Microbial Phospholipid Synthesis as a Marker for Microbial Protein Synthesis in the Rumen

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Phosphate uptake into intracellular inorganic phosphorus and cellular phospholipids and the relationship between cell growth and phospholipid synthesis were studied with suspensions of washed ruminal bacteria in vitro with $^{32}$P-phosphorus. It was shown that ruminal bacteria accumulated inorganic phosphate at a low rate when incubated without substrate. Upon the addition of substrate, the rate of inorganic phosphorus uptake into the cells increased markedly, and phospholipid synthesis and cell growth commenced. There was a highly significant relationship ($r = 0.98; P < 0.01$) between phospholipid synthesis and cell growth. The specific activity of the intracellular inorganic phosphorus did not equilibrate with phosphorus medium. When ruminal contents from sheep fed a high or low protein diet were incubated in vitro, the rate of $^{32}$P incorporation into microbial phospholipids was higher for the high protein diet. Since there was a high relationship between phospholipid synthesis and growth, rumen contents were collected before and various times after feeding and incubated with $^{32}$P-phosphorus in vitro. The short-term, zero time approach was used to measure the rate of microbial phospholipid synthesis in whole rumen contents. In these studies the average specific activity of the intracellular inorganic phosphorus was used to represent the precursor pool specific activity. Microbial phospholipid synthesis was then related to protein (N × 6.25) synthesis with appropriate nitrogen-to-phospholipid phosphorus ratios. Daily true protein synthesis in a 4-liter rumen was 185 g. This represents a rate of 22 g of protein synthesized per 100 g of organic matter digested. These data were also corrected for ruminal turnover. On this basis the rate of true protein synthesis in a 4-liter rumen was 16.1 g of protein per 100 g of organic matter digested. This value represents a 30-g digestible protein-to-Mcal digestible energy ratio which is adequate for growing calves and lambs.

Hungate (19) calculated adenosine triphosphate (ATP) yields from known pathways of ruminal fermentation of carbohydrates. By using a Y ATP = 10 (3, 34), he concluded that about 10 g of microbial protein (about 15 g of total cell mass) can be synthesized for each 100 g of carbohydrate fermented. This value was thought to represent an upper limit of the synthetic capacity of anaerobic ruminal fermentation (19). This level of protein synthesis in the rumen is equivalent to 18.3 g of digestible protein per Mcal of digestible energy (36) and is clearly below the requirement of growing ruminants (36). From a husbandry viewpoint, this result implied that, for optimal growth or production of ruminants, procedures to allow dietary protein to escape ruminal degradation must be developed.

Extensive direct experimental work on quantitative aspects of ruminal microbial protein synthesis indicates, however, that the limits set by Hungate (19) were too low. Thus, growth yield studies with strains of rumen bacteria (11, 12, 18) and ingesta passage studies with sheep by using purified diets or microbial cell markers (14, 15, 17, 27) indicated that ruminal microbial protein synthesis ranged from 15 to 22 g of microbial protein per 100 g of organic matter fermented. Other recent reports (13, 21) have also suggested that the ATP yield per mole of hexose fermented in the rumen is higher than previously anticipated.
The experiments described below were initiated to measure absolute bacterial and protozoal protein synthesis rates in whole rumen contents at various times after feeding with short-term, zero time in vitro (6) incubations. Since membrane (phospholipids) synthesis and growth are directly related (31, 33) and since growth and protein synthesis are directly related (28) in microorganisms, protein synthesis rates of ruminal microorganisms were assessed by measuring the rate of microbial phospholipid synthesis.

MATERIALS AND METHODS

Radioactive phosphorus-labeling pattern of cellular phosphorus containing constituents during in vitro incubations of mixed ruminal bacteria: experiment 1. The labeling patterns of cellular phosphorus by $^{32}$P-inorganic phosphorus were studied in suspensions of mixed ruminal bacteria in a high and low phosphorus medium in vitro. Rumen contents were collected as outlined by Purser and Moir (37) from sheep fitted with Jarret cannulae (fed ration 1, Table 1) before the morning feeding, placed in a vacuum bottle warmed to 39 C, gassed with oxygen-free CO$_2$, and transported quickly to the laboratory. Rumen contents from sheep are quite homogenous, and samples of 100 g or more are representative of whole rumen contents (37). The rumen contents were subsequently squeezed through two layers of cheesecloth. Rumen liquor (500 ml for high PO$_4$, and 800 ml for low PO$_4$, media) was then centrifuged at 500 x g for 15 min at 2 C. The pellet was discarded, and the supernatant was centrifuged at 10,000 x g for 15 min at 2 C. The resulting pellet (bacterial fractions; 300 to 400 mg dry weight for the high PO$_4$, and 150 to 200 mg dry weight for the low PO$_4$, media) was resuspended in the original rumen liquor volume in reduced anaerobic buffer (AB; Table 2) containing either 180 or 35 $\mu$g of phosphorous, pH 6.7, per ml. During the centrifugation steps, all tubes and beakers were gassed with O$_2$-free CO$_2$ to insure anaerobiosis. The ruminal bacteria fractions were then transferred into prewarmed fermentation flasks (1 liter) and incubated at 39 C under O$_2$-free CO$_2$. Radioactive phosphorus ($^{32}$P-P$_2$O$_5$; ca. 60 x $10^8$ DPM) dissolved in AB was then added to the fermentation flask, and initial subsamples (80 ml) were secured. For the experiments with the high PO$_4$ media, substrate (0.6% glucose, 0.5% soluble starch, and 0.15% urea; expressed as percent weight of the final volume of the fermentation system) was added and further subsamples were obtained at 30, 60, 120, 180, and 240 min. For the experiments with the low PO$_4$ media, inorganic phosphorus uptake by resting bacteria and actively growing bacteria was studied in the manner outlined by Mitchell and Moyle (31). Thus, substrate (as above) was added after 90 min of incubation. Subsamples (as above) were obtained at 30, 60, 90, 120, 150, 210, 270, and 330 min for the low PO$_4$ media fermentsations. To stop bacterial activity, subsamples were placed in prechilled beakers which were then placed in a solution of solid CO$_2$ in ethanol.

### Table 1. Experimental rations fed to sheep

| Ingredients                  | Ration (%) |
|------------------------------|------------|
| Corn cob pellets             | 10.0       |
| Alfalfa meal (deh)           | 15.0       |
| Rolled oats                  | 26.0       |
| Ground corn                  | 22.0       |
| Wheat bran                   | 10.0       |
| Soybean meal                 | 5.0        |
| Ground wheat straw           | 10.0       |
| Glucose monohydrate          | 10.0       |
| Corn starch                  | 14.0       |
| Urea (feed grade)            | 0.5        |
| Molasses                     | 9.0        |
| Mineral-vitamin mix$^a$      | 2.5        |

Crude protein (N x 6.25)$^b$

| Estimated digestible energy (kcal/kg)$^c$ |
|------------------------------------------|
| Sheep were fed at the rate of 158 kcal of digestible energy per bodyweight 0.75 kg per day (27) with equal portions offered at 8 a.m. and 5 p.m. |

$^a$ Sheep were fed at the rate of 158 kcal of digestible energy per bodyweight 0.75 kg per day (27) with equal portions offered at 8 a.m. and 5 p.m.

$^b$ Contents (in percent; 42.29 dicalcium phosphate; 42.29 high Zn trace mineral salt; 15.0 Na$_2$SO$_4$; 0.52 vitamin A premix [10,000 IU/g], and 0.10 vitamin D premix [8,000 IU/g]).

$^c$ Based on crude protein and digestible energy values from NRC publication 1684, U.S.-Canadian Tables of Feed Composition, 1969.

### Table 2. Anaerobic buffer

| Ingredients                  | Milliliters per 100 ml |
|------------------------------|------------------------|
|                             | High phosphorus media  | Low phosphorus media |
| Mineral solution I$^d$        | 7.5                    |                        |
| Mineral solution II$^d$       | 7.5                    |                        |
| Mineral solution III$^d$      | 7.5                    |                        |
| Water                       | 82.34                  | 90.84                  |
| 12% Na$_2$CO$_3$             | 1.11                   | 1.11                   |
| 3% Cysteine-hydrochloride    | 0.56                   | 0.56                   |

$^d$ The mineral-water solution was heated to 95 C and gassed with O$_2$-free CO$_2$, followed by the addition of Na$_2$CO$_3$ and cysteine; equilibrated under CO$_2$ at 39 C, and then finally adjusted to pH 6.7 with 1 N NaOH or 1 N HCl.

$^e$ Phosphorus, 180 $\mu$g/ml.

$^f$ Phosphorus, 35 $\mu$g/ml.

$^g$ K$_2$HPO$_4$, 0.3% (wt/vol).

$^h$ Contents: 0.3% KH$_2$PO$_4$; 1.2% Na$_2$SO$_4$; 0.6% NaCl; 0.6% MgSO$_4$·7H$_2$O; 0.06% CaCl$_2$·2H$_2$O (wt/vol).

$^i$ Contents: 0.58% tris(hydroxymethyl)aminomethane (mol wt 121.0); 1.28% Na$_2$SO$_4$; 1.2% NaCl; 0.12% MgSO$_4$·7H$_2$O; 0.12% CaCl$_2$·2H$_2$O; 7.47% K$_2$HPO$_4$ (wt/vol).
When the temperature of the subsample reached 2 to 5 C, the subsamples were centrifuged at 18,000 × g for 15 min at 3 C. The pellet was then resuspended and washed with a small quantity of deionized water and recovered by centrifugation. The pellets were then frozen, lyophilized, and stored for phospholipid, intracellular and total phosphorus, and 32P activity analysis. Increases in cellular dry matter and protein (N × 6.25) content were determined on separate subsamples. A sample of cell-free media was secured and frozen for inorganic phosphorus and 31P analysis.

Radioactive phosphorus incorporation into microbial phospholipids of rumen contents in vitro from sheep: experiment 2. Sheep (fitted with Jarret cannulae) were placed on ration 2 (high protein) or 3 (low protein) (Table 1, one sheep per ration) for a 3-week period. Rumen contents were collected, as described above, from the sheep before (0 h) and 2 and 4 h after the morning feeding. Upon arrival at the laboratory, 150 g of rumen contents was weighed into a wide-mouth fermentation flask (800 ml) (under an O2-free CO2 atmosphere), and 6 ml of a solution containing 32P-H3PO4 (13.2 × 104 DPM) was added. The flask was sealed and then shaken for 30 s, and an initial subsample was removed. Preliminary work showed that 6 ml of 1% crystal violet could be well mixed with 150 g of rumen contents within 30 s under these conditions. Further subsamples were obtained at 30, 60, 120, 180, and 240 min of the in vitro incubation. After each sampling the flask was flushed with O2-free CO2 and resealed. The microorganisms were killed by the addition of 0.05 volume of saturated HgCl2. After washing to remove unincorporated 32P, the samples were frozen and lyophilized.

Microbial phospholipid synthesis and microbial protein synthesis in whole rumen contents of sheep: experiment 3. Rumen contents were collected from sheep fed ration 1 (Table 1) before (0 h) and 2, 4, and 9 h after the morning feeding. One sheep served as the donor of rumen contents for two separate experiments. Short-term, zero time method (6, 20) in vitro incubations were conducted with rumen contents as described above, except 750 g of rumen contents was placed in the fermentation flasks. After the additions of 32P-H3PO4 (about 44 × 104 DPM), an initial subsample (350 g) was obtained. The final sample was obtained after 60 min. The microorganisms were killed with saturated HgCl2. Each subsample was divided in the following manner. From the well-mixed subsample, a 20-g sample was used to determine 32P incorporation into total microbial phospholipids. The particulate matter was spun down and then resuspended and washed in saline and centrifuged at 18,000 × g three times to remove unincorporated, free, and nonspecifically bound 32P. The residue was then frozen and lyophilized. The remaining rumen contents from the subsamples (305 g) were squeezed through two layers of cheesecloth. The particulate matter was then resuspended in 0.85% NaCl, stirred, and squeezed again through two layers of cheesecloth. Microscopy examination revealed that this procedure removed all except a few small protozoa from the residual plant matter and rumen contents. It was therefore assumed in subsequent calculations that total protozoal protoplasmic mass had been recovered quantitatively from rumen contents by this procedure. A small sample was removed from the rumen liquor for phosphorus and volatile fatty acid (VFA) analysis. The rumen liquor and extract from the second squeeze were then combined. The protozoa and bacteria were separated from the rumen fluid by differential centrifugation as described by Bergen et al. (4). Microscopy examination of the high-speed (bacterial) and 150 × g (protozoal) fractions were done in a separate (i.e., no isolate) study. It was found that the 150 × g (protozoal) and the high-speed (bacterial) fractions were devoid of gross plant material contamination. Previous work had shown that this differential centrifugation system (4) resulted in 150 × g (protozoal) and high-speed (bacterial) fractions which contained only 1.5 and 0.7% (based on dry matter) crude fiber (W. G. Bergen, unpublished data). The 150 × g (protozoal) and high-speed (bacterial) fractions were then frozen and lyophilized.

Analytical procedures. Preliminary experiments were conducted to assess the efficacy of various extraction procedures for phospholipids from ruminal microorganisms and the salt wash procedure of Folch et al. (10). During these studies, microbial preparations were extracted and reextracted in organic solvents, and the extracts were then monitored for phospholipids with thin-layer chromatography. Similarly, the salt wash procedure was checked to assure that only inorganic, but not phospholipid, phosphorus was lost during the wash. In a number of trials, upon addition of 32P-H3PO4 to chloroform-methanol (2:1), after the salt wash only 0.3% of the initial radioactivity remained in the solvent. For the experiments described above, microbial phospholipids were extracted from lyophilized rumen contents, high-speed (bacterial), or 150 × g (protozoal) preparations by a modification of the method described by Katz and Keeney (24). Approximately 30 mg of sample was extracted with 5 ml of chloroform-methanol (2:1; vol/vol) in 15 ml of Teflon-lined screw-capped culture tubes. The tubes were rotated from 16 to 20 h in room temperature. The extracts were filtered through a fritted glass Buchner funnel and the nonlipid impurities were removed by the salt wash procedure (10). Sonic treatment of microbial preparations did not improve the yield of total lipid extraction. Phospholipid phosphorus was determined in the washed extract by the ascorbic acid procedure of Chen et al. (7) as modified by Rhee and Dugan (39). Total cellular phosphorus and phosphorus concentration in incubation media were determined by the procedure of Chen et al. (7). Intracellular inorganic phosphorus (IC-P) was extracted from 30 to 100 mg of lyophilized microbial preparation with 4.0 ml of 5% perchloric acid (PCA) for 30 min at 5 C in an all-glass Potter-Elvehjem homogenizer (25, 41). The homogenates were centrifuged at 18,000 × g for 15 min. Inorganic phosphorus in the PCA extract was then determined by the isobutanol-benzene-ammonium molybdate procedure of Lindberg and Ernster.
Nitrogen was determined with a micro-Kjeldahl procedure. VFA were determined from media treated with metaphosphoric acid (9) on a Teflon column (198 by 0.05 cm) packed with Chromosorb 101 (60-80 mesh) at 188 C with nitrogen as carrier gas and a hydrogen flame detector. Dry matter of subsamples was determined by drying at 110 C to a constant weight (this took 20-24 h). Suitable samples of all phosphorus-containing extracts (i.e., phospholipids and intracellular phosphorus) were placed in vials containing 10 ml of scintillation fluid (5 g of 2,5-diphenyloxazole; 0.05 g 1,4 bis-[2-(4 methyl-5-phenyloxazole)]-benzene, 500 ml of toluene, and 500 ml of Triton X-100) and counted in a Nuclear Chicago 6848 liquid scintillation spectrometer. 32P-phosphorus activity (T1/2 = 25.3 days) in the counted samples was corrected for counting efficiency and decay, with decay factors derived by Robinson (40). The 32P-phosphorus was obtained from New England Nuclear Corp., Boston, Mass., as H32PO4 in 0.02 N HCl.

All glassware used in the experiments was washed with detergent, rinsed in deionized water-12 N HCl (2:1), followed by a final rinse in deionized water.

Calculations. To calculate the rate of microbial phospholipid phosphorus synthesis in whole rumen contents (experiment 3), the IC-P, specific activity (SA) was used as an indicator of precursor pool SA. Since the SA of IC-P, may differ between protozoa and bacteria, these were assessed separately. In this incubation system (experiment 3), the SA of the IC-P, was measured at the start (SA = 0) and the end of the incubation time. The rate of 32P uptake into cellular phospholipids is dependent on the rate of phospholipid synthesis as well as the rate of change of the SA of the precursor pool (IC-P1) during the incubation. To properly describe the SA of the IC-P, more frequent sampling would have been necessary. Thus, an approximation was made to determine the effective SA of the IC-P, pool during the incubation period. The following formulae describe the calculations:

(i) Intracellular phosphorus SA = (final IC-Pi-SA + initial IC-Pi-SA)/2.

(ii) Total 32P uptake into high-speed pellet (bacterial) phospholipids = total 32P uptake into rumen contents phospholipids - total 32P uptake into 150 × g pellet (protozoal) phospholipids.

(iii) Total phosphorus (micrograms) incorporation into microbial phospholipids = phosphorus incorporation into high-speed pellet (bacterial) phospholipids (net counts/min of 32P in the PL-Pi/SA of the IC-P1) + phosphorus incorporation into 150 × g pellet (protozoal) phospholipids (net counts/min of 32P in the PL-Pi/SA of the IC-P1).

(iv) Total microbial protein (N × 6.25) synthesis in the system = [µg of P] incorporation into high-speed pellet (bacterial) PL-Pi × high-speed pellet (bacterial) N/PL-Pi] + [µg of P] incorporation into 150 × g pellet (protozoal) PL-Pi × 150 × g pellet (protozoal) N/PL-Pi].

RESULTS

Physical separation of microbial fractions. Sampling of rumen contents and the subsequent fractionation of the rumen contents into microbial fractions is one of the most difficult aspects of microbial investigations in the rumen. Throughout this work rumen samples were withdrawn from the central and dorsal sac of the rumen. Moreover, at least 1 liter (from a 4-liter rumen volume of sheep) of contents was removed to insure that a representative sample had been secured. For experiment 1, mixed ruminal bacteria were prepared similar to the procedure outlined by Baldwin and Palmquist (2). It must be recognized that many large bacteria and clumps of bacteria may be lost during the initial low-speed centrifugation step. As Hungate (19) pointed out, suspensions of washed mixed ruminal bacteria contain all kinds of rumen bacteria, but they are not necessarily in the same proportions as found in the total contents. In experiment 3, the 150 × g pellet was designated the protozoal fraction. Although, the protozoa could be nearly quantitatively removed from the rumen fluid, this fraction may also contain sizeable amounts of bacteria (49). These bacteria are large bacteria as well as those harbored within the protozoa. The metabolic activity of these organisms will contribute to the total activity of the 150 × g (protozoal) fraction. In the remainder of the paper, the 150 × g pellet will be called the protozoal fraction, whereas the high-speed pellet will be called a bacterial fraction.

Experiment 1. The metabolism of 32P. H32PO4 in mixed ruminal bacteria incubated in high or low phosphate medium was studied. Figure 1 depicts the results for the high phosphate medium studies. The SA of inorganic phosphorus medium stayed constant throughout the incubation period. In the presence of substrate there was a linear rise in 32P incorporation into phospholipids and in 32P uptake into IC-Pi and total cellular phosphorus. The increase in dry cell mass and cellular protein (N × 6.25) were significantly correlated (r = 0.99; P < 0.01), and the rate of 32P incorporation into cellular phospholipids and the increase in dry cell mass or cellular protein were significantly correlated (r = 0.91, P < 0.01; r = 0.94, P < 0.01). This high correlation indicates that cellular phospholipid synthesis can be
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FIG. 1. Uptake of 33P-phosphorus into cellular phosphorus constituents and changes in cell mass of mixed ruminal bacteria during an in vitro incubation in high phosphorus buffer. (Mean of three separate experiments; bars represent ± standard error.)

used as a marker of total cellular growth. During the 240-min incubation period, the SA of the IC-P, did not equilibrate with the SA of the inorganic phosphorus medium, indicating that, if phospholipid synthesis is to be measured, the SA of the inorganic phosphorus medium will overestimate the SA of the phosphorus precursor pool.

Incubation of mixed ruminal bacteria in the low phosphate medium (Fig. 2) in the absence of substrate (0–90 min) resulted in some uptake of 33P into the IC-P, pool. 33P-phosphorus was not incorporated into the phospholipids during this period.

The addition of substrate caused a more rapid uptake of 33P into the IC-P, pool, the incorporation of 33P into PL-P1, and an increase (growth) of the bacterial cell mass. The SA of inorganic phosphorus medium showed little change. Again, the SA of the IC-P, pool did not reach the SA of the phosphorus medium after 240 min of incubation after substrate addition. The rate of 33P incorporation into cellular phospholipids and the increase in cell mass were significantly correlated (r = 0.98; P < 0.01), indicating that cellular phospholipid synthesis can be used as a marker of total cellular growth. Mitchell and Moyle (31) showed similar patterns of 32P uptake into phosphorus containing constituents of S. aureus. In this organism, some 32P uptake occurred into the IC-P, pool, but 32P incorporation into phospholipid did not occur in the

FIG. 2. Uptake of 33P-phosphorus into cellular phosphorus constituents and changes in cell mass of mixed ruminal bacteria during an in vitro incubation in low phosphorus buffer. (Mean of three separate experiments; bars represent ± standard error.)
absence of a carbon source. After the addition of substrate there was \(^{32}\)P uptake into both PL-P, and IC-P. As was the case for mixed ruminal bacteria, in *S. aureus* the SA of IC-P, did not equilibrate with the SA of the inorganic phosphorus in the incubation medium (31).

**Experiment 2.** Since experiment 1 showed that phospholipid synthesis was highly correlated with increases in cellular mass or protein content in mixed ruminal bacteria, experiment 2 was conducted to investigate whether rates of phospholipid synthesis in whole rumen contents (determined in vitro) could be related to dietary protein intakes of sheep. Under these experimental circumstances a significant amount of \(^{32}\)P incorporation into protozoal as well as bacterial phospholipid would be expected. Although protozoal phosphorus metabolism was not studied in detail as for mixed ruminal bacteria, it was assumed that for these organisms phospholipid synthesis would also reflect cellular growth. When a diet containing low levels of protein (N-limiting) is fed to sheep, an increase and then a decline in microbial growth (activity in the rumen) would be expected, whereas for a diet with adequate (or excess) protein a more sustained rate of microbial growth would be expected. Previous work had shown that, when urea is added to a low protein ration, microbial protein synthesis (16) and animal performance (23) are increased. As the results show (Fig. 3), before feeding and at 2 h after feeding the rate of \(^{32}\)P incorporation into microbial phospholipids (determined in vitro) did not differ between the two rations; however, for the high protein ration at 4 h after feeding the rate of \(^{32}\)P incorporation into phospholipids was still high, whereas for the low protein diet the rate of \(^{32}\)P incorporation into phospholipids declined to the prefeeding level.

**Experiment 3.** Experiment 1 showed that phospholipid synthesis and increases in cellular protein were highly correlated and experiment 2 showed that, as expected, the addition of a \(\text{NH}_4\) source to a low protein diet resulted in more sustained (increased) microbial activity (growth). Thus, these studies indicated that phospholipid synthesis can be used as a marker of microbial growth in whole rumen contents. In this experiment microbial protein synthesis, at various times after feeding, in the rumen of a sheep fed a standard ration was studied. The results were expressed as grams of protein \((N \times 6.25)\) synthesized per hour per hypothetical 4-liter rumen. Sheep used in this work showed a rumen volume of 3.5 to 4.0 liters from polyethylene glycol disappearance curves (21).
protozoal rate was substantially lower than the rate noted before feeding. There are no apparent reasons for a higher microbial protein synthesis rate at 15 h (0 h in Table 3, Fig. 4) than at 9 h after feeding. Since the 9-h rate was from a single experiment, the rate of protein synthesis may have been underestimated. These results expressed in terms of a 4-liter rumen are depicted in Fig. 4. The relative VFA production rate is plotted on the same graph and is parallel to the changes found for microbial protein synthesis. It is evident that immediately after feeding there was an increase in microbial activity (VFA production) and cellular growth (phospholipid and protein synthesis). Despite differences in rations, these results are in disagreement with the contention of Walker and Nader (46) that microbial protein synthesis in the rumen declines initially after feeding and then increases again to prefeeding rates.

**DISCUSSION**

Rumen microbial protein represents a major source of amino acids to the ruminant animal. Quantitative aspects of ruminal microbial protein synthesis have thus been the subject of extensive research efforts. In the past, procedures based on fermentation balances (19), ingesta passage studies with or without microbial cell markers (14), zero time in vitro incubations of rumen contents with 35S or 15N (1, 45), single dose or continuous infusion of 15N-urea into the rumen (32, 35), and rumen fermentation-turnover models with C, N, and H balance studies (21) have been used to assess microbial protein synthesis.

Hungate (19), from known pathways of ruminal VFA production and supposed ATP yields and using Y ATP = 10 (3), calculated that about 10 g of microbial protein can be synthesized for each 100 g of carbohydrate fermented. This value represented an upper limit of the synthetic capacity in the anaerobic ruminal fermentation. This level of protein synthesis in the rumen is equivalent to 18.3 g of digestible protein per Mcal of digestible energy (36). As Purser (36) pointed out, this protein-calorie ratio is below the required protein-calorie ratio to meet the protein requirements of growing ruminants and less than such ratios established from empirical balance studies with growing ruminants.

Growth yield studies with pure cultures of rumen bacteria (11, 12, 18) and ingesta passage studies with sheep, by using nonprotein nitrogen diets or markers for microbial cells (15, 17, 27), indicated that the microbial protein yield in the rumen was higher than predicted by Hungate (19). Overall, the above studies indicate that 15 to 22 g of microbial protein is formed per 100 g of organic matter fermented. There are a number of alternatives to explain these results. First, the Y ATP value may not
be universal among bacteria (however, this has been rejected by Payne [40]), or substrate phosphorylation (43) may result in an extra energy yield to the microorganisms. Although the latter process has been implicated in ruminal organisms (44), a more tenable alternative appears to be the recent suggestion that the Y ATP value of 10 is universal but that previously assumed ATP yields per mole of VFA are too low (13, 21).

To further evaluate the potential of microbial protein synthesis in the rumen, we decided to use the short-term, zero time method. Walker and Nader (45) had used this approach with 35S, but their actual results on protein synthesis rates were quite low. They were able to correct their data by determining a VFA-to-protein synthesis ratio from the in vitro incubation and then multiplying this ratio by an assumed VFA yield. The major problem in the approach of the above authors is that they assumed that the SA of the intracellular precursor pool (in this case 35S-cysteine or 35S-methionine) for protein synthesis equalled the SA of medium 35S-sulfide. Al-Rabbat et al. (1) made similar assumptions in their 35N incorporation studies with ruminal microorganisms. In the present work, it was decided to use phospholipid synthesis as a marker for cellular growth since membrane synthesis is closely related to total cell growth (33, 38, 50), and since IC-P1 equilibrates readily with phospholipid precursors (5, 48) and can be used to determine the SA of the intracellular precursor pool for phospholipid synthesis.

The results of experiment 1 showed clearly that, with ruminal bacteria, the SA of inorganic phosphorus medium did not equilibrate with the IC-P1 pool. A very high correlation between cell growth and phospholipid synthesis was noted for mixed ruminal bacteria similar to the observations of Ohki (33) for E. coli.

Preliminary work had shown that the N/PL-P1 ratios of the ruminal 150 × g fractions were not similar to the N/PL-P1 of ruminal bacteria. Since the 150 × g fraction is largely composed of protozoa, it was decided that the SA of the IC-P1 must be established for the 150 × g fraction and bacterial fraction separately. For all the calculations below, the rate of protein synthesis by both fractions have been combined to negate the implication (Table 3) that (apparent) protozoal protein synthesis was equal in magnitude to the bacterial protein synthesis.

The results from Table 3 and Fig. 4 were recalculated to estimate daily protein synthesis. The data (Table 4) are expressed as grams of protein produced in a 4-liter rumen per day.

To estimate daily protein synthesis, the various measured rates were arbitrarily designated to represent an average rate of various time intervals (summation interval). The estimated daily rate of microbial crude protein (N × 6.25) and true protein (N × 6.25 × 0.85) (42) synthesis in the rumen of a sheep with a 4-liter rumen consuming 158 kcal of digestible energy per 0.75 kg body weight per day was 218 and 185 g, respectively. These values represent a rate of microbial crude and true protein synthesis of 26 and 22 g per 100 g of organic matter digested (fermented; DOM) in the rumen, respectively. These values are higher than the theoretical upper limit proposed by Hungate (19) but similar to the upper values of ruminal microbial protein synthesis per 100 g of DOM in the range of values reported from direct measurements (15-17, 27).

The system used in the present work to assess microbial protein synthesis measured absolute but not net rates of microbial protein synthesis which are obtained from ingesta passage studies. The values given above can be recalculated by taking microbial protein turnover into account. Although the extent of turnover of microbial protein and bacterial-protozoal protein interconversions has not been accurately defined, it may be estimated from stud-

![Fig. 4. Microbial protein (N × 6.25) synthesis and relative rate of volatile fatty acid production in rumen contents at various times after feeding. (Protein synthesis results, mean of two separate experiments; VFA production represents a single experiment; bars represent ± standard error.)](http://aem.asm.org/Downloaded from)
ies of bacterial lysis in the rumen (22), from protozoa-bacteria interrelationships in the rumen (8, 47), from the recent report on N turnover in ruminants (92), and from microbial turnover data (29) that 25 or more of the total protein synthesized in the rumen may be involved in turnover. On a 25 turnover basis the estimated ruminal protein synthesis rate was 16.1 g of true protein synthesis/100 g of DOM. This value represents a 30-g digestible protein-to-Mcal of digestible energy ratio which is adequate for growing calves and lambs (36).

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Table 4. Estimated rate of ruminal microbial protein synthesis

| Inoculation time after feeding (h) | Summation interval (h) | Summation time (h) | Protein synthesis rate (g per h per 4-liter rumen) | Total microbial protein synthesis during summation interval (g) |
|-----------------------------------|-----------------------|--------------------|--------------------------------------------------|-----------------------------------------------------------|
| 0                                 | (T−T)                 | 1                  | 10.66 ± 0.70                                     | 9.06                                                      |
| 2                                 | (T−T)                 | 2                  | 13.17 ± 1.64                                     | 11.19                                                     |
| 4                                 | (T−T)                 | 4                  | 11.14 ± 1.70                                     | 9.47                                                      |
| 9                                 | (T−T)                 | 5                  | 5.45                                             | 4.63                                                      |
| Total                             | (T−T)                 | 12                 |                                                  | 109.00                                                    |

*True protein = N × 6.25 × 0.85 (42). Estimated rates of microbial crude protein and true protein synthesis per day equals 218.0 and 184.9 g, respectively. Estimated microbial crude protein and true protein synthesis per 100 g of organic matter digested in the rumen (75% digestion (11)) equal 26.0 and 22.0 g, respectively.*
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