Use of odd-chain fatty acids to estimate the microbial protein synthesis

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Introduction:

The microbial protein synthesis can supply most of amino acid requirements of ruminants, but its determination involves the use of cannulated animals. Most of the methods are laborious and requires the use of animals fistulated in the abomasum or small intestine, which may compromise animal welfare, and the estimation of digesta flow, laborious and inaccurate process (Vagnoni et al., 1997). According to Timmermans, Jr. et al. (2000), because of these limitations, there has been increasing interest in the development of noninvasive techniques to estimate the production of microbial N.

The accurate estimation of microbial protein synthesis is essential to determine the dietary protein requirements.

In nutrient requirements studies using the comparative slaughter technique, representative samples of the whole body are used to calculate the amount of retained nutrients. These samples are available to determine the amount of odd chain fatty acids in the body and, as odd chain fatty acids are synthesized only by ruminal microbes, its content in the body might be correlated to the microbial protein synthesis.

Objectives:

The aim of this study was to evaluate the correlation of body Odd-chain fatty acids with the digestible energy intake and microbial protein synthesis in goats fed different levels of energy.

Materials & Methods:

Sixty goats from different breed groups (20 Moxotó, 20 Canindé and 20 F1 Boer x non-descript goats), averaging 15 kg of initial BW, were alocated to different feeding levels: *ad libitum,* restricted fed (75% of *ad libitum*), and fed at maintenance level, with five animals from each breed group to each level of feeding. The experimental design provided ranges in ME intake, and as consequence on the mass of empty body and of fatty acids.

A baseline group of 15 randomly selected kids, (five from each breed group) was used to assess the initial body composition. The diets consisted of 60% of elephant grass and 40% of concentrate, on dry matter basis. The feeding period lasted 90 days, after a 30 days adaptation period.

After slaughter the carcasses were dissected and grounded and total body meat (muscle and carcass fat) and offal were quantified and sampled. The fatty acid content in meat and offal were determined by gas chromatography.

The total fat was determined by ether extraction. The mass of body odd-chain fatty acids ($C_{15:0}$, *iso* $C_{15:0}$, *anteiso* $C_{15:0}$, $C_{17:0}$, *iso* $C_{17:0}$, *anteiso* $C_{17:0}$, and $C_{17:1}$) and total fatty acids were determined.

The analyses of intake, dietary energy concentration, performance, and body composition were performed with PROC GLM, using a 3 x 3 factorial design with three levels of feeding (maintenance, *Ad libitum* or 0.75 restriction) and three genetic groups (Moxotó, Canindé and F1 Boer x NDG).

The odd-chain fatty acids in the body was regressed on energy intake and on the expected microbial protein synthesis using PROC GLM with the SOLUTION statement and the sum of squares type 3. The comparisons of means were performed using least squares means at P = 0.05 as significance level.

Results and Discussion:

There was an interaction between breed and level of feeding for DMI (kg/d). F1 Boer x NDG goats had a higher intake than Moxotó goats, whereas Canindé goats were intermediate. As expected, animal fed at maintenance level had the lowest intake of all nutrients and the greatest diet DE concentration.

The total fatty acid and MEI were not affected by breed (P>0.14) but there was effect of the level of feeding on those variables.

The higher intake levels provided more fermentable matter to rumen a microbe which in turn increases it mass and flux throughout abomasum and result in higher absorption of Odd-chain fatty acids on animals fed *ad libitum*.

The total and odd and branched-chain fatty acids were correlated (P<0.01) with the energy intake. In Figure 2, the estimated microbial protein synthesis (MP) was correlated with total OCFA: MP (g/day) = 37.54 + 2.113 x OCFA (r^2 = 0.780). Since there was no Odd-chain fatty acids in the diet, they were originated form microbial synthesis of fatty acids and, after digestion and absorption, retained on animal fat.

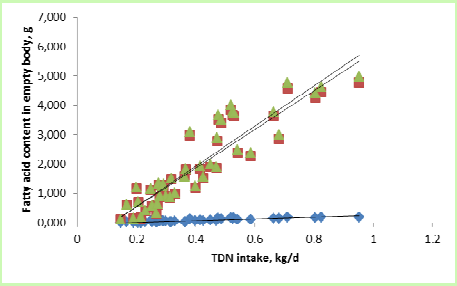

Figure 1. Relationship of fatty acid content in the empty body and the total digestible nutrients intake. Triangles are total fatty acids, squares are even-chain fatty acids and diamonds are odd-chain fatty acid content in the body

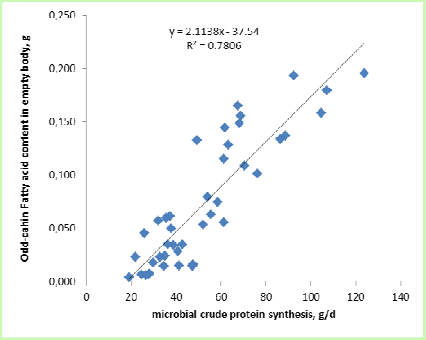

Figure 2. Regression of odd chain fatty acid content in the body on estimated microbial protein synthesis.

Implications:

We conclude that the mass of odd-chain fatty acid in the body can be used to estimate the microbial protein synthesis.

This technique might be useful in comparative slaughter studies, since a representative sample of the body is available.

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