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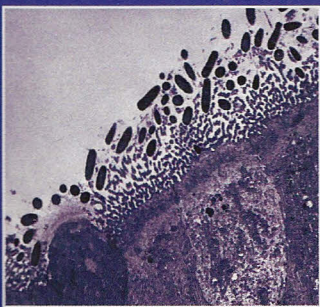
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Rowett-INRA 2010

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**Aberdeen Exhibition and
Conference Centre**



Gut Microbiology:
new insights into
gut microbial ecosystems

7th Joint Symposium organised by the **Rowett Institute of Nutrition and Health**, University of Aberdeen, Scotland (UK) & the **Institut National de la Recherche Agronomique**, Clermont-Ferrand-Theix (France)

Influence of dietary protein supply and carbohydrate type on rumen bacterial biodiversity

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High concentrations of protein tend to be used in dairy cows diets to maximize milk production. Some diets create a rumen imbalance between rapidly available nitrogen (N) and slowly available energy, which can limit microbial growth and increase excretion losses. The use of diets with a lower N concentration and the provision of more appropriate carbohydrate energy sources can increase rumen N use efficiency and help to solve potential pollution problems. However, it is unknown how these modifications in the diet affect the rumen microbial ecosystem.

Five Holstein rumen-cannulated cows in peak lactation (mean of 30.3 kg milk/d) were offered four different diets in to a 2² factorial design experiment. All diets were iso-energetic and based on grass silage and concentrate (70:30, DM basis) but differed in supplies of digestible N (110% vs. 80% of the requirements) and in the nature of the carbohydrates (NDF:Starch ratio of 2.85 vs. 1.31). After diet adaptation (4 weeks) nine samples of rumen contents were taken on alternate days at 0, 2.5 and 5h after feeding and pooled by time. Bacterial biodiversity was studied by TRFLP using 16S rRNA primers; 27F and 1389R. Amplicons were digested with either HaeIII, HhaI or MspI, and fragments length were determined. Low protein diets numerically decreased the amount of TRF's detected and, although an important animal effect was observed, results from UPGMA and PCA analysis suggest that the nature of the diets, and in particular the type of carbohydrate, can modify the rumen bacterial biodiversity.

Analysis of active bacteria in rainbow (*Oncorhynchus mykiss*) trout gut revealed by molecular analysis

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A limited supply of fish meal could hamper future growth in the aquaculture industry and therefore much effort has been made to study alternatives replacing fish meal. Influence of diet on the composition of salmonid gut microbiota is an important aspect considering its potential role on nutrition, the stimulation of the immune system and the competition with pathogens. AIMS: To evaluate the possible effect of diet on the intestinal microbiota composition of rainbow trout. The fish were fed one month with a diet 1 containing 50% replacement of fishmeal by vegetable proteins (corn, sunflower and soybean meal), diet 2 containing 50% replacement of fish oil by vegetable oils and a control diet with 100% of fish meal and 100% fish oil. We extracted DNA directly from intestinal contents and then the 16S rRNA gene was PCR amplified and analyzed by TTGE. Active bacterial populations were determined after RNA extraction, reverse transcription, PCR and TTGE analysis of the 16S rRNA amplicons. Results showed that the DNA profiles from all samples showed an intense band due to wheat component present in the three diets. Comparison of microbiota profiles from DNA and RNA showed important differences indicating that active bacterial populations were more diverse and better described by RNA analysis. The inclusion of vegetable protein or vegetable oil did not significantly alter the intestinal microbiota composition after one month. We observed a common band present in all fishes that was identified as *Ralstonia* sp.