ο, Mg treatment.

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