Rumen microbial community and nitrogen metabolism in goats fed blend of palm oil and canola oil

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ABSTRACT
This study assessed the influence of dietary blend of 20% palm oil and 80% canola oil on the population of rumen microbiota and nitrogen economy in goats. Twenty-four Boer bucks (4–5 months old; initial BW, 20.54 ± 0.474 kg) were randomly allotted to diets containing on a dry matter basis, 0, 4 or 8% oil blend, fed daily for 100 days and slaughtered. The rumen microbiota was examined by quantitative real-time polymerase chain reaction (PCR) using the 16S rRNA gene. The population of total protozoa and methanogens was lower \((p < 0.05)\) while the population of \(Fibrobacter succinogenes\) was greater \((p < 0.05)\) in goats fed oil blend compared with the control goats. The population of total bacteria was greater \((p < 0.05)\) in goats fed 8% oil blend compared with those fed other diets. The population of \(Ruminococcus albus\) and \(Ruminococcus flavefaciens\) was greater \((p < 0.05)\) in goats fed 4% oil blend compared with those fed other diets. Diet had no effect \((p > 0.05)\) on microbial N yield, microbial protein synthesis, efficiency of microbial protein synthesis and the intake, retention and excretion of N. Dietary supplementation of blend of palm oil and canola oil altered rumen microbial profile but did not affect nitrogen metabolism in goats.

Introduction
The manipulation of the rumen ecosystem is an effective strategy for ensuring efficient feed utilisation to achieve desired production targets at a least cost with minimal negative impact on the environment. Dietary fats are commonly used in ruminant nutrition due to their high energy density and low price and could be utilised to modify the fatty acid profile of ruminant milk and meat (Adeyemi et al. 2016). Nonetheless, unsaturated fats could have detrimental effect on rumen microbial ecology (Mao et al. 2010), which could affect fibre digestibility and voluntary feed intake in ruminants. The impact of lipid supplementation on rumen microbiota in sheep (Mao et al. 2010) and cattle (Lee et al. 2011; Ivan et al. 2013) has been documented. However, similar in vivo studies are seldom reported for goats. Erstwhile companion \(in vitro\) study showed that the blend of 20% palm oil and 80% canola oil had no effect \(in vitro\) organic matter (OM) and dry matter (DM) digestibility (Adeyemi et al. 2015).

Similarly, the oil blend did not affect growth performance and the intake and digestibility of DM and OM, but depressed methane concentration, total volatile fatty acids, and molar proportion of acetate and butyrate in goats (Adeyemi et al. 2016). The response of rumen microbiota to dietary blend of palm oil and canola oil remain obscure but could offer insights into some of the previous findings.

The N requirement of ruminants is a combination of the need of the rumen microbiota and that of the host animal. A shortfall in N supply or excess N beyond its basal requirements could have environmental and economic consequences (Lee et al. 2011). Thus, optimising N efficiency to reduce production cost and limit environmental pollution is warranted. One major strategy for enhancing N efficiency is increasing ruminal microbial protein synthesis, which can be maximised by defaunation (Doreau & Ferlay 1995; Lee et al. 2011). Dietary fat can reduce the population of rumen protozoa (Mao et al. 2010; Ivan et al. 2013).
Nonetheless, the effects of dietary fat on the population of rumen protozoa and nitrogen metabolism in ruminants are highly variable and inconsistent in the published literature. Therefore, there is need for additional studies in different production systems. The objective of this study was to determine the effects of graded levels of blend of 20% palm oil and 80% canola oil on the population of rumen microbiota and nitrogen economy in goats.

Materials and methods

Animal welfare and ethics

The study was conducted according to the guidelines approved by the Universiti Putra Malaysia Institutional Animal Care and Use Committee.

Experimental site, animals and diet

The feeding trial was conducted at Ar-Raudhah Biotech Farm, Pty Ltd., Kuang, Selangor, Malaysia. The geographical coordinates of Kuang are 3° 16’ 0” North, 101° 35’ 0” East. Annual rainfall was about 2670 mm. During the trial, the ambient temperature ranged from 26°C to 33°C while relative humidity ranged from 81% to 85%.

Twenty-four, 4–5 months old Boer crossbred bucks weighing 20.54 ± 0.474 kg (mean ± standard deviation) were used in this study. The goats were drenched against parasites and randomly allotted to diets containing on a DM basis 0, 4 and 8% oil blend and fed daily for 100 d following a two-week adaptation period. Each diet consisted of 50% concentrate mixture (22% corn grain, 17% soybean meal, 7.5% palm kernel cake, 2% rice bran, 0.5% limestone, 0.5% salt and 0.5% mineral-vitamin premix) on a DM basis (Adeyemi et al. 2016). The ingredients in the concentrate portion were adjusted (Adeyemi et al. 2016) to make the diets isocaloric and isonitrogenous (Table 1). The oil-supplemented diets were prepared by manually incorporating the oil blend into the ground concentrate thoroughly. The diets were prepared fresh twice a day and no antioxidant was added. The diets were offered as complete ration mix (forage and concentrate) in two equal meals at 0830 and 1530 h with ad libitum access to water. Daily faeces from individual goat was collected and weighed in the morning prior to feeding. After thorough mixing, approximately 100 g/kg of the daily faeces from each goat were sampled and stored at −20°C pending subsequent analysis. Urine samples were collected for 10 days. The goats were fed twice daily at 0830 and 1530 h with ad libitum access to water. Daily faeces from individual goat was collected and weighed in the morning prior to feeding. After thorough mixing, approximately 100 g/kg of the daily faeces from each goat were sampled and stored at −20°C pending subsequent analysis. Urine sample was collected in plastic containers and acidified with 15 mL of 10% H2SO4 and stored at −20°C until analysis. Microbial nitrogen yield was estimated following the equation proposed by ARC (1984) as follows:

\[
\text{Microbial Nitrogen yield} = 32g/kg \text{ of organic matter digested in the rumen (OMDR)}.
\]

where OMDR = dry matter intake (kg) × organic matter content × organic matter digestibility ×0.65.

| Levels of oil blend, % | 0  | 4  | 8  | BCOPOa |
|-----------------------|----|----|----|--------|
| Chemical composition  |    |    |    |        |
| Dry matter, g/kg      | 676.96 | 678.99 | 680.73 |
| Crude protein, g/kg DM| 147.2  | 143.7  | 143.9  |
| Ether extract, g/kg DM| 23.00  | 63.50  | 111.10 |
| Ash, g/kg DM          | 68.40  | 65.80  | 62.60  |
| Nitrogen free extract, g/kg DM | 165.56 | 139.67 | 124.51 |
| Acid detergent fibre, g/kg DM | 350.40 | 332.80 | 325.20 |
| Neutral detergent fibre, g/kg DM | 635.24 | 626.72 | 620.60 |
| Metabolizable energy, MJ/Kg DM | 11.59 | 11.61 | 11.62 |
| Ca %                  | 1.02  | 1.05  | 1.04  |
| P %                   | 0.52  | 0.54  | 0.54  |
| Fatty acid, g/100 g of total FA |     |    |    |        |
| C12:0                 | 0.07  | 0.07  | 0.08  | 0.11  |
| C14:0                 | 3.35  | 1.38  | 0.99  | 0.63  |
| C16:0                 | 12.64 | 16.14 | 14.92 | 13.42 |
| C16:1                 | 0.52  | 0.31  | 0.29  | 0.24  |
| C18:0                 | 3.53  | 3.02  | 2.74  | 2.87  |
| C18:1n-9              | 24.19 | 40.10 | 50.37 | 57.85 |
| C18:2n-6              | 44.59 | 32.01 | 23.08 | 18.15 |
| C18:3n-3              | 6.70  | 7.04  | 7.90  | 8.52  |
| n-6:n-3               | 6.66  | 4.54  | 2.92  | 2.13  |
| Total FA, g/kg DM     | 15.83 | 37.09 | 52.27 |

Table 1. Chemical and fatty acid composition of dietary treatments.

Blend of 80% canola oil and 20% palm oil, %.

\[
\text{SFA} = \frac{\text{C12:0} + \text{C14:0} + \text{C16:0} + \text{C18:0}}{\text{Total FA}}, \quad \text{MUFA} = \frac{(\text{C16:1} + \text{C18:1})}{\text{Total FA}}, \quad \text{PUFA} = \frac{(\text{C18:2n-6} + \text{C18:3n-3})}{\text{n-6:n-3}}.
\]
Sampling of rumen fluid

After the 100 d feeding trial, the goats were fasted for 12 h with ad libitum access to water and slaughtered according to the Halal procedure. After evisceration, within 10 min post-mortem, the rumen contents were sampled from the dorsal caudal, ventral caudal, dorsal cranial and ventral cranial parts of the rumen, pooled together and strained through four layers of cheesecloth to obtain the rumen fluid. The rumen fluid was snap frozen in liquid nitrogen and stored at −80 °C until analysis.

Extraction of DNA from rumen microbes

The DNA was extracted from rumen fluid using the hexadecyltrimethylammonium bromide (CTAB) DNA extraction method. Each sample (1.5 mL) was centrifuged at 12,000 g for 5 min. The supernatant was transferred into a clean autoclaved 1.5 mL centrifuge tubes and 200 mg silica beads was added. Thereafter, 800 µL CTAB isolation buffer (100 mM Tris-HCl, pH 8; 1.4M NaCl; 20 mM EDTA (Sodium salt); 2% CTAB) was added and beat for 2 min (fast prep setting 5). The bead beating was repeated twice. The samples were incubated at 70 °C for 20 min, and centrifuged at 15,000 g for 15 min. The supernatant was dispensed into a new tube, 500 µL phenol was added and the mixture was vortex to form a white emulsion. Thereafter, the samples were centrifuged at 15,000 g for 15 min and 500 µL of the upper aqueous layer was removed into another Eppendorf tube. A 300 µL of isopropanol was added mixed gently. The samples were incubated at room temperature for 10 min for the DNA to precipitate. The samples were centrifuged at 15,000 g for 20 min. The supernatant was decanted off leaving behind a grey pellet of DNA. The pellet was washed in 1 mL 70% ethanol, incubated at 70 °C for 10 min with continuous agitation and centrifuged at 13,000 g for 10 min. The ethanol was poured off and the pellet was dried at 70 °C. The pellet was re-suspended in 50 µL of RNA-free water. The samples were stored at −80 °C until further analysis. The concentration and purity of the DNA was measured with a BioPhotometer Plus (Eppendorf, Hamburg, Germany).

Quantitative real-time PCR

A standard curve method in real-time PCR was used to quantify rumen bacteria, protozoa and methanogen populations. The standard curves were constructed using the number of copies of the 16S rRNA gene plotted against quantification cycle (Cq) that was obtained from ten-fold serial dilutions of PCR products from a pure culture of each group of rumen microorganism. The DNA was extracted from the pure culture of each targeted rumen microorganisms in order to prepare the standard curves. The bacterial DNA was amplified using conventional PCR. The PCR products of the targeted rumen microorganisms were run in 1% agarose gel and specific bands were purified using the mEGAquick-spinTM purification kit (iNtRON Biotechnology, Seongnam, Korea).

The concentration and purity of 16S rRNA gene in each sample was determined using a Nanodrop ND-1000 spectrophotometer (Implen NanoPhotometerTM, Munich, Germany). The number of copies of the 16S rRNA gene per ml of elution buffer was quantified using the formula obtained online in URI Genomics and Sequencing Centre web-based calculator (www.uri.edu/research/gsc/resources/cndna.html).

\[
\text{Number of copies} = \frac{\text{Amount of DNA (1µg/mL)} \times 6.022 \times 10^{23}}{\text{Length (bp)} \times 10^9 \times 650}
\]

Since the amplification efficiency among templates and primers may be variable, the amplification efficiency (E) of each primer-template combination was estimated based on the slope value of the linear

| Microorganism | Sequence 5’–3’ | Product size, bp | Annealing temperature, °C | Reference |
|---------------|---------------|-----------------|--------------------------|-----------|
| Total bacteria F<sup>a</sup> | CCG CAA CGA GGC CAA CCC | 145 | 55 | Denman and McSweeney (2006) |
| Total bacteria R<sup>b</sup> | CCA TAG TAG CTC GTG TGC ACG C | 223 | 55 | Sylvester et al. (2004) |
| Total protozoa F<sup>a</sup> | CCA TCT CTG YAA TCG GTA TT | 140 | 55 | Denman et al. (2007) |
| Total protozoa R<sup>b</sup> | GCT GGT GTG AAG GTA TT | 122 | 55 | Denman and McSweeney (2006) |
| Methanogens F<sup>a</sup> | TCC GCT GGA TCD CAR AGR GC | 175 | 55 | Koike and Kobayashi (2001) |
| Methanogens R<sup>b</sup> | CGC TCC CCC CTC TAT C | 295 | 55 | Koike and Kobayashi (2001) |
| Fibrobacter succinogenes F<sup>a</sup> | GTG CAG AAT TAC TCG TGC TAA A | 122 | 55 | Denman and McSweeney (2006) |
| Fibrobacter succinogenes R<sup>b</sup> | CGC CTG CCG CTC TAT T | 122 | 55 | Denman and McSweeney (2006) |
| Ruminococcus albus F<sup>a</sup> | CCC TAA AAG CAG TCT TAG TTC G | 175 | 55 | Koike and Kobayashi (2001) |
| Ruminococcus albus R<sup>b</sup> | CCT CCT GCC TAG GAC A | 295 | 55 | Koike and Kobayashi (2001) |
| Ruminococcus flavefaciens F<sup>a</sup> | TCT GGA AAC GGA TGG TA | 175 | 55 | Koike and Kobayashi (2001) |
| Ruminococcus flavefaciens R<sup>b</sup> | CCT TTA AGA CAG TTA ACA A | 295 | 55 | Koike and Kobayashi (2001) |

<sup>a</sup>Forward.  
<sup>b</sup>Reverse.
regression of each standard curve determined by the equation below:

\[
E(\%) = \left(10^{\frac{-1}{\text{slope}}} - 1\right) \times 100
\]

where \(E\) is 100% if a ten-fold dilution of DNA template results in a Cq difference of 3.32.

The sequences and primers used to quantify the number of different microbes are shown in Table 2. The Real-time PCR was conducted with the Bio-Rad CFX96 Touch (Bio-Rad Laboratories, Hercules, CA) using optical grade plates. The PCR reaction was performed on a total volume of 25 \(\mu\)L using the iTQ SYBR Green Supermix (Bio-Rad Laboratories, Hercules, CA). Each reaction included 12.5 \(\mu\)L SYBR Green Supermix, 1 \(\mu\)L of forward primer, 1 \(\mu\)L of reverse primer 2 \(\mu\)L of DNA samples and 8.5 \(\mu\)L RNase-free water. The conditions applied to each well included an initial incubation at 94°C for 5 min; 40 cycles of denaturation at 94°C for 20 s, annealing for 30 s and for 20 s at 72°C. A melting curve analysis was conducted after the last cycle of each amplification to confirm the specificity of the amplification.

**Statistical analysis**

The experiment followed a completely randomised design model. Some real-time PCR data, which did not meet the ANOVA requirement of normality were subjected to logarithm transformation prior to analysis. The real-time PCR and nitrogen metabolism data were subjected to the generalised linear model (GLM) procedure of SAS. The level of significance was set at \(p < .05\). Linear and quadratic orthogonal contrasts were tested using the contrast statement of SAS with coefficients estimated based on the levels of dietary oil blend.

**Results**

**Rumen microbiota**

The rumen microbial populations of goats fed graded levels of oil blend are presented in Table 3. The population of total protozoa decreased \((p < .05)\) as the level of oil blend increased in diet. The 4% and 8% oil blend reduced the population of total protozoa by 71% and 86% respectively. The population of total methanogens did not differ \((p > .05)\) between goats fed 4 and 8% oil blend but was lower \((p < .05)\) than that of the control goats. The 4% and 8% oil blend reduced the population of methanogens by 62% and 66%, respectively.

Goats fed 8% oil blend had higher \((p < .05)\) total rumen bacteria compared with those fed other diets. The population of total bacteria did not differ \((p > .05)\) between goats fed 0 and 4% oil blend. The population of *Fibrobacter succinogenes* did not differ \((p > .05)\) between goats fed 4 and 8% oil blend but was higher \((p < .05)\) than that of the control goats. The population of *F. succinogenes* increased by 32% and 34% in response to 4% and 8% oil blend respectively. The populations of *Ruminococcus flavefaciens* and *Ruminococcus albus* were higher \((p < .05)\) in goats fed 4% oil blend compared with those fed other diets. The 8% oil blend had greater \((p < .05)\) population of *R. flavefaciens* and *R. albus* compared with the control goats. The 4 and 8% oil blend increased the population of *R. flavefaciens* by 106% and 48% respectively. The population of *R. albus* increased by 80% and 44% in response to 4% and 8% oil blend respectively.

**Nitrogen metabolism**

Table 4 presents the components of nitrogen metabolism in goats fed graded level of oil blend. Nitrogen intake, retention and excretion (faecal and urine) did not differ \((p > .05)\) among diets. Similarly, diet had no effect \((p > .05)\) on microbial N yield, microbial protein synthesis and efficiency of microbial protein synthesis in goats.

**Discussion**

Diet is one of the major determinants of rumen microbial populations (Mao et al. 2010). Dietary oil blend

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**Table 3. Mean population of total bacteria, protozoa, methanogen, *Fibrobacter succinogenes*, *Ruminococcus albus* and *Ruminococcus flavefaciens* in ruminal fluid (copy no/mL) of goats fed dietary oil blend.**

| Microorganism                  | 0                   | 4                   | 8                   | SEM     | Linear    | Quadratic |
|--------------------------------|---------------------|---------------------|---------------------|---------|-----------|-----------|
| Total bacteria \(\times 10^{11}\) | 5.28<sup>a</sup>    | 5.49<sup>b</sup>    | 7.41<sup>a</sup>    | 0.212   | 0.040     | 0.424     |
| Total protozoa \(\times 10^{5}\) | 7.16<sup>a</sup>    | 2.06<sup>b</sup>    | 0.97<sup>c</sup>    | 0.094   | 0.001     | 0.018     |
| Methanogens \(\times 10^{4}\)   | 5.92<sup>a</sup>    | 2.30<sup>b</sup>    | 2.06<sup>b</sup>    | 0.107   | 0.016     | 0.684     |
| *Fibrobacter succinogenes* \(\times 10^{6}\) | 4.19<sup>b</sup>    | 5.53<sup>a</sup>    | 5.63<sup>a</sup>    | 0.303   | 0.015     | 0.764     |
| *Ruminococcus albus* \(\times 10^{5}\) | 393<sup>a</sup>     | 709<sup>a</sup>     | 565<sup>a</sup>     | 42.25   | 0.002     | 0.042     |
| *Ruminococcus flavefaciens* \(\times 10^{6}\) | 3.13<sup>a</sup>     | 6.44<sup>a</sup>     | 4.62<sup>a</sup>     | 0.108   | 0.004     | 0.111     |

<sup>a,b,c</sup>Means having different superscript along the same row are significantly different \((p < .05)\). SEM: standard error of mean.
decreased the population of rumen protozoa. Rumen protozoa have a limited capacity to take up, assimilate and transform dietary lipids and high concentrations of dietary lipids are toxic to protozoa (Liu et al. 2012; Ivan et al. 2013). In line with the current observation, a decrease in the population of protozoa in response to dietary fat (Mao et al. 2010; Liu et al. 2012) and oil seeds (Ivan et al. 2013) has been documented. The decrease in the population of protozoa could be responsible for the increase in the population of cellulolytic bacteria in the oil-supplemented goats. Rumen protozoa are predators of bacteria (Mao et al. 2010; Liu et al. 2012). The consumption and digestion of bacteria by rumen protozoa is a wasteful process, which causes undesirable recycling of nitrogen in the rumen (Lee et al. 2011).

The decrease in the population of protozoa following oil supplementation was accompanied by a decrease in the population of methanogens. However, the reduction in the population of methanogens was lower than that of protozoa. This implies that rumen protozoa were more sensitive to the oil blend than the methanogens. This observation is similar to that of Mao et al. (2010) who observed that dietary soybean oil reduced the population of methanogens in lambs. Rumen protozoa are implicated in methane production because of the endo- and ecto-symbiotic relationships between rumen protozoa and methanogens (Lee et al. 2011). The reduction in the population of protozoa and methanogen in oil-supplemented goats lends credence to the reduction in the methane concentration in the goats (Adeyemi et al. 2016).

The R. albus, R. flavefaciens and F. succinogenes are the most predominant culturable cellulolytic species in the rumen and as such, changes in their relative population could potentially affect ruminal fibre metabolism and concentrations of VFA (Liu et al. 2012). Oil-supplemented goats had higher population of R. flavefaciens and F. succinogenes compared with the control goats. This finding could be due to the reduction in the population of rumen protozoa. The response of cellulolytic bacteria to fat supplementation has yielded inconsistent results in the published literature. Mao et al. (2010) found that the supplementation of 3% soybean oil reduced the population of F. succinogenes and R. flavefaciens. In addition, Zhang et al. (2008) reported that supplementation of C18:3n-3, C18:2n-6, C18:1n-9 and C18:0 at 35 and 70 g/kg DM of substrate decreased the population of R. flavefaciens and F. succinogenes in vitro. In contrast, supplementation of different blends (1:1, 2.5:1.5 and 1:2.5) of sunflower oil and fish oil at 4% reduced the population of F. succinogenes but did not affect the populations of R. albus and R. flavefaciens in steers (Liu et al. 2012). In addition, Ivan et al. (2013) observed that feeding oil-seeds rich in C18:2n-6 and C18:3n-3 increased the population of R. albus and R. flavefaciens but depressed the population F. succinogenes in dairy cows.

The population of total bacteria did not differ between goats fed the 4% oil blend and those fed the control diet. This observation was contrary to our expectation given the decrease in the concentration of ruminal protozoa in goats fed the 4% oil blend compared with the control goats. This observation suggests that the increase in the population of F. succinogenes, R. albus and R. flavefaciens in goats fed 4% oil blend was at the expense of other bacteria species that were not considered in the present study. The significant increase in the population of total bacteria in goats supplemented with 8% oil blend is consistent with the decrease in the population of rumen protozoa. It could be inferred that the decrease in rumen protozoa instigates an increase in the

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**Table 4. Mean nitrogen intake, retention, excretion, and microbial protein synthesis in goats fed graded levels of oil blend.**

| Parameter                          | Levels of oil blend, % | p Value |
|------------------------------------|------------------------|---------|
|                                    | 0          | 4        | 8        | SEM  | Linear | Quadratic |
| N intake, g/d                      | 19.49      | 19.59    | 19.70    | 0.431| .136   | .101      |
| Faecal N, g/d                      | 5.02       | 4.83     | 5.55     | 0.120| .091   | .112      |
| Urine N, g/d                       | 1.90       | 2.07     | 1.84     | 0.060| .241   | .201      |
| Total N excreted                   | 6.92       | 6.90     | 7.39     | 0.303| .112   | .216      |
| N absorbed, g/d                   | 14.46      | 14.67    | 14.18    | 0.312| .143   | .108      |
| N retained, g/d                   | 12.57      | 12.69    | 12.34    | 0.214| .100   | .121      |
| N retained, % of intake           | 63.67      | 64.77    | 62.64    | 0.591| .085   | .092      |
| N retained, % of N absorbed       | 86.92      | 86.50    | 87.70    | 0.540| .105   | .209      |
| Microbial N yield, g/d            | 13.34      | 12.90    | 12.96    | 0.309| .210   | .101      |
| Microbial protein synthesis, MPS, g/d | 83.40   | 80.64    | 80.98    | 1.607| .221   | .145      |
| Efficiency of MPS (g/d)           | 44.62      | 45.29    | 46.33    | 1.495| .092   | .109      |

SEM: standard error of mean.

TDN intake kg/g microbial crude protein.
population of some species of bacteria other than the cellulolytic bacteria.

The population of *R. albus* and *R. flavefaciens* bacteria differed between goats fed 4 and 8% oil blend. Goats fed 4% oil blend had greater population of *R. albus* and *R. flavefaciens* compared with other treatments. This suggests a possible interaction between the level of dietary oil, protozoa population and the population of cellulolytic bacteria. It could be inferred that there is a limit of level of oil blend that the cellulolytic bacteria could tolerate and the 4% oil blend seemed to be the limit. Nonetheless, despite the significant changes in the population of cellulolytic bacteria between the oil-supplemented goats and the control goats, the NDF and ADF intake and digestibility did not differ among the diets (Adeyemi et al. 2016).

Dietary oil blend had no effect on the N intake, N retention and faecal and urine excretion of N in goats. This finding could be attributed to the homogenous DM and crude protein intake (Adeyemi et al. 2016). The current observation is consistent with the similarity in the concentration of ammonia nitrogen among the diets as shown in a companion study (Adeyemi et al. 2016). Similarly, dietary oil blend had no effect on the microbial nitrogen, microbial protein synthesis and the efficiency of microbial protein synthesis. This observation was unexpected given the significant decrease in the population of rumen protozoa in the oil-supplemented goats compared with the control goats. A decrease in protozoa population results into less engulfment of bacteria and shortens nitrogen cycle in the rumen (Lee et al. 2011). However, Doreau and Ferlay (1995) posited that reduction in protozoa population by dietary fat would bring about an increase in efficiency of microbial protein synthesis only if the dietary fat reduce OM digestibility in the rumen. The current observation is consistent with the findings of Freitas Júnior et al. (2014) who observed that dietary 3% soybean oil or calcium salt of unsaturated fatty acids did not affect microbial protein synthesis in dairy cows. In contrast, free or protected linseed oil and coconut oil (Sutton et al. 1983) reduced OM digestibility in the rumen, and the population of rumen protozoa and enhanced microbial protein synthesis in sheep.

**Conclusions**

The results of this study showed that rumen microbial profile in goats varied in response to dietary oil blend. The population of protozoa and methanogens was lower while that of *R. flavefaciens*, *R. albus* and *F. succinogenes* was higher in oil-supplemented goats compared with the control goats. Goats fed 4% oil blend had higher population of *R. flavefaciens* and *R. albus* compared to those fed other diets. Dietary oil blend had no effect on nitrogen metabolism in goats. The 4% oil blend seems optimal for manipulating the rumen microbiota in goats. Further research is suggested to determine other groups of rumen bacteria that could be influenced by the oil blend.

**Disclosure statement**

The authors declare that they have no conflicts of interest.

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