METHANE PRODUCTION AND EFFICIENCY OF FEED ENERGY UTILIZATION BY INCLUSION OF UREA TREATED COCOA FEED AS BARLEY GRAIN SUBSTITUTION IN RUMINANT RATION

Despal
Dept. Animal Nutrition & Feed Technology, Fac. Animal Science, Bogor Agricultural University, Indonesia Jl. Agatis, Kampus IPB Darmaga, 16680 Bogor email: despal@ipb.ac.id]

BACKGROUND

According to US-EPA (2009), enteric fermentation in ruminant stomach is the largest anthropogenic source of CH_4 emissions in the United States in year 2007 (24 percent of total CH_4 emissions). The gas represent energy loses and therefore reduced feed energy efficiency (Pelchen and Peters, 1994). Methane production was higher in ruminant fed low quality feedstuff such as cocoa pod, the major feed resources available in Indonesia. In opposite, feeds that allow a high efficiency of microbial protein cell synthesis produce low amounts of methane per unit of feed digested (Leng, 1982). Improvement fibrous feed quality using urea treatment (Chenost, 2001) can reduce up to 20% of CH_4 emission and improve feed energy conversion simultaneously. Despal (2005) have been found that 20 g urea per kg cocoa pods (w/w fresh material) improved cocoa pods digestibility better than applications of 10 and 30 g urea.

METHODS

The improved urea treated cocoa pod (CPs) was used as substitute (0, 25, 50, 75 and 100%) of barley enriched with soybean (barley) in ruminant ration. The study was conducted in rumen simulation technique according to Czerkawski and Breckendridge (1977) procedures (figure 1) to observe the effect of the rations on CH_4 production and energy feed utilization by rumen microbial. Composition of the rations fed daily to fermenters were 10 g hay as basal ration (R1), 10 g hay + 4 g barley (R2), 10 g hay + 3 g barley + 1 g CPs (R3), 10 g hay + 2 g barley + 2 g CPs (R4), 10 g hay + 1 g barley + 3 g CPs (R5) and 10 g hay + 4 g CPs (R6).

RESULTS

Up to 25% of cocoa pods could replace barley grain in ruminant ration. Decreasing CH_4 production in ration contained > 25% urea treated cocoa pod were caused by the low activities of microbial which lead to low digestibility and feed efficiency.

Table 2: Efficiency of microbial protein synthesis expressed in different terms

Parameters	Treatments					
	R1	R2	R3	R4	R5	R6
TOMD (HF + MC) g/d	2.95^{a}	4.14^{e}	3.91^{de}	3.72^{cd}	3.61^{bc}	3.37^{b}
Microbial-N/OMAD (mg/g)	13.3^{b}	12.4^{ab}	11.9^{ab}	11.6^{a}	12.9^{ab}	12.5^{ab}
Microbial-N/TOMD (mg/g)	19.1^{c}	16.6^{a}	16.8^{a}	16.9^{a}	17.7^{ab}	18.5^{bc}
Microbial-N/HF (mg/g)	25.1^{c}	21.0^{a}	21.3^{a}	21.5^{a}	22.7^{ab}	24.0^{bc}
Microbial-N/SCFA (mg/mmol)	2.27^{c}	1.93^{a}	1.96^{ab}	1.97^{ab}	2.07^{abc}	2.16^{bc}
Microbial-N/ATP* (mg/mmol)	1.27^{b}	1.09^{a}	1.10^{a}	1.10^{a}	1.15^{a}	1.20^{ab}
CH_4/SCFA (mmol/mmol)	0.22	0.21	0.23	0.22	0.21	0.21
CH_4/OMAD (mmol/g)	1.29	1.37	1.40	1.29	1.28	1.23
CH_4/TOMD (mmol/g)	1.84	1.83	1.99	1.88	1.78	1.82
CH_4/NDF disappearance (mmol/g)	2.86^{ab}	3.55^{c}	3.29^{bc}	2.97^{abc}	2.89^{ab}	2.42^{a}

TOMD = truly organic matter digested; HF = hexose fermented; MC = microbial cell; OMAD = Organic matter digestibility; SCFA = Short chain fatty acid, ATP = Adenosine tri-phosphate; *) ATP = 2 Acetate + Propionate + 3 Butyrate (mmol/day); different superscript at the same row represent significantly different at P < 0.05.

Table 1: Effect of replacing barley/soybean meal-mixture by urea treated cocoa pod on fermentation characteristics in Rusitec

Parameter	Treatment					
	R1	R2	R3	R4	R5	R6
PH	6.63^{d}	6.51^{a}	6.52^{ab}	6.54^{b}	6.59^{c}	6.63^{d}
Protozoa (cts/ml)	17475	17868	16310	14267	13672	12436
CH_4 (mmol/d)	5.45^{a}	7.51^{de}	7.71^{e}	6.95^{cd}	6.38^{bc}	6.02^{ab}
NH_4^+ (mmol/l)	5.64^{a}	8.31^{d}	7.42^{c}	7.28^{c}	6.68^{b}	6.48^{b}
SCFA (mmol/d)	24.88^{a}	35.61^{b}	33.59^{b}	31.94^{ab}	30.94^{ab}	28.78^{ab}
acetate	14.46^{a}	18.84^{b}	18.47^{b}	17.85^{ab}	17.80^{ab}	17.26^{ab}
propionate	6.07^{a}	9.20^{b}	8.57^{b}	7.76^{ab}	7.52^{ab}	6.59^{a}
iso-butyrate	0.17	0.25	0.18	0.16	0.15	0.20
n-butyrate	3.02	5.14	4.58	4.45	3.94	3.41
iso-valerate	0.60^{a}	1.12^{d}	0.98^{cd}	0.88^{bc}	0.79^{abc}	0.70^{ab}
n-valerate	0.56	1.06	0.81	0.84	0.75	0.63
Microbial cells (mgDM/d)	700^{a}	859^{c}	821^{b}	782^{b}	793^{b}	776^{b}

CH4 = methane; NH4+ = ammonia concentration; SCFA = Short chain fatty acid; different superscript at the same row represent significantly different at P < 0.05.

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